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*1503     1:50-58 9     AQRDSEESY     1.389559     1.325826     -0.619367     2.715385     2.096018     4.162618
HLA B*1503     1:86-94 9     RQSQRAEIY     1.602945     1.384149     -0.991398     2.987094     1.995696     9.803882
HLA B*1517     1:25-33 9     RTALFNWAY     1.425350     1.394077     -0.885540     2.819427     1.933887     7.683157
HLA B*1517     1:33-41 9     YARHTGGTF     1.316740     1.201894     -0.597164     2.518634     1.921470     3.955159
HLA A*8001     1:25-33 9     RTALFNWAY     1.425350     1.394077     -0.949817     2.819427     1.869610     8.908753
HLA A*3002     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.010997     2.819427     1.808429     10.256460
HLA A*0101     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.172478     2.819427     1.646949     14.875706
HLA A*0202     1:205-213     9     ALMKITHVL     1.662500     0.455646     -0.471988     2.118146     1.646158     2.964750
HLA A*0250     1:60-68 9     ALLDALRWL     1.537707     0.516755     -0.418133     2.054462     1.636329     2.618986
HLA A*0250     1:205-213     9     ALMKITHVL     1.662500     0.455646     -0.497494     2.118146     1.620652     3.144083
HLA A*0219     1:205-213     9     ALMKITHVL     1.662500     0.455646     -0.516328     2.118146     1.601818     3.283428
HLA B*1503     1:440-448     9     LALKPRKAF     1.407943     1.119240     -0.986586     2.527183     1.540597     9.695860
HLA B*1503     1:100-108     9     RLLAAGEAY     1.333942     1.459540     -1.271696     2.793482     1.521785     18.693747
HLA B*1503     1:33-41 9     YARHTGGTF     1.316740     1.201894     -1.032881     2.518634     1.485753     10.786501
HLA A*0101     1:139-147     9     LTDAQRAAY     1.167960     1.175930     -0.877288     2.343890     1.466602     7.538558
HLA A*0211     1:60-68 9     ALLDALRWL     1.537707     0.516755     -0.629272     2.054462     1.425190     4.258650
HLA A*0212     1:205-213     9     ALMKITHVL     1.662500     0.455646     -0.700649     2.118146     1.417496     5.019371
HLA A*3201     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.430437     2.819427     1.388990     26.942442
HLA A*2902     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.433327     2.819427     1.386100     27.122319
HLA A*2902     1:275-283     9     FIPEGLLNY     1.273574     1.265061     -1.154156     2.538635     1.384479     14.261208
HLA B*1517     1:457-465     9     GTTVSPPLF     1.234422     1.000737     -0.852309     2.235159     1.382850     7.117190
HLA A*2403     1:35-43 9     RHTGGTFVF     1.667665     1.260092     -1.596024     2.927757     1.331733     39.447906
HLA B*5801     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.496768     2.819427     1.322659     31.388287
HLA B*1502     1:100-108     9     RLLAAGEAY     1.333942     1.459540     -1.499004     2.793482     1.294477     31.550360
HLA B*1501     1:86-94 9     RQSQRAEIY     1.602945     1.384149     -1.707888     2.987094     1.279207     51.037294
HLA A*0211     1:283-291     9     YLALLGWSI     1.492210     0.300064     -0.522666     1.792274     1.269608     3.331704
HLA A*2403     1:57-65 9     SYLALLDAL     1.498520     0.489384     -0.723049     1.987904     1.264855     5.285053
HLA A*0250     1:283-291     9     YLALLGWSI     1.492210     0.300064     -0.529649     1.792274     1.262625     3.385705
HLA A*0250     1:375-383     9     VLGDAWELL     1.509402     0.401696     -0.658495     1.911098     1.252603     4.555068
HLA A*2602     1:77-85 9     EVGGPYGPY     0.951232     1.107356     -0.818730     2.058588     1.239859     6.587638
HLA A*1101     1:25-33 9     RTALFNWAY     1.425350     1.394077     -1.588515     2.819427     1.230912     38.771714
HLA B*1517     1:177-185     9     FAAGSVPDF     1.283549     1.092903     -1.177886     2.376452     1.198566     15.062120
HLA B*1517     1:139-147     9     LTDAQRAAY     1.167960     1.175930     -1.147620     2.343890     1.196270     14.048179
HLA A*0202     1:283-291     9     YLALLGWSI     1.492210     0.300064     -0.606435     1.792274     1.185839     4.040499
HLA A*0211     1:205-213     9     ALMKITHVL     1.662500     0.455646     -0.937233     2.118146     1.180913     8.654322
HLA A*0250     1:409-417     9     VLDAALAAL     1.329115     0.442767     -0.606078     1.771882     1.165804     4.037178
HLA A*0250     1:250-258     9     VLGEGTKKL     1.458243     0.385551     -0.687351     1.843794     1.156443     4.868007
HLA A*2603     1:77-85 9     EVGGPYGPY     0.951232     1.107356     -0.927671     2.058588     1.130918     8.465852
HLA A*0212     1:283-291     9     YLALLGWSI     1.492210     0.300064     -0.692670     1.792274     1.099604     4.927997
HLA B*1501     1:100-108     9     RLLAAGEAY     1.333942     1.459540     -1.696281     2.793482     1.097201     49.691394
HLA B*1501     1:50-58 9     AQRDSEESY     1.389559     1.325826     -1.631186     2.715385     1.084198     42.774639
HLA A*0211     1:409-417     9     VLDAALAAL     1.329115     0.442767     -0.692807     1.771882     1.079076     4.929544
HLA A*8001     1:275-283     9     FIPEGLLNY     1.273574     1.265061     -1.466854     2.538635     1.071781     29.299079
HLA A*0219     1:60-68 9     ALLDALRWL     1.537707     0.516755     -0.983043     2.054462     1.071419     9.617082
HLA A*0203     1:205-213     9     ALMKITHVL     1.662500     0.455646     -1.047302     2.118146     1.070844     11.150690
HLA B*1517     1:360-368     9     AAFAAAAEL     1.357907     0.478008     -0.766966     1.835915     1.068949     5.847441
HLA A*8001     1:100-108     9     RLLAAGEAY     1.333942     1.459540     -1.726138     2.793482     1.067343     53.227790
HLA B*1517     1:187-195     9     LTRASGDPL     1.250089     0.497067     -0.697567     1.747156     1.049589     4.983871
HLA A*0211     1:279-287     9     GLLNYLALL     1.290918     0.282433     -0.523968     1.573351     1.049383     3.341705
HLA A*0250     1:279-287     9     GLLNYLALL     1.290918     0.282433     -0.524311     1.573351     1.049040     3.344345
HLA A*3101     1:206-214     9     LMKITHVLR     1.064507     0.764456     -0.782642     1.828963     1.046321     6.062359
HLA A*0216     1:283-291     9     YLALLGWSI     1.492210     0.300064     -0.755035     1.792274     1.037239     5.688990
HLA A*0212     1:409-417     9     VLDAALAAL     1.329115     0.442767     -0.748184     1.771882     1.023698     5.599949
HLA A*0212     1:279-287     9     GLLNYLALL     1.290918     0.282433     -0.573105     1.573351     1.000246     3.742012
HLA A*0219     1:409-417     9     VLDAALAAL     1.329115     0.442767     -0.779855     1.771882     0.992027     6.023587
HLA B*1503     1:383-391     9     LKFFNDDQY     1.359636     1.362684     -1.756762     2.722320     0.965558     57.116505
HLA A*3002     1:188-196     9     TRASGDPLY     1.277550     1.378138     -1.693034     2.655688     0.962654     49.321263
HLA A*0250     1:374-382     9     VVLGDAWEL     1.258066     0.515443     -0.812006     1.773509     0.961503     6.486427
```

HLA B*1501	1:33-41	9	YARHTGGTF	1.316740	1.201894	-1.560373	2.518634	0.958261	36.338992
HLA A*0216	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.100428	2.054462	0.954034	12.601675
HLA A*0211	1:375-383	9	VLGDAWELL	1.509402	0.401696	-0.958721	1.911098	0.952376	9.093299
HLA A*0201	1:205-213	9	ALMKITHVL	1.662500	0.455646	-1.178083	2.118146	0.940062	15.068967
HLA A*2602	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-1.601216	2.538635	0.937419	39.922370
HLA A*0250	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.372694	1.307776	0.935082	2.358816
HLA B*1503	1:224-232	9	RQLALHQAL	1.264243	0.500053	-0.835308	1.764296	0.928989	6.843964
HLA B*1517	1:440-448	9	LALKPRKAF	1.407943	1.119240	-1.608829	2.527183	0.918355	40.628300
HLA A*3101	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.067465	1.962632	0.895167	11.680596
HLA A*0250	1:227-235	9	ALHQALIRI	1.220562	0.336437	-0.667874	1.556999	0.889125	4.654510
HLA A*0219	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.418810	1.307776	0.888966	2.623070
HLA A*3101	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-0.824322	1.708081	0.883759	6.673006
HLA A*0211	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.433912	1.307776	0.873863	2.715891
HLA B*0702	1:33-41	9	YARHTGGTF	1.316740	1.201894	-1.648977	2.518634	0.869657	44.563229
HLA A*6801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-0.801959	1.650564	0.848605	6.338100
HLA A*0203	1:283-291	9	YLALLGWSI	1.492210	0.300064	-0.943774	1.792274	0.848500	8.785653
HLA B*1503	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-2.080422	2.927757	0.847335	120.343318
HLA B*3501	1:354-362	9	HIALDEAAF	1.481866	1.112955	-1.759097	2.594821	0.835724	57.424472
HLA A*0212	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.225689	2.054462	0.828773	16.814685
HLA B*1517	1:59-67	9	LALLDALRW	1.480034	0.393544	-1.046827	1.873578	0.826751	11.138511
HLA A*0219	1:375-383	9	VLGDAWELL	1.509402	0.401696	-1.085114	1.911098	0.825983	12.165063
HLA A*0219	1:283-291	9	YLALLGWSI	1.492210	0.300064	-0.970873	1.792274	0.821401	9.351322
HLA A*0202	1:375-383	9	VLGDAWELL	1.509402	0.401696	-1.090358	1.911098	0.820739	12.312845
HLA A*2902	1:188-196	9	TRASGDPLY	1.277550	1.378138	-1.844515	2.655688	0.811173	69.906070
HLA A*0212	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.496864	1.307776	0.810911	3.139528
HLA A*0216	1:375-383	9	VLGDAWELL	1.509402	0.401696	-1.101429	1.911098	0.809669	12.630751
HLA A*0250	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-0.716114	1.517234	0.801121	5.201321
HLA A*0216	1:205-213	9	ALMKITHVL	1.662500	0.455646	-1.317192	2.118146	0.800954	20.758300
HLA A*0206	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-0.973119	1.773509	0.800390	9.399810
HLA A*0211	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-1.257195	2.055046	0.797851	18.079871
HLA A*2601	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-1.263299	2.058588	0.795289	18.335776
HLA B*5801	1:59-67	9	LALLDALRW	1.480034	0.393544	-1.081834	1.873578	0.791744	12.073536
HLA B*1503	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-1.584779	2.376452	0.791673	38.439641
HLA B*5701	1:25-33	9	RTALFNWAY	1.425350	1.394077	-2.032995	2.819427	0.786432	107.893498
HLA B*1517	1:3-11	9	ATETVRVRF	1.431229	1.094515	-1.742867	2.525744	0.782878	55.318038
HLA A*3201	1:205-213	9	ALMKITHVL	1.662500	0.455646	-1.336989	2.118146	0.781157	21.726438
HLA A*0250	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-1.275108	2.055046	0.779938	18.841167
HLA A*0201	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.274995	2.054462	0.779467	18.836275
HLA A*0206	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.276607	2.054462	0.777855	18.906310
HLA A*0202	1:409-417	9	VLDAALAAL	1.329115	0.442767	-0.999701	1.771882	0.772181	9.993122
HLA B*1517	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-2.035349	2.793482	0.758132	108.479946
HLA B*3501	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-1.618852	2.376452	0.757601	41.576847
HLA B*1502	1:33-41	9	YARHTGGTF	1.316740	1.201894	-1.764299	2.518634	0.754335	58.116409
HLA B*1517	1:415-423	9	AALTSVTDW	1.150326	0.497710	-0.893970	1.648036	0.754067	7.833749
HLA A*0203	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.303100	2.054462	0.751363	20.095535
HLA A*0201	1:283-291	9	YLALLGWSI	1.492210	0.300064	-1.046498	1.792274	0.745776	11.130078
HLA B*3501	1:33-41	9	YARHTGGTF	1.316740	1.201894	-1.774500	2.518634	0.744133	59.497708
HLA A*3101	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-0.909739	1.650564	0.740825	8.123429
HLA A*0211	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-1.105221	1.843794	0.738573	12.741520
HLA A*6801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-0.910759	1.609246	0.698487	8.142524
HLA A*2501	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-1.843444	2.538635	0.695192	69.733831
HLA A*3001	1:479-487	9	RLRAARQLV	1.087444	0.249933	-0.649891	1.337377	0.687486	4.465715
HLA A*0216	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.627609	1.307776	0.680167	4.242370
HLA A*0202	1:279-287	9	GLLNYLALL	1.290918	0.282433	-0.907249	1.573351	0.666102	8.076979
HLA A*0211	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-1.108365	1.773509	0.665144	12.834083
HLA A*0219	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-1.129712	1.773509	0.643797	13.480695
HLA A*6801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-1.117128	1.749555	0.632427	13.095691
HLA A*6901	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-0.886376	1.517234	0.630858	7.697968
HLA A*0219	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-1.216916	1.843794	0.626878	16.478427
HLA B*1503	1:25-33	9	RTALFNWAY	1.425350	1.394077	-2.195354	2.819427	0.624073	156.802899
HLA B*1517	1:23-31	9	LVRTALFNW	1.553174	0.453372	-1.385933	2.006546	0.620613	24.318289
HLA A*0216	1:279-287	9	GLLNYLALL	1.290918	0.282433	-0.955136	1.573351	0.618215	9.018538
HLA A*0202	1:60-68	9	ALLDALRWL	1.537707	0.516755	-1.439158	2.054462	0.615304	27.488956
HLA A*6801	1:58-66	9	YLALLDALR	0.982293	0.674716	-1.060995	1.657009	0.596014	11.507859
HLA A*0216	1:409-417	9	VLDAALAAL	1.329115	0.442767	-1.176777	1.771882	0.595105	15.023709

HLA A*6802	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-0.928136	1.517234	0.589099	8.474925
HLA A*0211	1:227-235	9	ALHQALIRI	1.220562	0.336437	-0.969797	1.556999	0.587202	9.328180
HLA A*2601	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-1.953320	2.538635	0.585316	89.808934
HLA B*1517	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-1.561064	2.144780	0.583716	36.396835
HLA B*1503	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-1.438505	2.012396	0.573890	27.447645
HLA B*1503	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-1.937710	2.500040	0.562331	86.638228
HLA B*4001	1:428-436	9	IEAALKDAL	1.293005	0.395561	-1.126686	1.688566	0.561880	13.387089
HLA A*0211	1:463-471	9	PLFESLELL	1.291656	0.202256	-0.945494	1.493912	0.548418	8.820513
HLA A*2902	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-2.246023	2.793482	0.547459	176.206969
HLA A*6802	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-1.316177	1.854767	0.538590	20.709843
HLA A*0250	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.260755	0.790220	0.529464	1.822868
HLA A*0201	1:279-287	9	GLLNYLALL	1.290918	0.282433	-1.044520	1.573351	0.528831	11.079494
HLA A*0202	1:225-233	9	QLALHQALI	1.319205	0.310263	-1.117796	1.629468	0.511672	13.115827
HLA B*3901	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-2.416708	2.927757	0.511048	261.040845
HLA A*0206	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.009578	1.517234	0.507656	10.223001
HLA A*0219	1:279-287	9	GLLNYLALL	1.290918	0.282433	-1.073621	1.573351	0.499731	11.847335
HLA A*2602	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-1.303504	1.792234	0.488730	20.114242
HLA A*0206	1:412-420	9	AALAALTSV	1.136579	0.168474	-0.818819	1.305053	0.486234	6.588993
HLA A*0211	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.315569	0.790220	0.474651	2.068087
HLA A*1101	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.492012	1.962632	0.470620	31.046472
HLA B*2705	1:478-486	9	QRLRAARQL	1.551442	0.535207	-1.616065	2.086649	0.470584	41.310939
HLA A*3201	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-2.326047	2.793482	0.467435	211.858815
HLA A*3301	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-1.196381	1.650564	0.454183	15.717420
HLA A*3002	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-2.536542	2.987094	0.450553	343.986660
HLA B*3901	1:205-213	9	ALMKITHVL	1.662500	0.455646	-1.673604	2.118146	0.444542	47.163275
HLA A*0206	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.320039	1.764296	0.444257	20.894855
HLA A*0206	1:279-287	9	GLLNYLALL	1.290918	0.282433	-1.132198	1.573351	0.441153	13.558075
HLA A*2603	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-2.099143	2.538635	0.439493	125.644267
HLA A*0250	1:479-487	9	RLRAARQLV	1.087444	0.249933	-0.899872	1.337377	0.437505	7.940933
HLA A*0206	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-0.872712	1.307776	0.435064	7.459531
HLA A*0201	1:409-417	9	VLDAALAAL	1.329115	0.442767	-1.337313	1.771882	0.434570	21.742665
HLA A*0206	1:283-291	9	YLALLGWSI	1.492210	0.300064	-1.360107	1.792274	0.432167	22.914346
HLA A*0206	1:409-417	9	VLDAALAAL	1.329115	0.442767	-1.343177	1.771882	0.428705	22.038249
HLA A*2602	1:25-33	9	RTALFNWAY	1.425350	1.394077	-2.395793	2.819427	0.423634	248.767334
HLA A*6801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-1.704504	2.126210	0.421706	50.641246
HLA A*6901	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-1.834699	2.255532	0.420833	68.343740
HLA B*5801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-1.965650	2.376452	0.410802	92.395248
HLA B*5801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-1.581081	1.990887	0.409806	38.113711
HLA B*1517	1:236-244	9	GVAERIPKF	1.580848	1.093055	-2.274630	2.673903	0.399273	188.204676
HLA B*3501	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-2.102808	2.500040	0.397233	126.709119
HLA A*3201	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-2.452430	2.845028	0.392598	283.419702
HLA A*0202	1:463-471	9	PLFESLELL	1.291656	0.202256	-1.113595	1.493912	0.380317	12.989571
HLA A*2602	1:354-362	9	HIALDEAAF	1.481866	1.112955	-2.220479	2.594821	0.374341	166.142017
HLA B*3901	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.393174	1.764296	0.371122	24.727153
HLA A*0212	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-1.061032	1.429823	0.368791	11.508855
HLA B*5301	1:59-67	9	LALLDALRW	1.480034	0.393544	-1.513064	1.873578	0.360515	32.588445
HLA A*6802	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-1.897092	2.255532	0.358440	78.902664
HLA A*0250	1:463-471	9	PLFESLELL	1.291656	0.202256	-1.138034	1.493912	0.355877	13.741500
HLA A*0203	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.439255	0.790220	0.350964	2.749508
HLA A*0216	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-1.502533	1.843794	0.341261	31.807772
HLA A*0206	1:205-213	9	ALMKITHVL	1.662500	0.455646	-1.780158	2.118146	0.337988	60.277856
HLA A*3002	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-2.010501	2.343890	0.333389	102.447486
HLA A*0250	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-0.772736	1.104589	0.331853	5.925653
HLA A*0211	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-0.641743	0.954860	0.313117	4.382713
HLA A*0203	1:279-287	9	GLLNYLALL	1.290918	0.282433	-1.262045	1.573351	0.311307	18.282882
HLA A*0216	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-1.464998	1.773509	0.308511	29.174128
HLA A*2602	1:311-319	9	DVNSSPARF	1.154757	1.048756	-1.896735	2.203513	0.306779	78.837808
HLA A*0219	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.484027	0.790220	0.306193	3.048083
HLA A*0203	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.114060	1.419915	0.305855	13.003492
HLA A*3201	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-2.625521	2.927757	0.302235	422.202982
HLA B*3501	1:25-33	9	RTALFNWAY	1.425350	1.394077	-2.522854	2.819427	0.296573	333.313958
HLA B*1517	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-2.210908	2.500040	0.289133	162.520323
HLA A*0211	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-1.787535	2.064809	0.277274	61.310545
HLA B*1502	1:50-58	9	AQRDSEESY	1.389559	1.325826	-2.441378	2.715385	0.274007	276.298203
HLA A*8001	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-2.715441	2.987094	0.271654	519.326861

HLA B*1503	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-2.577653	2.845028	0.267376	378.140234
HLA B*3901	1:94-102	9	YRDVLARLL	1.616307	0.425031	-1.783987	2.041338	0.257350	60.811744
HLA B*4801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.507542	1.764296	0.256754	32.176763
HLA A*0203	1:409-417	9	VLDAALAAL	1.329115	0.442767	-1.516968	1.771882	0.254914	32.882777
HLA A*6801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-1.460285	1.710050	0.249765	28.859235
HLA A*0211	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-1.051634	1.299885	0.248250	11.262484
HLA A*0201	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-1.076088	1.307776	0.231688	11.914824
HLA A*3002	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-2.563866	2.793482	0.229616	366.324622
HLA A*2602	1:378-386	9	DAWELLKFF	1.666410	1.046728	-2.485948	2.713138	0.227191	306.159535
HLA A*0203	1:225-233	9	QLALHQALI	1.319205	0.310263	-1.415485	1.629468	0.213983	26.030639
HLA B*0702	1:187-195	9	LTRASGDPL	1.250089	0.497067	-1.535675	1.747156	0.211481	34.330101
HLA A*6801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-1.456272	1.661630	0.205358	28.593801
HLA A*0212	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-1.642661	1.843794	0.201133	43.919889
HLA B*1517	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-2.373309	2.560573	0.187264	236.215711
HLA B*1502	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-2.351741	2.538635	0.186895	224.771119
HLA B*1501	1:25-33	9	RTALFNWAY	1.425350	1.394077	-2.638631	2.819427	0.180796	435.142420
HLA A*0206	1:375-383	9	VLGDAWELL	1.509402	0.401696	-1.732656	1.911098	0.178442	54.032605
HLA A*0250	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-0.781129	0.954860	0.173731	6.041275
HLA B*5801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-2.066546	2.235159	0.168613	116.559029
HLA A*0216	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.621754	0.790220	0.168466	4.185560
HLA A*0212	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-0.790578	0.954860	0.164282	6.174165
HLA A*3201	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.798357	1.962632	0.164275	62.857472
HLA A*0216	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-1.136460	1.299885	0.163425	13.691783
HLA A*3201	1:3-11	9	ATETVRVRF	1.431229	1.094515	-2.374723	2.525744	0.151021	236.986262
HLA A*0250	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.271579	1.419915	0.148336	18.688691
HLA B*5701	1:59-67	9	LALLDALRW	1.480034	0.393544	-1.725828	1.873578	0.147750	53.189794
HLA A*2402	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-2.780630	2.927757	0.147127	603.433751
HLA A*0206	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-2.399007	2.538635	0.139628	250.615223
HLA A*0206	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.654252	0.790220	0.135968	4.510780
HLA A*0212	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.663307	0.790220	0.126913	4.605816
HLA A*3201	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-2.243829	2.361023	0.117194	175.318870
HLA A*0250	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-1.189864	1.299885	0.110021	15.483309
HLA A*0212	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-1.670390	1.773509	0.103119	46.815521
HLA A*6801	1:2-10	9	TATETVRVR	1.064509	0.662041	-1.624862	1.726550	0.101689	42.156208
HLA B*1501	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-2.399797	2.500040	0.100244	251.071186
HLA B*4001	1:54-62	9	SEESYLALL	1.352077	0.257378	-1.514309	1.609455	0.095146	32.682018
HLA A*0202	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-1.743830	1.835915	0.092085	55.440873
HLA A*0250	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-1.144857	1.234017	0.089160	13.959088
HLA A*0206	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-1.038961	1.117129	0.078168	10.938583
HLA A*6801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.885358	1.962632	0.077274	76.799490
HLA A*2602	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-2.768976	2.845028	0.076052	587.457092
HLA A*0201	1:375-383	9	VLGDAWELL	1.509402	0.401696	-1.836780	1.911098	0.074317	68.672109
HLA A*0206	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-0.882932	0.954860	0.071928	7.637158
HLA A*0216	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-0.886846	0.954860	0.068014	7.706302
HLA A*6801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-1.719085	1.780575	0.061489	52.370327
HLA B*5801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-1.946764	2.006546	0.059781	88.463573
HLA B*0702	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-0.865541	0.923460	0.057919	7.337378
HLA B*4001	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.709011	1.764296	0.055286	51.169443
HLA A*0211	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.910268	1.962632	0.052364	81.333147
HLA B*1503	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-2.611716	2.663942	0.052226	408.992856
HLA A*3301	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-1.913999	1.962632	0.048633	82.034882
HLA A*0206	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.372687	1.419915	0.047228	23.587755
HLA A*3201	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.719701	1.764296	0.044596	52.444609
HLA A*2602	1:290-298	9	SIADDHDLF	1.324197	1.161129	-2.444240	2.485326	0.041086	278.124810
HLA B*5801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-2.886892	2.927757	0.040864	770.711971
HLA A*6802	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-1.097473	1.137355	0.039882	12.516204
HLA A*0203	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.477920	1.517234	0.039314	30.055229
HLA A*0203	1:227-235	9	ALHQALIRI	1.220562	0.336437	-1.521249	1.556999	0.035749	33.208499
HLA A*1101	1:181-189	9	SVPDFALTR	1.418756	0.707454	-2.090609	2.126210	0.035601	123.199614
HLA A*3301	1:206-214	9	LMKITHVLR	1.064507	0.764456	-1.796562	1.828963	0.032401	62.598208
HLA B*1801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-2.681862	2.713138	0.031276	480.686524
HLA A*0201	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.491538	1.517234	0.025697	31.012563
HLA B*1517	1:281-289	9	LNYLALLGW	1.664731	0.421452	-2.066945	2.086183	0.019237	116.666276
HLA B*5801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-1.628945	1.648036	0.019091	42.554446
HLA A*0202	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-1.305816	1.307776	0.001960	20.221603

HLA B*0801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-2.378637	2.378256	-0.000382	239.131844
HLA A*0202	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.792251	0.790220	-0.002032	6.197992
HLA A*0211	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-0.778370	0.775701	-0.002670	6.003027
HLA B*3501	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-2.350735	2.343890	-0.006845	224.251279
HLA A*3001	1:187-195	9	LTRASGDPL	1.250089	0.497067	-1.759153	1.747156	-0.011998	57.431929
HLA A*0250	1:412-420	9	AALAALTSV	1.136579	0.168474	-1.322807	1.305053	-0.017754	21.028440
HLA B*0801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-2.151588	2.118146	-0.033442	141.771156
HLA B*1503	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-2.210748	2.177014	-0.033734	162.460548
HLA A*0211	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.552469	1.517234	-0.035235	35.683645
HLA A*3101	1:232-240	9	LIRIGVAER	0.803790	0.789705	-1.629622	1.593495	-0.036127	42.620800
HLA A*0211	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-1.144890	1.104589	-0.040301	13.960145
HLA B*1517	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-2.043803	2.003005	-0.040798	110.612168
HLA A*2601	1:236-244	9	GVAERIPKF	1.580848	1.093055	-2.716587	2.673903	-0.042684	520.699709
HLA A*0216	1:463-471	9	PLFESLELL	1.291656	0.202256	-1.540398	1.493912	-0.046486	34.705440
HLA A*0203	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-2.104246	2.055046	-0.049200	127.129330
HLA B*3501	1:378-386	9	DAWELLKFF	1.666410	1.046728	-2.762802	2.713138	-0.049663	579.164195
HLA B*4501	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-0.959520	0.905846	-0.053674	9.110040
HLA A*6802	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-2.090468	2.032901	-0.057567	123.159631
HLA B*2705	1:94-102	9	YRDVLARLL	1.616307	0.425031	-2.099791	2.041338	-0.058453	125.832010
HLA A*0203	1:479-487	9	RLRAARQLV	1.087444	0.249933	-1.397455	1.337377	-0.060078	24.972090
HLA A*2902	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-2.785446	2.722320	-0.063126	610.163242
HLA B*3501	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-1.917861	1.852642	-0.065219	82.767743
HLA B*1502	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-2.912398	2.845028	-0.067370	817.331268
HLA A*0202	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.595479	1.517234	-0.078244	39.398427
HLA A*2602	1:236-244	9	GVAERIPKF	1.580848	1.093055	-2.755885	2.673903	-0.081982	570.013079
HLA B*3501	1:440-448	9	LALKPRKAF	1.407943	1.119240	-2.610062	2.527183	-0.082878	407.438144
HLA A*2301	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.016842	2.927757	-0.089086	1039.542190
HLA B*1501	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-2.466536	2.376452	-0.090084	292.776588
HLA A*3301	1:118-126	9	EARHVAAGR	0.989892	0.619354	-1.699693	1.609246	-0.090446	50.083265
HLA A*0201	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-1.864782	1.773509	-0.091273	73.245601
HLA B*3501	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-2.885844	2.793482	-0.092363	768.854631
HLA A*3002	1:50-58	9	AQRDSEESY	1.389559	1.325826	-2.813466	2.715385	-0.098081	650.827656
HLA A*0212	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.618339	1.517234	-0.101105	41.527842
HLA B*4601	1:33-41	9	YARHTGGTF	1.316740	1.201894	-2.639637	2.518634	-0.121003	436.151130
HLA A*2301	1:93-101	9	IYRDVLARL	1.447955	0.489591	-2.058685	1.937546	-0.121139	114.468119
HLA A*6802	1:429-437	9	EAALKDALI	1.091740	0.176549	-1.395148	1.268289	-0.126859	24.839777
HLA A*6802	1:1-9	9	VTATETVRV	1.280980	0.156043	-1.565561	1.437023	-0.128538	36.775665
HLA A*0250	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-2.509245	2.378256	-0.130990	323.031804
HLA A*0212	1:375-383	9	VLGDAWELL	1.509402	0.401696	-2.042877	1.911098	-0.131779	110.376650
HLA B*1501	1:224-232	9	RQLALHQAL	1.264243	0.500053	-1.898671	1.764296	-0.134374	79.190032
HLA A*0219	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-1.089813	0.954860	-0.134953	12.297400
HLA A*6801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-1.863226	1.713576	-0.149650	72.983752
HLA B*1502	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.137122	2.987094	-0.150027	1371.265834
HLA B*5701	1:23-31	9	LVRTALFNW	1.553174	0.453372	-2.163692	2.006546	-0.157147	145.778148
HLA B*1517	1:21-29	9	VGLVRTALF	1.226065	1.008655	-2.392382	2.234720	-0.157662	246.820882
HLA A*3301	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-1.876411	1.708081	-0.168331	75.233540
HLA A*3201	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-2.314196	2.144780	-0.169416	206.155885
HLA A*0206	1:236-244	9	GVAERIPKF	1.580848	1.093055	-2.852228	2.673903	-0.178325	711.586668
HLA A*0206	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.015167	1.835915	-0.179252	103.554120
HLA A*2603	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-1.976072	1.792234	-0.183838	94.639394
HLA A*0301	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-2.152810	1.962632	-0.190178	142.170540
HLA A*0201	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-0.982963	0.790220	-0.192744	9.615313
HLA A*2403	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-2.629285	2.431527	-0.197759	425.877966
HLA B*3501	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.046159	2.845028	-0.201131	1112.138804
HLA A*3301	1:325-333	9	DALNAEHIR	1.176166	0.604409	-1.985442	1.780575	-0.204867	96.703390
HLA A*6801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-2.037008	1.828963	-0.208046	108.895064
HLA A*2403	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-2.708717	2.500040	-0.208676	511.347998
HLA A*2602	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-2.063722	1.854767	-0.208955	115.803541
HLA A*3001	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-0.936331	0.726109	-0.210222	8.636362
HLA A*0212	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-1.316703	1.104589	-0.212114	20.734954
HLA A*0206	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-1.204182	0.990658	-0.213524	16.002268
HLA A*6801	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.034675	2.819427	-0.215248	1083.115351
HLA B*4501	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-1.441108	1.222401	-0.218708	27.612664
HLA A*6801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-2.011949	1.790732	-0.221217	102.789461
HLA B*1517	1:378-386	9	DAWELLKFF	1.666410	1.046728	-2.938938	2.713138	-0.225800	868.836178

HLA A*6901	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-1.017125	0.790220	-0.226905	10.402194
HLA A*6802	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-0.840998	0.612666	-0.228333	6.934229
HLA A*0212	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-2.295123	2.064809	-0.230313	197.297971
HLA A*0202	1:361-369	9	AFAAAAELV	0.982214	0.345272	-1.558287	1.327486	-0.230800	36.164838
HLA A*0219	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-1.350973	1.104589	-0.246384	22.437407
HLA A*0202	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-1.783048	1.536595	-0.246452	60.680292
HLA A*0202	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-2.100487	1.852642	-0.247844	126.033670
HLA A*2301	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.093351	2.845028	-0.248322	1239.797481
HLA B*4002	1:224-232	9	RQLALHQAL	1.264243	0.500053	-2.013546	1.764296	-0.249250	103.168292
HLA B*5801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-2.337517	2.086183	-0.251334	217.528781
HLA A*6901	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-1.596005	1.338560	-0.257446	39.446199
HLA A*0216	1:227-235	9	ALHQALIRI	1.220562	0.336437	-1.815879	1.556999	-0.258881	65.445436
HLA A*3001	1:93-101	9	IYRDVLARL	1.447955	0.489591	-2.203967	1.937546	-0.266421	159.943759
HLA A*3101	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-1.917231	1.648791	-0.268441	82.647829
HLA A*0301	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.066684	2.793482	-0.273202	1165.961190
HLA A*6801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-1.873526	1.600184	-0.273342	74.735394
HLA A*6802	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-1.266457	0.990658	-0.275799	18.469579
HLA A*0211	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-1.705872	1.429823	-0.276049	50.800944
HLA B*1503	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-1.728751	1.448126	-0.280625	53.548963
HLA A*3002	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.018491	2.722320	-0.296172	1043.497610
HLA A*0216	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-1.814925	1.517234	-0.297691	65.301849
HLA A*2602	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-2.676275	2.376452	-0.299823	474.542235
HLA A*0211	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.723671	1.419915	-0.303757	52.926293
HLA A*0216	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.726881	1.419915	-0.306966	53.318862
HLA B*1503	1:188-196	9	TRASGDPLY	1.277550	1.378138	-2.964209	2.655688	-0.308521	920.892545
HLA B*1517	1:50-58	9	AQRDSEESY	1.389559	1.325826	-3.024624	2.715385	-0.309239	1058.336110
HLA A*0250	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-1.380238	1.067176	-0.313061	24.001471
HLA A*0250	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-1.747613	1.429823	-0.317790	55.925868
HLA A*2902	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-2.669513	2.343890	-0.325623	467.210994
HLA A*0201	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-1.291578	0.954860	-0.336718	19.569408
HLA B*1501	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-2.682628	2.343890	-0.338737	481.535022
HLA A*3101	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-2.055095	1.713576	-0.341518	113.525790
HLA A*3101	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.167129	2.819427	-0.347702	1469.363603
HLA A*3301	1:58-66	9	YLALLDALR	0.982293	0.674716	-2.012268	1.657009	-0.355259	102.865116
HLA A*6802	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-1.660973	1.299885	-0.361088	45.811353
HLA B*1502	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-2.923182	2.560573	-0.362609	837.880822
HLA A*0216	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-1.794128	1.429823	-0.364305	62.248349
HLA B*1501	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-2.911562	2.538635	-0.372926	815.758668
HLA A*2403	1:93-101	9	IYRDVLARL	1.447955	0.489591	-2.312311	1.937546	-0.374765	205.263368
HLA B*1503	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.215574	1.835915	-0.379659	164.275862
HLA B*0702	1:452-460	9	RVAATGTTV	1.107071	0.312844	-1.807036	1.419915	-0.387121	64.126259
HLA A*3001	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.208494	2.819427	-0.389067	1616.197054
HLA A*1101	1:314-322	9	SSPARFDQK	0.878945	0.297758	-1.574724	1.176703	-0.398020	37.559822
HLA A*0211	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.193664	2.793482	-0.400183	1561.940052
HLA B*1501	1:354-362	9	HIALDEAAF	1.481866	1.112955	-2.995208	2.594821	-0.400388	989.026805
HLA B*3501	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.125407	2.722320	-0.403087	1334.772109
HLA A*3001	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-1.468752	1.062125	-0.406627	29.427431
HLA B*2705	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.395396	2.987094	-0.408301	2485.397417
HLA A*0219	1:463-471	9	PLFESLELL	1.291656	0.202256	-1.904652	1.493912	-0.410741	80.288308
HLA B*1503	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.007580	2.594821	-0.412760	1017.607854
HLA A*0250	1:1-9	9	VTATETVRV	1.280980	0.156043	-1.850356	1.437023	-0.413333	70.852587
HLA A*2902	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-2.481709	2.058588	-0.423121	303.186123
HLA B*1501	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-2.985021	2.560573	-0.424448	966.096915
HLA A*3101	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-2.139413	1.710050	-0.429363	137.851929
HLA B*1501	1:187-195	9	LTRASGDPL	1.250089	0.497067	-2.179166	1.747156	-0.432010	151.065793
HLA B*0702	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-2.208286	1.776041	-0.432245	161.542073
HLA A*2501	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.032903	2.594821	-0.438083	1078.706261
HLA B*1517	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.425944	2.987094	-0.438849	2666.513868
HLA A*0206	1:229-237	9	HQALIRIGV	1.172366	0.156389	-1.768222	1.328755	-0.439467	58.643842
HLA A*2603	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.285609	2.845028	-0.440581	1930.230205
HLA A*0250	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-1.689294	1.241782	-0.447512	48.898306
HLA B*1503	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.166598	2.713138	-0.453460	1467.568205
HLA B*1517	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-1.793014	1.338560	-0.454455	62.088930
HLA A*1101	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-2.105453	1.650564	-0.454889	127.483328
HLA B*5301	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-2.832450	2.376452	-0.455998	679.907510

HLA B*1501	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-2.821285	2.361023	-0.460262	662.651348
HLA A*3201	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.451201	2.987094	-0.464106	2826.186454
HLA A*2603	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.284289	2.819427	-0.464862	1924.370528
HLA A*2902	1:290-298	9	SIADDHDLF	1.324197	1.161129	-2.956780	2.485326	-0.471454	905.273663
HLA B*1501	1:205-213	9	ALMKITHVL	1.662500	0.455646	-2.589889	2.118146	-0.471743	388.945729
HLA A*2603	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-2.336553	1.861442	-0.475111	217.046825
HLA A*6802	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.313806	1.835915	-0.477891	205.970832
HLA A*0216	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-1.781901	1.300706	-0.481195	60.520306
HLA A*0301	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.306153	2.819427	-0.486726	2023.732025
HLA B*0801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-2.489176	2.001284	-0.487892	308.443756
HLA A*0203	1:412-420	9	AALAALTSV	1.136579	0.168474	-1.793930	1.305053	-0.488878	62.220067
HLA B*5701	1:415-423	9	AALTSVTDW	1.150326	0.497710	-2.138013	1.648036	-0.489976	137.408170
HLA A*3001	1:206-214	9	LMKITHVLR	1.064507	0.764456	-2.322522	1.828963	-0.493560	210.146573
HLA A*6901	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-1.642017	1.137355	-0.504662	43.854834
HLA B*1801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-1.557441	1.048747	-0.508693	36.094474
HLA A*0206	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-1.671132	1.162401	-0.508732	46.895621
HLA B*3801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.438941	2.927757	-0.511185	2747.522121
HLA A*0211	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-1.650410	1.137355	-0.513055	44.710532
HLA B*1801	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.334986	2.819427	-0.515559	2162.648231
HLA A*3201	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-2.507925	1.990887	-0.517038	322.051164
HLA A*0250	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-1.906161	1.384650	-0.521511	80.567646
HLA B*3501	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-2.585303	2.058588	-0.526714	384.860032
HLA B*1502	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-2.970731	2.431527	-0.539205	934.826742
HLA B*4501	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-1.725241	1.181912	-0.543329	53.117905
HLA A*0250	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-1.536704	0.990658	-0.546046	34.411544
HLA A*2501	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-2.605480	2.058588	-0.546892	403.162555
HLA A*0211	1:224-232	9	RQLALHQAL	1.264243	0.500053	-2.312377	1.764296	-0.548081	205.294463
HLA A*2602	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.065329	1.517234	-0.548094	116.232850
HLA B*5801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-2.911745	2.361023	-0.550722	816.102967
HLA B*1502	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-2.618731	2.058588	-0.560143	415.653349
HLA A*6802	1:229-237	9	HQALIRIGV	1.172366	0.156389	-1.890203	1.328755	-0.561448	77.660999
HLA A*2601	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.393309	2.819427	-0.573883	2473.486247
HLA A*0202	1:227-235	9	ALHQALIRI	1.220562	0.336437	-2.132529	1.556999	-0.575530	135.684069
HLA A*0203	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-2.423273	1.843794	-0.579479	265.016509
HLA B*1503	1:205-213	9	ALMKITHVL	1.662500	0.455646	-2.698919	2.118146	-0.580773	499.941521
HLA B*4501	1:366-374	9	AELVQTRIV	1.123749	0.213984	-1.926188	1.337733	-0.588454	84.369930
HLA A*0201	1:463-471	9	PLFESLELL	1.291656	0.202256	-2.090736	1.493912	-0.596825	123.235610
HLA A*0202	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-1.554156	0.954860	-0.599296	35.822520
HLA A*0250	1:225-233	9	QLALHQALI	1.319205	0.310263	-2.229534	1.629468	-0.600067	169.642395
HLA A*0206	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-2.665608	2.064809	-0.600799	463.029018
HLA A*0216	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-1.377461	0.775701	-0.601760	23.848483
HLA B*2705	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-2.244233	1.642298	-0.601935	175.482080
HLA B*1501	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.131201	2.527183	-0.604018	1352.698328
HLA B*2705	1:224-232	9	RQLALHQAL	1.264243	0.500053	-2.368990	1.764296	-0.604694	233.878568
HLA B*4002	1:428-436	9	IEAALKDAL	1.293005	0.395561	-2.295879	1.688566	-0.607313	197.641960
HLA A*6802	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-2.463271	1.852642	-0.610628	290.583239
HLA A*0211	1:412-420	9	AALAALTSV	1.136579	0.168474	-1.916583	1.305053	-0.611530	82.524517
HLA A*6901	1:283-291	9	YLALLGWSI	1.492210	0.300064	-2.416314	1.792274	-0.624040	260.803703
HLA A*2402	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.469588	2.845028	-0.624559	2948.410031
HLA B*1503	1:187-195	9	LTRASGDPL	1.250089	0.497067	-2.373173	1.747156	-0.626017	236.141605
HLA A*6901	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-1.619721	0.990658	-0.629063	41.660153
HLA B*2705	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-2.809246	2.177014	-0.632232	644.534731
HLA B*1501	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-2.706710	2.064809	-0.641901	508.990996
HLA A*2601	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.165285	1.517234	-0.648051	146.313830
HLA B*0702	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-2.495097	1.846931	-0.648166	312.677539
HLA A*3301	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-2.398970	1.749555	-0.649414	250.593531
HLA A*0201	1:227-235	9	ALHQALIRI	1.220562	0.336437	-2.207632	1.556999	-0.650634	161.299305
HLA A*3201	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-2.716949	2.064809	-0.652140	521.133696
HLA B*3901	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.490003	1.835915	-0.654088	309.031679
HLA B*1502	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.255902	2.594821	-0.661082	1802.611839
HLA A*0212	1:227-235	9	ALHQALIRI	1.220562	0.336437	-2.219168	1.556999	-0.662170	165.641238
HLA B*1517	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-2.653541	1.990887	-0.662654	450.340758
HLA B*1801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-2.352220	1.688566	-0.663654	225.019317
HLA A*6801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-1.389941	0.726109	-0.663832	24.543768
HLA A*3301	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.379889	2.713138	-0.666751	2398.221221

HLA A*6901	1:412-420	9	AALAALTSV	1.136579	0.168474	-1.971857	1.305053	-0.666804	93.725330
HLA B*4501	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-1.323587	0.655319	-0.668268	21.066242
HLA B*4002	1:366-374	9	AELVQTRIV	1.123749	0.213984	-2.006418	1.337733	-0.668685	101.488749
HLA A*0202	1:57-65	9	SYLALLDAL	1.498520	0.489384	-2.658297	1.987904	-0.670393	455.298911
HLA A*0206	1:57-65	9	SYLALLDAL	1.498520	0.489384	-2.662079	1.987904	-0.674175	459.281849
HLA A*0202	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-2.840292	2.164532	-0.675760	692.296951
HLA A*6802	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-2.452143	1.776041	-0.676103	283.232705
HLA A*0206	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-1.789650	1.112802	-0.676848	61.609788
HLA A*3002	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.240269	2.560573	-0.679696	1738.876531
HLA B*5301	1:23-31	9	LVRTALFNW	1.553174	0.453372	-2.694643	2.006546	-0.688097	495.043252
HLA B*4002	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-1.912387	1.222401	-0.689986	81.731000
HLA A*0202	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-2.466917	1.773509	-0.693408	293.033290
HLA B*5401	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-1.384119	0.686428	-0.697691	24.216937
HLA A*0216	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-1.803084	1.104589	-0.698495	63.545393
HLA A*0211	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-2.042548	1.338560	-0.703989	110.293084
HLA B*1517	1:289-297	9	WSIADDHDL	1.275539	0.438866	-2.421563	1.714405	-0.707158	263.974820
HLA A*6802	1:460-468	9	VSPPLFESL	1.613644	0.458549	-2.780376	2.072193	-0.708183	603.081286
HLA A*0211	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-2.009186	1.300706	-0.708480	102.137587
HLA A*0202	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-2.775550	2.064809	-0.710741	596.416995
HLA B*3501	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-2.911726	2.199112	-0.712614	816.067648
HLA A*6802	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-1.503365	0.790220	-0.713145	31.868746
HLA A*3101	1:58-66	9	YLALLDALR	0.982293	0.674716	-2.375827	1.657009	-0.718819	237.589601
HLA A*2403	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-2.808335	2.089268	-0.719066	643.183247
HLA B*2705	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-1.950467	1.230828	-0.719639	89.221037
HLA B*1801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-1.375511	0.655319	-0.720192	23.741639
HLA B*1503	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-2.684169	1.962632	-0.721537	483.246971
HLA A*2402	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-2.886389	2.164532	-0.721857	769.820221
HLA A*3001	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-1.109681	0.387024	-0.722657	12.873024
HLA B*4601	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.107965	2.376452	-0.731512	1282.225904
HLA A*0203	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-1.368218	0.635887	-0.732331	23.346291
HLA A*0250	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-2.695437	1.962632	-0.732805	495.949288
HLA A*2402	1:93-101	9	IYRDVLARL	1.447955	0.489591	-2.673000	1.937546	-0.735454	470.976989
HLA A*0211	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-2.882146	2.144780	-0.737366	762.335501
HLA A*0206	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.531544	2.793482	-0.738062	3400.507989
HLA B*5801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.244968	2.500040	-0.744927	1757.792940
HLA B*0702	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.276174	2.527183	-0.748990	1888.746079
HLA A*0202	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-2.602525	1.843794	-0.758731	400.428091
HLA A*0216	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-2.814002	2.055046	-0.758956	651.630918
HLA A*6901	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-2.539164	1.773509	-0.765655	346.069739
HLA A*0206	1:460-468	9	VSPPLFESL	1.613644	0.458549	-2.838728	2.072193	-0.766535	689.807103
HLA B*2705	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.696008	2.927757	-0.768251	4966.011829
HLA A*0202	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-2.823959	2.055046	-0.768913	666.743514
HLA A*3001	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.330912	2.560573	-0.770339	2142.455831
HLA B*1509	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.701585	2.927757	-0.773829	5030.202018
HLA A*3101	1:364-372	9	AAAELVQTR	0.986953	0.803779	-2.569674	1.790732	-0.778942	371.256476
HLA B*1502	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.502998	2.722320	-0.780678	3184.179608
HLA A*0219	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-2.081564	1.299885	-0.781679	120.660141
HLA B*1502	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.606008	2.819427	-0.786581	4036.531791
HLA A*3101	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-2.105430	1.313812	-0.791618	127.476432
HLA B*1502	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.319244	2.527183	-0.792061	2085.663951
HLA A*0203	1:375-383	9	VLGDAWELL	1.509402	0.401696	-2.708045	1.911098	-0.796947	510.557438
HLA A*3301	1:232-240	9	LIRIGVAER	0.803790	0.789705	-2.390855	1.593495	-0.797360	245.954478
HLA A*0206	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.282776	2.485326	-0.797449	1917.677746
HLA A*0206	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.175160	2.376452	-0.798708	1496.786362
HLA A*0211	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-2.042844	1.241782	-0.801063	110.368291
HLA A*0206	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-2.656267	1.854767	-0.801500	453.175744
HLA B*3501	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.729356	2.927757	-0.801600	5362.364606
HLA B*5701	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.330263	2.527183	-0.803080	2139.259254
HLA A*0201	1:412-420	9	AALAALTSV	1.136579	0.168474	-2.110054	1.305053	-0.805001	128.840881
HLA A*0202	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-2.660970	1.854767	-0.806204	458.110584
HLA B*1501	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.291694	2.485326	-0.806368	1957.466208
HLA B*0702	1:205-213	9	ALMKITHVL	1.662500	0.455646	-2.924987	2.118146	-0.806841	841.369287
HLA A*0216	1:412-420	9	AALAALTSV	1.136579	0.168474	-2.114198	1.305053	-0.809145	130.076300
HLA A*0203	1:463-471	9	PLFESLELL	1.291656	0.202256	-2.304149	1.493912	-0.810238	201.441682
HLA A*2602	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-2.957226	2.144780	-0.812446	906.204653

HLA B*0702	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-2.937195	2.123741	-0.813454	865.355540
HLA A*2902	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.801091	2.987094	-0.813996	6325.441097
HLA A*3201	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.332432	1.517234	-0.815198	214.997020
HLA B*5301	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-2.662201	1.846931	-0.815270	459.411070
HLA B*5701	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.337030	2.518634	-0.818396	2172.850950
HLA A*2501	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.637910	2.819427	-0.818483	4344.198733
HLA A*0250	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.357386	2.538635	-0.818750	2277.119772
HLA B*2705	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.479385	2.655688	-0.823697	3015.679838
HLA B*3501	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-2.689366	1.861442	-0.827924	489.064570
HLA A*0206	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-1.615990	0.775701	-0.840289	41.303788
HLA B*1502	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.496245	2.655688	-0.840557	3135.054802
HLA A*2902	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.770350	2.927757	-0.842594	5893.186077
HLA B*3501	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.381778	2.538635	-0.843143	2408.675125
HLA A*6802	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-2.638006	1.792234	-0.845773	434.516687
HLA B*5301	1:415-423	9	AALTSVTDW	1.150326	0.497710	-2.494857	1.648036	-0.846821	312.505048
HLA A*3201	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.012980	2.164532	-0.848447	1030.337643
HLA A*0202	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-2.749193	1.900474	-0.848720	561.297991
HLA A*0250	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-2.743038	1.891829	-0.851208	553.398321
HLA A*0202	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-2.997271	2.144780	-0.852491	993.735741
HLA A*2603	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-1.879095	1.020365	-0.858730	75.699779
HLA B*1503	1:3-11	9	ATETVRVRF	1.431229	1.094515	-3.390481	2.525744	-0.864736	2457.427534
HLA B*1517	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-2.988620	2.123741	-0.864879	974.137151
HLA B*1503	1:478-486	9	QRLRAARQL	1.551442	0.535207	-2.951973	2.086649	-0.865324	895.308771
HLA A*0202	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-2.296490	1.429823	-0.866667	197.920153
HLA A*0202	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.352988	2.485326	-0.867661	2254.175049
HLA B*1501	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.246655	2.378256	-0.868399	1764.634014
HLA B*5701	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.583759	2.713138	-0.870620	3834.941596
HLA A*0211	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-1.863508	0.990658	-0.872850	73.031148
HLA A*0250	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.709050	1.835915	-0.873135	511.740969
HLA A*1101	1:435-443	9	ALIEGLALK	0.478643	0.243793	-1.599017	0.722436	-0.876581	39.720728
HLA A*3101	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-2.204973	1.328104	-0.876869	160.314527
HLA A*0206	1:463-471	9	PLFESLELL	1.291656	0.202256	-2.371819	1.493912	-0.877908	235.406910
HLA A*2902	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.114148	2.235159	-0.878990	1300.613900
HLA A*0219	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-2.934168	2.055046	-0.879123	859.346756
HLA A*6802	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-1.794612	0.914083	-0.880528	62.317759
HLA A*3002	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.423124	2.538635	-0.884489	2649.259282
HLA B*1503	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.448988	2.560573	-0.888414	2811.820517
HLA A*2301	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.389282	2.500040	-0.889242	2450.656730
HLA B*1501	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.564516	2.673903	-0.890613	3668.736091
HLA B*1517	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-2.492667	1.601532	-0.891135	310.933358
HLA A*2603	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.684641	2.793482	-0.891159	4837.722371
HLA A*3001	1:23-31	9	LVRTALFNW	1.553174	0.453372	-2.898301	2.006546	-0.891755	791.227191
HLA A*0202	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.314572	1.419915	-0.894657	206.334407
HLA B*1517	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.104873	2.203513	-0.901359	1273.129625
HLA B*1517	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.265967	2.361023	-0.904945	1844.876984
HLA B*3501	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.561504	2.655688	-0.905816	3643.379684
HLA B*1503	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.141196	2.235159	-0.906037	1384.189856
HLA A*1101	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-2.619897	1.713576	-0.906320	416.770172
HLA A*0203	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-2.214343	1.307776	-0.906567	163.810835
HLA B*3501	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-2.808349	1.900474	-0.907875	643.204125
HLA A*3001	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.701590	2.793482	-0.908108	5030.256444
HLA A*0202	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-1.545684	0.635887	-0.909797	35.130465
HLA A*0203	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.453658	2.538635	-0.915023	2842.224454
HLA B*5301	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.116789	2.199112	-0.917677	1308.546657
HLA A*0206	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.296976	2.378256	-0.918720	1981.417142
HLA B*1501	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.764350	2.845028	-0.919321	5812.320708
HLA B*2705	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-3.587955	2.663942	-0.924013	3872.174623
HLA B*1503	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-2.062073	1.137355	-0.924717	115.364583
HLA A*3201	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.523424	2.594821	-0.928603	3337.520788
HLA A*2403	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-2.704445	1.773509	-0.930936	506.343450
HLA B*3501	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.141604	2.203513	-0.938091	1385.493436
HLA A*0212	1:463-471	9	PLFESLELL	1.291656	0.202256	-2.434123	1.493912	-0.940211	271.720778
HLA B*4001	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.869057	2.927757	-0.941300	7397.018724
HLA B*1801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-1.847983	0.905846	-0.942137	70.466505
HLA A*0202	1:412-420	9	AALAALTSV	1.136579	0.168474	-2.250088	1.305053	-0.945035	177.863850

HLA A*6801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-2.594245	1.648791	-0.945454	392.866458
HLA A*3001	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-1.901918	0.952354	-0.949563	79.784313
HLA B*1502	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.877755	2.927757	-0.949998	7546.655263
HLA A*3001	1:50-58	9	AQRDSEESY	1.389559	1.325826	-3.666541	2.715385	-0.951156	4640.240698
HLA B*5701	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-2.942500	1.990887	-0.951613	875.991144
HLA A*8001	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.607954	2.655688	-0.952265	4054.653540
HLA A*6901	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.668030	2.713138	-0.954892	4656.183444
HLA B*0801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.487378	2.527183	-0.960195	3071.695634
HLA B*1501	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.020235	2.058588	-0.961646	1047.694771
HLA A*1101	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-1.823713	0.860662	-0.963051	66.636557
HLA B*1502	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.340286	2.376452	-0.963834	2189.204451
HLA A*1101	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.758664	2.793482	-0.965182	5736.722147
HLA B*1517	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-2.865775	1.900474	-0.965301	734.133316
HLA A*0206	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-2.818400	1.852642	-0.965757	658.263717
HLA B*2705	1:233-241	9	IRIGVAERI	1.016372	0.381644	-2.363953	1.398016	-0.965937	231.181528
HLA A*1101	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-2.674931	1.708081	-0.966850	473.076054
HLA A*0206	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.788502	2.819427	-0.969075	6144.722509
HLA A*2603	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.685266	2.713138	-0.972128	4844.689012
HLA B*4501	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-1.820672	0.846543	-0.974130	66.171704
HLA A*3002	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.905977	2.927757	-0.978220	8053.349098
HLA A*2403	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.052738	2.072193	-0.980545	1129.113375
HLA A*8001	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.327768	2.343890	-0.983878	2127.003803
HLA A*6801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-2.693511	1.708081	-0.985430	493.754075
HLA A*0206	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.487218	2.500040	-0.987178	3070.565850
HLA A*3001	1:224-232	9	RQLALHQAL	1.264243	0.500053	-2.752182	1.764296	-0.987886	565.173815
HLA A*0250	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.246077	2.255532	-0.990545	1762.287143
HLA A*3001	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-2.457792	1.466619	-0.991173	286.940309
HLA A*0219	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.509532	1.517234	-0.992297	323.245078
HLA A*2501	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.668256	2.673903	-0.994352	4658.602258
HLA A*2601	1:378-386	9	DAWELLKFF	1.666410	1.046728	-3.710932	2.713138	-0.997793	5139.627905
HLA A*2403	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.379292	2.376452	-1.002840	2394.928060
HLA A*2403	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.530350	2.527183	-1.003167	3391.175463
HLA B*1503	1:206-214	9	LMKITHVLR	1.064507	0.764456	-2.833803	1.828963	-1.004841	682.029471
HLA B*3801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-3.992673	2.987094	-1.005578	9832.693957
HLA A*0250	1:435-443	9	ALIEGLALK	0.478643	0.243793	-1.728699	0.722436	-1.006263	53.542590
HLA A*3001	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.525120	2.518634	-1.006487	3350.582436
HLA A*1101	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-1.734404	0.726109	-1.008295	54.250523
HLA B*3501	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.494243	2.485326	-1.008917	3120.637878
HLA A*3001	1:232-240	9	LIRIGVAER	0.803790	0.789705	-2.612388	1.593495	-1.018893	409.626151
HLA A*0206	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-1.631623	0.612666	-1.018958	42.817702
HLA A*0250	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.084540	2.064809	-1.019731	1214.899018
HLA A*0202	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.461861	1.437023	-1.024838	289.641555
HLA A*2301	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.263900	2.234720	-1.029180	1836.114947
HLA A*0216	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-2.369493	1.338560	-1.030934	234.149490
HLA A*2602	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.531055	2.500040	-1.031015	3396.683696
HLA B*1517	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.625970	2.594821	-1.031149	4226.390308
HLA A*2602	1:60-68	9	ALLDALRWL	1.537707	0.516755	-3.085753	2.054462	-1.031290	1218.295150
HLA A*0206	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.179149	2.144780	-1.034369	1510.599175
HLA B*5801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.024381	2.987094	-1.037287	10577.454639
HLA B*0702	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.416198	2.378256	-1.037943	2607.343095
HLA A*0211	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.578660	2.538635	-1.040025	3790.184679
HLA A*2403	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.714465	2.673903	-1.040562	5181.616940
HLA A*0301	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.027666	2.987094	-1.040571	10657.755469
HLA B*3501	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.031669	2.987094	-1.044575	10756.457708
HLA B*1501	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.767301	2.722320	-1.044981	5851.948866
HLA A*1101	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.033229	2.987094	-1.046135	10795.166176
HLA A*0202	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-1.771507	0.725139	-1.046368	59.089048
HLA A*2403	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.165207	2.118146	-1.047062	1462.875610
HLA A*0211	1:479-487	9	RLRAARQLV	1.087444	0.249933	-2.384859	1.337377	-1.047482	242.582154
HLA A*0203	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.426127	2.378256	-1.047872	2667.639298
HLA B*0702	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-3.975789	2.927757	-1.048033	9457.778153
HLA B*1503	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.588218	2.538635	-1.049583	3874.521514
HLA A*2902	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.723586	2.673903	-1.049683	5291.587778
HLA B*1517	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-2.907102	1.852707	-1.054395	807.425339
HLA B*1801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.899591	2.845028	-1.054562	7935.798375

HLA A*0211	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-2.289108	1.234017	-1.055091	194.584363
HLA A*6901	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-2.849253	1.792234	-1.057019	706.729720
HLA A*0301	1:435-443	9	ALIEGLALK	0.478643	0.243793	-1.780228	0.722436	-1.057792	60.287640
HLA B*4403	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.045202	2.987094	-1.058108	11096.916231
HLA B*1503	1:415-423	9	AALTSVTDW	1.150326	0.497710	-2.706719	1.648036	-1.058683	509.002011
HLA A*0250	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-1.697287	0.635887	-1.061400	49.806585
HLA B*1501	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.492984	2.431527	-1.061458	3111.602070
HLA A*2601	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.656668	2.594821	-1.061847	4535.947015
HLA A*6901	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-2.167414	1.104589	-1.062825	147.032727
HLA A*2602	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.857168	2.793482	-1.063687	7197.278762
HLA A*6802	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.182128	2.118146	-1.063983	1520.997114
HLA A*3001	1:227-235	9	ALHQALIRI	1.220562	0.336437	-2.622758	1.556999	-1.065760	419.525440
HLA A*3201	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.489871	1.419915	-1.069957	308.938071
HLA B*0801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-2.862800	1.792274	-1.070526	729.122475
HLA A*2403	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.237106	2.164532	-1.072574	1726.260523
HLA A*2301	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.239719	2.164532	-1.075187	1736.676655
HLA A*2902	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-3.921666	2.845028	-1.076638	8349.613761
HLA B*3901	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.597116	1.517234	-1.079882	395.472257
HLA B*5701	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.442409	2.361023	-1.081386	2769.548900
HLA A*2601	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-2.874261	1.792234	-1.082027	748.619738
HLA B*5801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-2.938938	1.854767	-1.084171	868.836178
HLA A*2902	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.467163	2.376452	-1.090711	2931.994907
HLA B*0801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-2.014928	0.923460	-1.091467	103.496994
HLA A*0202	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.472680	2.378256	-1.094424	2969.475882
HLA A*0202	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-2.394999	1.299885	-1.095115	248.312868
HLA A*2403	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.456337	2.361023	-1.095314	2859.807394
HLA A*2601	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.474089	2.376452	-1.097637	2979.130263
HLA A*3001	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-2.215964	1.117129	-1.098835	164.423455
HLA A*3001	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.937209	1.835915	-1.101294	865.383630
HLA A*6901	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-2.336145	1.234017	-1.102128	216.842610
HLA A*3201	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.358283	2.255532	-1.102752	2281.830483
HLA A*0301	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-1.832288	0.726109	-1.106179	67.965446
HLA B*4001	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.094668	2.987094	-1.107574	12435.646406
HLA B*5801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.902048	2.793482	-1.108566	7980.832324
HLA A*2603	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.671075	2.560573	-1.110502	4688.943664
HLA B*4403	1:54-62	9	SEESYLALL	1.352077	0.257378	-2.720027	1.609455	-1.110572	524.840065
HLA A*0216	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-2.344636	1.234017	-1.110619	221.123890
HLA B*1517	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.649507	2.538635	-1.110871	4461.765515
HLA A*3101	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-2.817977	1.705831	-1.112146	657.623025
HLA A*0201	1:225-233	9	QLALHQALI	1.319205	0.310263	-2.742122	1.629468	-1.112654	552.231960
HLA A*0101	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.658477	2.538635	-1.119842	4554.881431
HLA B*2705	1:25-33	9	RTALFNWAY	1.425350	1.394077	-3.939945	2.819427	-1.120518	8708.540573
HLA A*3201	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.794446	2.673903	-1.120543	6229.403640
HLA A*0203	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-2.184213	1.062125	-1.122088	152.831484
HLA A*3201	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-2.915913	1.792234	-1.123679	823.972929
HLA B*1501	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.959881	1.835915	-1.123966	911.761408
HLA B*1517	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.052044	2.927757	-1.124287	11273.116832
HLA B*3901	1:51-59	9	QRDSEESYL	1.503495	0.502197	-3.130581	2.005692	-1.124889	1350.767768
HLA A*0203	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-2.119466	0.990658	-1.128808	131.663599
HLA B*4501	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-1.537573	0.407915	-1.129659	34.480493
HLA B*1503	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.806307	2.673903	-1.132403	6401.867372
HLA B*1501	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.060897	2.927757	-1.133140	11505.271391
HLA A*0202	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-2.376062	1.241782	-1.134281	237.718169
HLA B*2705	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.138935	2.001284	-1.137652	1377.004811
HLA A*0203	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.574683	1.437023	-1.137661	375.563294
HLA B*1517	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.210247	2.072193	-1.138054	1622.732845
HLA A*0211	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-2.974208	1.835915	-1.138293	942.341604
HLA A*6802	1:283-291	9	YLALLGWSI	1.492210	0.300064	-2.932810	1.792274	-1.140536	856.663848
HLA A*0250	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.147051	2.003005	-1.144046	1402.977089
HLA A*0206	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.131363	2.987094	-1.144268	13532.019708
HLA B*4402	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.133017	2.987094	-1.145922	13583.655510
HLA A*0203	1:304-312	9	VAAFDVADV	0.706341	0.208036	-2.060794	0.914377	-1.146418	115.025567
HLA A*6801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-3.019624	1.870150	-1.149474	1046.222150
HLA A*0203	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-2.105275	0.954860	-1.150415	127.430924
HLA A*3301	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-2.813616	1.661630	-1.151986	651.053033

HLA A*2602	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.410442	2.255532	-1.154910	2573.012788
HLA A*2902	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.723656	2.560573	-1.163083	5292.446654
HLA A*6801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.886316	2.722320	-1.163996	7696.903380
HLA B*1517	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.009335	2.845028	-1.164307	10217.274692
HLA A*0101	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.152099	2.987094	-1.165005	14193.816172
HLA A*0202	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-1.778048	0.612666	-1.165382	59.985731
HLA B*1503	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-2.423217	1.257536	-1.165680	264.982102
HLA A*0202	1:432-440	9	LKDALIEGL	1.577897	0.430413	-3.175611	2.008310	-1.167301	1498.341880
HLA A*0206	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-2.505975	1.338560	-1.167415	320.608329
HLA B*1502	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.653242	2.485326	-1.167916	4500.309926
HLA A*0212	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.963027	2.793482	-1.169545	9183.890991
HLA A*0101	1:3-11	9	ATETVRVRF	1.431229	1.094515	-3.697107	2.525744	-1.171363	4978.600847
HLA A*3101	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.965231	2.793482	-1.171749	9230.612870
HLA A*6802	1:225-233	9	QLALHQALI	1.319205	0.310263	-2.804947	1.629468	-1.175479	638.185256
HLA A*3001	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.162724	2.987094	-1.175629	14545.328949
HLA A*0216	1:479-487	9	RLRAARQLV	1.087444	0.249933	-2.514339	1.337377	-1.176962	326.842833
HLA B*2705	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.970916	2.793482	-1.177435	9352.253944
HLA A*3101	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-2.479186	1.300814	-1.178372	301.429652
HLA A*2902	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.610609	2.431527	-1.179082	4079.516264
HLA B*5801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-2.518263	1.338560	-1.179703	329.809079
HLA A*6901	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-2.489143	1.307776	-1.181367	308.420395
HLA A*0202	1:479-487	9	RLRAARQLV	1.087444	0.249933	-2.521730	1.337377	-1.184354	332.453146
HLA B*1801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.171562	2.987094	-1.184468	14844.388433
HLA A*2301	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.172547	1.987904	-1.184643	1487.809030
HLA B*1503	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.420145	2.234720	-1.185425	2631.148243
HLA A*0211	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.624271	1.437023	-1.187249	420.989603
HLA A*0212	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-1.963145	0.775701	-1.187444	91.863944
HLA A*0211	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.567049	2.378256	-1.188794	3690.194157
HLA B*4801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.117242	2.927757	-1.189486	13099.122898
HLA A*2501	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.034752	2.845028	-1.189723	10833.076209
HLA A*0203	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.026729	1.835915	-1.190814	1063.478595
HLA B*3901	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.180944	1.987904	-1.193040	1516.855636
HLA A*0250	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-2.496140	1.300706	-1.195434	313.429490
HLA B*1503	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.556810	2.361023	-1.195787	3604.210614
HLA A*2403	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-2.732846	1.536595	-1.196250	540.562321
HLA A*6802	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-2.465977	1.269415	-1.196562	292.399865
HLA B*3501	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.033956	1.835915	-1.198041	1081.323817
HLA A*8001	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.126307	2.927757	-1.198550	13375.392336
HLA B*1502	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-3.061891	1.861442	-1.200449	1153.164185
HLA B*0802	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.721927	2.518634	-1.203294	5271.415731
HLA A*0212	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.166096	1.962632	-1.203464	1465.870161
HLA B*1503	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.408830	2.203513	-1.205317	2563.481561
HLA B*5701	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-3.999801	2.793482	-1.206319	9995.415671
HLA B*1801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.001305	2.793482	-1.207823	10030.083069
HLA A*2601	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.693390	2.485326	-1.208064	4936.173582
HLA A*3001	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-2.668573	1.459786	-1.208787	466.201063
HLA A*0250	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.053975	2.845028	-1.208947	11323.359210
HLA A*0201	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.274186	2.064809	-1.209377	1880.121481
HLA B*3901	1:478-486	9	QRLRAARQL	1.551442	0.535207	-3.296638	2.086649	-1.209988	1979.874171
HLA A*3002	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.330531	2.118146	-1.212385	2140.579001
HLA B*3901	1:409-417	9	VLDAALAAL	1.329115	0.442767	-2.985345	1.771882	-1.213463	966.818438
HLA A*0202	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.286897	2.072193	-1.214704	1935.961094
HLA B*5801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.380049	2.164532	-1.215517	2399.103623
HLA A*0301	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-2.866837	1.650564	-1.216273	735.930667
HLA A*0203	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.282080	2.064809	-1.217271	1914.609374
HLA B*1503	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.218931	2.001284	-1.217647	1655.505863
HLA B*1801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.145511	2.927757	-1.217755	13980.130335
HLA A*6901	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.054706	1.835915	-1.218791	1134.243817
HLA B*1503	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.705020	2.485326	-1.219694	5070.144934
HLA B*3501	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.651274	2.431527	-1.219747	4479.954006
HLA A*3001	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-2.873688	1.650564	-1.223124	747.632202
HLA A*6801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-2.754315	1.530697	-1.223618	567.956880
HLA B*1801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-3.946670	2.722320	-1.224350	8844.425043
HLA A*0211	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.069468	2.845028	-1.224439	11734.586448
HLA B*3501	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-3.258571	2.032901	-1.225670	1813.724143

HLA A*0201	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.061713	1.835915	-1.225798	1152.690157
HLA B*1502	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-2.018067	0.790220	-1.227847	104.247740
HLA A*0202	1:58-66	9	YLALLDALR	0.982293	0.674716	-2.885990	1.657009	-1.228981	769.112558
HLA A*0201	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.609326	2.378256	-1.231070	4067.483970
HLA B*1503	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.609486	2.378256	-1.231230	4068.980560
HLA A*6901	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.052533	2.819427	-1.233106	11285.809125
HLA B*5801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.577453	2.343890	-1.233562	3779.660017
HLA B*0702	1:479-487	9	RLRAARQLV	1.087444	0.249933	-2.571944	1.337377	-1.234567	373.201723
HLA A*6801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-2.419744	1.184382	-1.235362	262.871802
HLA B*3501	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.755354	1.517234	-1.238119	569.316587
HLA B*0702	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.130247	1.891829	-1.238418	1349.730501
HLA A*6801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-2.832065	1.593495	-1.238570	679.304549
HLA A*3201	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.227680	1.987904	-1.239776	1689.196626
HLA A*0250	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.033558	2.793482	-1.240077	10803.345364
HLA A*6802	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.063871	2.819427	-1.244444	11584.340531
HLA A*0212	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.665195	1.419915	-1.245280	462.588359
HLA A*0202	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.065178	2.819427	-1.245751	11619.237506
HLA A*2402	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.677390	2.431527	-1.245864	4757.627442
HLA A*2603	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.501644	2.255532	-1.246113	3174.272842
HLA B*4601	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.784837	2.538635	-1.246202	6093.082783
HLA A*2603	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-2.899363	1.650564	-1.248799	793.164323
HLA B*4601	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.749069	2.500040	-1.249028	5611.365000
HLA A*0202	1:229-237	9	HQALIRIGV	1.172366	0.156389	-2.579655	1.328755	-1.250900	379.887191
HLA B*1503	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.597306	2.343890	-1.253415	3956.451850
HLA A*6901	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.372277	2.118146	-1.254131	2356.551364
HLA A*6802	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.255630	2.001284	-1.254346	1801.480970
HLA B*5801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.489215	2.234720	-1.254496	3084.718072
HLA A*0202	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.852446	2.594821	-1.257625	7119.440406
HLA A*3101	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.246393	2.987094	-1.259299	17635.728624
HLA A*0202	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.024205	1.764296	-1.259909	1057.317465
HLA B*5701	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.247639	2.987094	-1.260544	17686.367074
HLA B*1503	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-2.648246	1.386690	-1.261555	444.882697
HLA A*2603	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.606281	2.343890	-1.262391	4039.065700
HLA B*1503	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.694081	2.431527	-1.262555	4944.030850
HLA B*1517	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.057070	1.792234	-1.264836	1140.433595
HLA A*2403	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.252580	2.987094	-1.265485	17888.733797
HLA B*1503	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-2.725750	1.459786	-1.265964	531.802441
HLA A*2602	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.267640	2.001284	-1.266357	1851.996861
HLA A*0206	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.862102	2.594821	-1.267282	7279.511600
HLA A*2902	1:50-58	9	AQRDSEESY	1.389559	1.325826	-3.982983	2.715385	-1.267598	9615.751821
HLA A*0202	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.062885	2.793482	-1.269403	11558.049012
HLA A*8001	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-3.830187	2.560573	-1.269614	6763.738962
HLA B*4801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-3.124228	1.852707	-1.271521	1331.152100
HLA B*0801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-2.323110	1.050133	-1.272977	210.430983
HLA A*0250	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-1.998763	0.725139	-1.273625	99.715640
HLA A*3101	1:181-189	9	SVPDFALTR	1.418756	0.707454	-3.400569	2.126210	-1.274359	2515.181955
HLA A*2602	1:50-58	9	AQRDSEESY	1.389559	1.325826	-3.993199	2.715385	-1.277814	9844.616588
HLA A*0216	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.075154	2.793482	-1.281672	11889.224902
HLA A*2902	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.801518	2.518634	-1.282885	6331.672192
HLA A*0212	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-3.338294	2.055046	-1.283248	2179.184289
HLA A*2301	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-3.716575	2.431527	-1.285049	5206.850897
HLA A*3001	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-2.336972	1.050133	-1.286838	217.255933
HLA B*4002	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.214849	2.927757	-1.287093	16400.202923
HLA B*1801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.814859	2.527183	-1.287675	6529.182351
HLA B*5301	1:462-470	9	PPLFESLEL	1.313352	0.107023	-2.708825	1.420375	-1.288449	511.475265
HLA B*3501	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.003633	1.714405	-1.289229	1008.401111
HLA A*0211	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.963450	2.673903	-1.289546	9192.838437
HLA B*7301	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.945500	2.655688	-1.289811	8820.629127
HLA A*6801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.775265	2.485326	-1.289939	5960.260984
HLA A*2602	1:188-196	9	TRASGDPLY	1.277550	1.378138	-3.945659	2.655688	-1.289971	8823.874591
HLA A*3201	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.668726	2.378256	-1.290470	4663.645490
HLA B*3801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-3.957830	2.663942	-1.293888	9074.645312
HLA B*5301	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.008057	2.713138	-1.294919	10187.249664
HLA A*2402	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.114935	2.819427	-1.295508	13029.718181
HLA A*3101	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-2.763676	1.466619	-1.297057	580.330924

HLA A*2902	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.010562	2.713138	-1.297423	10246.168668
HLA B*1503	1:51-59	9	QRDSEESYL	1.503495	0.502197	-3.304269	2.005692	-1.298577	2014.970616
HLA B*0803	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.286833	2.987094	-1.299738	19356.763469
HLA A*0212	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.447465	2.144780	-1.302685	2801.980634
HLA B*4801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.289812	2.987094	-1.302717	19490.002291
HLA B*1801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.806725	2.500040	-1.306684	6408.035085
HLA A*3201	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.083464	1.776041	-1.307424	1211.892553
HLA A*2403	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.127275	2.819427	-1.307848	13405.237653
HLA A*3002	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.368048	2.058588	-1.309459	2333.715105
HLA B*3901	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-3.974257	2.663942	-1.310316	9424.476992
HLA A*0203	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.985154	2.673903	-1.311251	9663.938777
HLA B*3501	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.985225	2.673903	-1.311321	9665.507330
HLA A*0216	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.850646	2.538635	-1.312011	7089.998668
HLA A*2403	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.106312	2.793482	-1.312831	12773.573536
HLA A*3001	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.240921	2.927757	-1.313165	17414.918918
HLA B*1503	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-2.368615	1.054023	-1.314592	233.676215
HLA A*1101	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-3.185606	1.870150	-1.315456	1533.224067
HLA B*3901	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.006659	1.688566	-1.318093	1015.452124
HLA B*5701	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.553450	2.235159	-1.318292	3576.435505
HLA A*0250	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.256494	1.937546	-1.318948	1805.071001
HLA B*1517	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.043008	2.722320	-1.320688	11040.986749
HLA B*1502	1:236-244	9	GVAERIPKF	1.580848	1.093055	-3.995576	2.673903	-1.321673	9898.661780
HLA B*1509	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.308951	2.987094	-1.321856	20368.112966
HLA A*3201	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.807552	2.485326	-1.322226	6420.249411
HLA B*5401	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-2.246216	0.923460	-1.322755	176.285154
HLA B*0702	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-2.841697	1.517234	-1.324463	694.540237
HLA B*0801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.312026	2.987094	-1.324932	20512.862593
HLA B*3501	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.143329	1.817618	-1.325711	1391.005972
HLA B*1502	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.390749	2.064809	-1.325939	2458.943564
HLA A*1101	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.669858	2.343890	-1.325968	4675.822125
HLA B*3501	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.390932	2.064809	-1.326122	2459.981387
HLA A*2403	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.845548	2.518634	-1.326914	7007.252563
HLA A*6802	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.709137	2.378256	-1.330881	5118.428865
HLA A*2603	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.048294	2.715385	-1.332909	11176.201671
HLA B*5301	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.261169	2.927757	-1.333413	18246.069237
HLA A*0202	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-2.634393	1.300706	-1.333687	430.916329
HLA B*3901	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.321610	2.987094	-1.334515	20970.549963
HLA A*2402	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.834656	2.500040	-1.334615	6833.694482
HLA A*3201	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.406885	2.072193	-1.334692	2552.024411
HLA A*2601	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.180504	2.845028	-1.335476	15153.203301
HLA A*2402	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.570235	2.234720	-1.335515	3717.364255
HLA A*6801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.394475	2.058588	-1.335886	2480.132278
HLA B*3901	1:54-62	9	SEESYLALL	1.352077	0.257378	-2.945968	1.609455	-1.336512	883.013931
HLA A*2301	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.713084	2.376452	-1.336632	5165.160328
HLA B*0801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-2.357436	1.020365	-1.337071	227.738082
HLA A*3002	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.001192	2.663942	-1.337250	10027.478848
HLA B*3901	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.338759	2.001284	-1.337475	2181.519790
HLA B*0802	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.328473	2.987094	-1.341378	21304.564743
HLA A*1101	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-2.451495	1.109528	-1.341967	282.810117
HLA B*0702	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.937497	2.594821	-1.342677	8659.587725
HLA A*0203	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-2.773201	1.429823	-1.343378	593.199157
HLA A*0212	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.722158	2.378256	-1.343902	5274.211214
HLA B*5701	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.722627	2.376452	-1.346175	5279.920882
HLA A*0203	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.333331	2.987094	-1.346237	21544.251036
HLA A*0202	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.602963	2.255532	-1.347432	4008.329774
HLA A*0212	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-2.652094	1.300706	-1.351388	448.842499
HLA B*1502	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.852606	2.500040	-1.352565	7122.059934
HLA A*3101	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.281600	2.927757	-1.353844	19124.955799
HLA B*5301	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.881514	2.527183	-1.354330	7612.261300
HLA B*5801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.030372	2.673903	-1.356469	10724.384056
HLA B*4402	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.284742	2.927757	-1.356985	19263.788505
HLA A*2402	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.345276	2.987094	-1.358182	22145.025394
HLA B*4601	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.349280	2.987094	-1.362185	22350.112066
HLA A*6801	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.072689	1.710232	-1.362458	1182.195709
HLA B*1503	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-2.596167	1.230828	-1.365338	394.608859

HLA A*0206	1:227-235	9	ALHQALIRI	1.220562	0.336437	-2.922637	1.556999	-1.365639	836.829862
HLA A*8001	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.088423	2.722320	-1.366104	12258.107728
HLA A*2501	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.079838	2.713138	-1.366700	12018.172009
HLA B*1502	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.713516	2.343890	-1.369626	5170.304390
HLA B*4501	1:54-62	9	SEESYLALL	1.352077	0.257378	-2.979405	1.609455	-1.369950	953.686041
HLA B*3901	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.748448	2.378256	-1.370193	5603.356509
HLA B*1503	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.791451	1.419915	-1.371537	618.658985
HLA B*0702	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.872022	2.500040	-1.371981	7447.693030
HLA A*2603	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-3.342636	1.970233	-1.372403	2201.079898
HLA A*2603	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.119815	1.747156	-1.372659	1317.696368
HLA B*0801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.892744	2.518634	-1.374111	7811.676069
HLA A*6801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.030509	2.655688	-1.374820	10727.749612
HLA A*3002	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.971165	2.594821	-1.376345	9357.618516
HLA A*0250	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-2.513991	1.137355	-1.376636	326.581247
HLA A*2301	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.895564	2.518634	-1.376930	7862.553396
HLA A*0206	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.306091	2.927757	-1.378335	20234.453149
HLA B*4002	1:377-385	9	GDAWELLKF	1.384021	0.916265	-3.678805	2.300286	-1.378518	4773.147119
HLA A*2602	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.722707	2.343890	-1.378817	5280.892140
HLA B*3501	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-1.647468	0.268538	-1.378931	44.408723
HLA A*8001	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.095110	2.715385	-1.379725	12448.300628
HLA B*1503	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.172355	1.792274	-1.380080	1487.149168
HLA A*0216	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.054135	2.673903	-1.380232	11327.525529
HLA B*4402	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.096529	2.715385	-1.381144	12489.042888
HLA B*5701	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.468761	2.086183	-1.382578	2942.800772
HLA A*2402	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.902607	2.518634	-1.383974	7991.114692
HLA A*0201	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.528823	2.144780	-1.384043	3379.271580
HLA B*1517	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.202715	1.817618	-1.385096	1594.830665
HLA A*2403	1:3-11	9	ATETVRVRF	1.431229	1.094515	-3.911277	2.525744	-1.385533	8152.240128
HLA A*2902	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.980582	2.594821	-1.385762	9562.733926
HLA B*4403	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.314117	2.927757	-1.386361	20611.866101
HLA B*3901	1:354-362	9	HIALDEAAF	1.481866	1.112955	-3.981517	2.594821	-1.386697	9583.345974
HLA A*2601	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.373884	2.987094	-1.386789	23652.851873
HLA A*0250	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-2.505383	1.117129	-1.388254	320.171544
HLA A*2403	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.233871	2.845028	-1.388842	17134.469085
HLA B*1509	1:210-218	9	THVLRGEDL	1.116170	0.447749	-2.953425	1.563919	-1.389506	898.307077
HLA A*2602	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.376710	2.987094	-1.389615	23807.288919
HLA B*5801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-3.908674	2.518634	-1.390040	8103.520482
HLA A*3002	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.064120	2.673903	-1.390217	11590.985455
HLA B*3501	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.106073	2.715385	-1.390688	12766.526912
HLA A*2603	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.391984	2.001284	-1.390701	2465.950703
HLA A*2402	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.055892	2.663942	-1.391951	11373.456329
HLA A*2603	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.379377	2.987094	-1.392282	23953.920726
HLA B*1501	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.813306	1.419915	-1.393391	650.588278
HLA A*0201	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.380563	2.987094	-1.393469	24019.452169
HLA A*6901	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.381421	2.987094	-1.394326	24066.928066
HLA A*6901	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-2.308919	0.914083	-1.394835	203.666122
HLA A*2402	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.187415	1.792274	-1.395141	1539.624209
HLA A*2301	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.069223	2.673903	-1.395320	11727.986093
HLA B*1517	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.815393	1.419915	-1.395478	653.721212
HLA A*2602	1:3-11	9	ATETVRVRF	1.431229	1.094515	-3.922174	2.525744	-1.396429	8359.376289
HLA B*0801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.241894	2.845028	-1.396866	17453.966720
HLA A*0219	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.653379	2.255532	-1.397847	4501.722226
HLA B*4601	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.325980	2.927757	-1.398223	21182.629117
HLA A*0206	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.111571	2.713138	-1.398432	12929.167444
HLA B*0802	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.326847	2.927757	-1.399090	21224.957156
HLA B*4403	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.115001	2.715385	-1.399616	13031.692032
HLA B*5701	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.328623	2.927757	-1.400866	21311.942361
HLA A*0202	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-2.538276	1.137355	-1.400920	345.362771
HLA B*0802	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.247601	2.845028	-1.402573	17684.836240
HLA A*3301	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.222720	2.819427	-1.403293	16700.135560
HLA A*3201	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-3.903552	2.500040	-1.403511	8008.512483
HLA A*2602	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.154400	1.749555	-1.404844	1426.920469
HLA A*0219	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.199427	2.793482	-1.405945	15828.042297
HLA B*1517	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.198955	1.789240	-1.409716	1581.085667
HLA A*2301	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.645113	2.235159	-1.409955	4416.855645

HLA A*3301	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-3.124256	1.713576	-1.410680	1331.238519
HLA A*0212	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.401436	2.987094	-1.414341	25202.053121
HLA A*2402	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.088724	2.673903	-1.414821	12266.598988
HLA A*6802	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.834907	1.419915	-1.414993	683.765839
HLA A*0219	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.343157	2.927757	-1.415400	22037.227097
HLA A*1101	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.343721	2.927757	-1.415964	22065.858229
HLA A*3101	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.180907	1.764296	-1.416610	1516.724345
HLA B*1509	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.261663	2.845028	-1.416634	18266.809951
HLA B*1501	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-2.803462	1.386690	-1.416772	636.006995
HLA A*0216	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.481988	2.064809	-1.417179	3033.810582
HLA A*0206	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.266874	2.845028	-1.421845	18487.316149
HLA A*2602	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.350079	2.927757	-1.422322	22391.259851
HLA A*0219	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.411052	2.987094	-1.423958	25766.318138
HLA A*2501	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.139887	2.715385	-1.424502	13800.237265
HLA A*0216	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.863021	1.437023	-1.425999	729.493350
HLA A*2301	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-2.963274	1.536595	-1.426679	918.911871
HLA A*0206	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.142363	2.715385	-1.426978	13879.151309
HLA A*0206	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-2.857213	1.429823	-1.427391	719.802598
HLA A*0250	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-2.628458	1.200757	-1.427701	425.067746
HLA A*0301	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.355487	2.927757	-1.427731	22671.854431
HLA B*1503	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.500225	2.072193	-1.428033	3163.917601
HLA B*0702	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.416177	2.987094	-1.429082	26072.134719
HLA A*0211	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.058555	1.629468	-1.429087	1144.339468
HLA A*0301	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.967726	2.538635	-1.429090	9283.798168
HLA A*6801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.806363	2.376452	-1.429911	6402.698628
HLA B*4601	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.145478	2.715385	-1.430094	13979.071542
HLA A*6801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.025208	2.594821	-1.430388	10597.616275
HLA A*0219	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-2.206373	0.775701	-1.430672	160.832263
HLA A*2501	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.419283	2.987094	-1.432188	26259.267705
HLA A*0212	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.278412	2.845028	-1.433384	18985.069396
HLA B*5801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.278462	2.845028	-1.433433	18987.226368
HLA A*0212	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.362075	2.927757	-1.434318	23018.392987
HLA B*0801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.363252	2.927757	-1.435496	23080.865615
HLA B*4403	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.148993	2.713138	-1.435855	14092.665933
HLA B*0702	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.231528	2.793482	-1.438047	17042.300380
HLA B*1517	1:60-68	9	ALLDALRWL	1.537707	0.516755	-3.493402	2.054462	-1.438940	3114.599862
HLA A*3001	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.284335	2.845028	-1.439307	19245.767752
HLA B*3901	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.284392	2.845028	-1.439363	19248.266733
HLA B*4402	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.259224	2.819427	-1.439797	18164.520790
HLA A*2301	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.558234	2.118146	-1.440088	3616.046022
HLA A*2403	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.036072	2.594821	-1.441252	10866.062755
HLA B*4601	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.969427	2.527183	-1.442243	9320.231879
HLA A*2603	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.646748	2.203513	-1.443235	4433.517705
HLA A*0219	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.288651	2.845028	-1.443623	19437.985087
HLA B*0702	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.263058	2.819427	-1.443631	18325.604289
HLA A*2402	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.432452	1.987904	-1.444548	2706.773526
HLA A*0203	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.238116	2.793482	-1.444634	17302.791386
HLA B*0803	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.372476	2.927757	-1.444720	23576.328304
HLA B*1509	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.267128	2.819427	-1.447701	18498.120853
HLA A*3201	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.223108	1.773509	-1.449599	1671.506645
HLA A*6801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-3.214941	1.764418	-1.450523	1640.368034
HLA A*0216	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.295756	2.845028	-1.450728	19758.596266
HLA A*0216	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.438757	2.987094	-1.451663	27463.601695
HLA A*6901	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.596568	2.144780	-1.451788	3949.736710
HLA A*0202	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-3.990652	2.538635	-1.452017	9787.053556
HLA A*0211	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.708267	2.255532	-1.452736	5108.193763
HLA B*4601	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.272362	2.819427	-1.452935	18722.432137
HLA A*3201	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.245621	1.792274	-1.453347	1760.438560
HLA A*6901	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.874520	1.419915	-1.454605	749.065365
HLA A*0101	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.382422	2.927757	-1.454665	24122.456977
HLA A*6901	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.382863	2.927757	-1.455107	24147.003424
HLA A*2601	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.383035	2.927757	-1.455278	24156.541488
HLA B*4403	1:366-374	9	AELVQTRIV	1.123749	0.213984	-2.793270	1.337733	-1.455537	621.254899
HLA A*6901	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.301092	2.845028	-1.456063	20002.844909
HLA A*6802	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.444377	2.987094	-1.457283	27821.302607

HLA A*0101	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.250815	2.793482	-1.457333	17816.202411
HLA A*0201	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.385269	2.927757	-1.457513	24281.142422
HLA A*0203	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-2.526730	1.067176	-1.459554	336.302543
HLA B*4601	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.304964	2.845028	-1.459935	20181.977560
HLA A*2402	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.945786	2.485326	-1.460460	8826.452721
HLA B*3501	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.821592	2.361023	-1.460570	6631.204511
HLA A*3001	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.839195	2.378256	-1.460939	6905.494182
HLA B*1517	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.234513	1.773509	-1.461004	1715.981129
HLA A*0201	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-2.891638	1.429823	-1.461815	779.180481
HLA A*0202	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.137716	2.673903	-1.463812	13731.425630
HLA B*1502	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.582039	2.118146	-1.463893	3819.785108
HLA A*2601	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.120386	2.655688	-1.464698	13194.283997
HLA A*6901	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.902009	1.437023	-1.464986	798.010657
HLA A*2403	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.129084	2.663942	-1.465142	13461.195175
HLA A*3201	1:181-189	9	SVPDFALTR	1.418756	0.707454	-3.591794	2.126210	-1.465584	3906.555449
HLA B*1517	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.320546	1.854767	-1.465779	2091.924226
HLA B*1503	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.632290	2.164532	-1.467757	4288.344991
HLA B*5801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-3.995304	2.527183	-1.468121	9892.451852
HLA B*1509	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.124385	2.655688	-1.468696	13316.333129
HLA A*0211	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.289250	2.819427	-1.469823	19464.818714
HLA B*5401	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-2.471339	1.000328	-1.471011	296.032023
HLA A*0203	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.399303	2.927757	-1.471546	25078.559675
HLA A*0201	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-3.315795	1.843794	-1.472001	2069.165796
HLA B*5801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.185448	2.713138	-1.472309	15326.668578
HLA A*0202	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.319949	2.845028	-1.474920	20890.495173
HLA B*4402	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.197402	2.722320	-1.475082	15754.402836
HLA A*0250	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.149515	2.673903	-1.475612	14109.601327
HLA A*2602	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.190906	1.714405	-1.476502	1552.051279
HLA A*2501	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.404575	2.927757	-1.476818	25384.863625
HLA A*0211	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.014183	1.536595	-1.477587	1033.195493
HLA A*0202	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-3.511667	2.032901	-1.478766	3248.382457
HLA B*5301	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.468612	2.987094	-1.481518	29417.949480
HLA A*0202	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.373997	1.892220	-1.481777	2365.901901
HLA A*2602	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.470250	1.987904	-1.482346	2952.911525
HLA B*4601	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.276288	2.793482	-1.482807	18892.448826
HLA B*1503	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-3.538071	2.055046	-1.483025	3451.999061
HLA A*0201	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.303061	2.819427	-1.483634	20093.733413
HLA A*2902	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.148091	2.663942	-1.484149	14063.420253
HLA B*2705	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.330305	2.845028	-1.485277	21394.653844
HLA B*5801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.080670	2.594821	-1.485850	12041.210073
HLA B*2705	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-3.523697	2.037348	-1.486348	3339.615897
HLA B*1517	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.865180	2.378256	-1.486924	7331.284409
HLA B*1509	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.083062	2.594821	-1.488241	12107.707174
HLA B*5101	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.475619	2.987094	-1.488524	29896.377046
HLA B*4001	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.308732	2.819427	-1.489305	20357.867945
HLA A*2402	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.203360	2.713138	-1.490222	15972.034516
HLA B*4403	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.309790	2.819427	-1.490363	20407.488534
HLA B*1503	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.384226	1.891829	-1.492397	2422.291420
HLA A*8001	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.337607	2.845028	-1.492579	21757.423419
HLA A*6802	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.207836	1.714405	-1.493432	1613.750742
HLA A*0206	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.930851	1.437023	-1.493828	852.807417
HLA A*2902	1:377-385	9	GDAWELLKF	1.384021	0.916265	-3.794197	2.300286	-1.493911	6225.832424
HLA A*1101	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.033516	2.538635	-1.494881	10802.293407
HLA B*4403	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-2.544098	1.048747	-1.495350	350.023775
HLA B*1517	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-3.239141	1.743756	-1.495385	1734.366966
HLA B*0803	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.695510	2.199112	-1.496398	4960.319592
HLA A*0216	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.424712	2.927757	-1.496956	26589.628559
HLA B*0801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.171008	2.673903	-1.497105	14825.448194
HLA B*1801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.212514	2.715385	-1.497129	16312.248679
HLA A*2403	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.875739	2.378256	-1.497483	7511.707239
HLA B*4501	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-2.546452	1.048747	-1.497705	351.926303
HLA A*3101	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.343521	2.845028	-1.498493	22055.713785
HLA A*3301	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.344928	2.845028	-1.499900	22127.301774
HLA A*0212	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.036587	1.536595	-1.499992	1087.895529
HLA A*0203	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.319639	2.819427	-1.500212	20875.582484

HLA A*2301	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.214210	2.713138	-1.501072	16376.087938
HLA A*0250	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.354167	1.852642	-1.501525	2260.305177
HLA B*4601	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.215202	2.713138	-1.502063	16413.516816
HLA A*6802	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.431263	2.927757	-1.503506	26993.713536
HLA A*2601	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-3.364965	1.861442	-1.503523	2317.209567
HLA A*0301	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.348725	2.845028	-1.503697	22321.595129
HLA A*0203	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.349085	2.845028	-1.504056	22340.078653
HLA A*3101	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.217311	2.713138	-1.504173	16493.449003
HLA A*8001	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.168245	2.663942	-1.504303	14731.427651
HLA B*1501	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-3.495282	1.990887	-1.504395	3128.108786
HLA A*6802	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.349498	2.845028	-1.504470	22361.359676
HLA B*4801	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.324291	2.819427	-1.504864	21100.394864
HLA B*4501	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.324417	2.819427	-1.504990	21106.559908
HLA A*0212	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.324584	2.819427	-1.505157	21114.668540
HLA A*2402	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.623597	2.118146	-1.505451	4203.360337
HLA B*5301	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.005881	2.500040	-1.505841	10136.343667
HLA A*2403	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.219116	2.713138	-1.505978	16562.118455
HLA B*5701	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.006224	2.500040	-1.506184	10144.352958
HLA B*0803	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.221855	2.715385	-1.506471	16666.921348
HLA B*3901	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.326741	2.819427	-1.507314	21219.790675
HLA A*2603	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.435076	2.927757	-1.507319	27231.768654
HLA A*0211	1:432-440	9	LKDALIEGL	1.577897	0.430413	-3.515863	2.008310	-1.507553	3279.920647
HLA A*3002	1:290-298	9	SIADDHDLF	1.324197	1.161129	-3.993340	2.485326	-1.508014	9847.812603
HLA B*0702	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.708169	2.199112	-1.509057	5107.033234
HLA B*5301	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.329034	2.819427	-1.509607	21332.128583
HLA B*1503	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.575005	2.064809	-1.510195	3758.413619
HLA A*2601	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.303843	2.793482	-1.510361	20129.964760
HLA B*1503	1:432-440	9	LKDALIEGL	1.577897	0.430413	-3.519190	2.008310	-1.510880	3305.142643
HLA A*6801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.357639	2.845028	-1.512611	22784.482696
HLA B*5701	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.357820	2.845028	-1.512792	22793.975810
HLA B*1503	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-2.436599	0.923460	-1.513139	273.274562
HLA B*3801	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.334149	2.819427	-1.514722	21584.849339
HLA A*6901	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-2.944751	1.429823	-1.514928	880.542905
HLA A*3101	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.225340	1.710232	-1.515109	1680.119290
HLA B*3501	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.179193	2.663942	-1.515252	15107.529025
HLA B*1801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.307638	1.792234	-1.515404	2030.663108
HLA B*4402	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.310025	2.793482	-1.516543	20418.531745
HLA B*4801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.310466	2.793482	-1.516984	20439.309164
HLA A*0211	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.505173	2.987094	-1.518078	32001.676739
HLA A*6901	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.335700	1.817618	-1.518082	2166.207862
HLA A*0202	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.446006	2.927757	-1.518249	27925.801914
HLA A*0211	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.507255	1.987904	-1.519351	3215.546717
HLA A*6901	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-2.636916	1.117129	-1.519787	433.427336
HLA B*2705	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.236159	2.715385	-1.520774	17224.992864
HLA B*1501	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.176468	2.655688	-1.520780	15013.019016
HLA B*0801	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.340335	2.819427	-1.520908	21894.509272
HLA A*0202	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.235520	2.713138	-1.522382	17199.665102
HLA B*4403	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-2.704986	1.181912	-1.523074	506.973872
HLA A*0250	1:304-312	9	VAAFDVADV	0.706341	0.208036	-2.437506	0.914377	-1.523130	273.845815
HLA A*0301	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.083800	2.560573	-1.523227	12128.292078
HLA A*0250	1:361-369	9	AFAAAAELV	0.982214	0.345272	-2.851128	1.327486	-1.523642	709.787332
HLA B*3801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.369041	2.845028	-1.524013	23390.592526
HLA B*1502	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.724972	2.199112	-1.525860	5308.504634
HLA B*4601	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.248867	2.722320	-1.526547	17736.479246
HLA A*2301	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.514373	2.987094	-1.527279	32686.868601
HLA A*0202	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.514463	2.987094	-1.527368	32693.588920
HLA B*4801	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.372481	2.845028	-1.527452	23576.583396
HLA B*5701	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.053477	2.525744	-1.527733	11310.379934
HLA B*4402	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.372934	2.845028	-1.527906	23601.212765
HLA B*1503	1:479-487	9	RLRAARQLV	1.087444	0.249933	-2.865296	1.337377	-1.527919	733.323561
HLA A*3002	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.028798	2.500040	-1.528758	10685.582540
HLA A*0101	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.373832	2.845028	-1.528803	23650.036936
HLA B*4501	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.516236	2.987094	-1.529142	32827.397866
HLA A*0211	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.458138	2.927757	-1.530382	28716.955400
HLA A*6901	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.387558	1.854767	-1.532791	2440.944813

HLA A*0201	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.326769	2.793482	-1.533288	21221.168280
HLA B*4403	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.256304	2.722320	-1.533984	18042.783381
HLA A*3201	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.371375	1.835915	-1.535460	2351.660952
HLA B*2705	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-2.922383	1.386690	-1.535693	836.341072
HLA B*1801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-2.919296	1.383422	-1.535875	830.416944
HLA B*0802	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.356241	2.819427	-1.536814	22711.259999
HLA A*0202	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.913274	2.376452	-1.536822	8189.813759
HLA B*1517	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.602061	2.064809	-1.537252	4000.011523
HLA A*6901	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.331529	2.793482	-1.538048	21455.040856
HLA B*4001	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.331656	2.793482	-1.538175	21461.309519
HLA B*5101	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.251461	2.713138	-1.538323	17842.727650
HLA B*4001	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.383921	2.845028	-1.538892	24205.859711
HLA A*0202	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.501555	1.962632	-1.538923	3173.620355
HLA A*2501	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.884775	2.343890	-1.540884	7669.636350
HLA A*3001	1:452-460	9	RVAATGTTV	1.107071	0.312844	-2.961079	1.419915	-1.541165	914.280470
HLA A*3001	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.215094	2.673903	-1.541190	16409.432741
HLA B*5301	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.080280	2.538635	-1.541645	12030.401419
HLA B*2705	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.264788	2.722320	-1.542468	18398.716410
HLA B*0803	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.361908	2.819427	-1.542481	23009.553271
HLA A*3201	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.255648	2.713138	-1.542510	18015.570884
HLA A*6801	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.530387	2.987094	-1.543293	33914.655270
HLA A*0201	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.217260	2.673903	-1.543357	16491.486110
HLA B*1517	1:1-9	9	VTATETVRV	1.280980	0.156043	-2.980580	1.437023	-1.543558	956.269201
HLA B*5701	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.888229	2.343890	-1.544338	7730.872587
HLA A*2402	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.616642	2.072193	-1.544450	4136.586843
HLA A*2603	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.144161	1.599646	-1.544515	1393.672442
HLA A*2603	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.044662	2.500040	-1.544621	11083.117208
HLA B*0801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.338174	2.793482	-1.544692	21785.808884
HLA B*5101	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.473377	2.927757	-1.545621	29742.478300
HLA A*0202	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.483257	1.937546	-1.545711	3042.686333
HLA A*0201	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.391892	2.845028	-1.546864	24654.279465
HLA B*1503	1:412-420	9	AALAALTSV	1.136579	0.168474	-2.852171	1.305053	-1.547119	711.494284
HLA B*1509	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.269449	2.722320	-1.547129	18597.257468
HLA A*0201	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.086610	2.538635	-1.547974	12207.019303
HLA B*3901	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.262396	1.714405	-1.547992	1829.768706
HLA A*3001	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.270570	2.722320	-1.548250	18645.309983
HLA B*1801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.067057	2.518634	-1.548424	11669.633512
HLA B*4501	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.477517	2.927757	-1.549760	30027.345839
HLA B*0801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.144792	2.594821	-1.549972	13957.006408
HLA A*0219	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.369908	2.819427	-1.550481	23437.332612
HLA A*1101	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.266479	2.715385	-1.551094	18470.521375
HLA A*6801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.265640	2.713138	-1.552502	18434.883121
HLA B*5301	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.276004	2.722320	-1.553684	18880.085940
HLA A*0301	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.898078	2.343890	-1.554187	7908.198409
HLA B*4402	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.267926	2.713138	-1.554788	18532.176911
HLA A*2602	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.073871	2.518634	-1.555237	11854.158331
HLA A*3001	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-2.469779	0.914083	-1.555695	294.970534
HLA A*0202	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.558915	2.003005	-1.555910	3621.723573
HLA A*0206	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-2.470131	0.914083	-1.556048	295.209995
HLA B*1501	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.269270	2.713138	-1.556132	18589.612748
HLA A*0301	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.272160	2.715385	-1.556775	18713.723542
HLA A*3001	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.082794	2.525744	-1.557050	12100.242322
HLA A*3101	1:2-10	9	TATETVRVR	1.064509	0.662041	-3.283739	1.726550	-1.557189	1921.935981
HLA A*0216	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.376628	2.819427	-1.557201	23802.781528
HLA A*6801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.901184	2.343890	-1.557293	7964.959575
HLA B*3801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.214459	2.655688	-1.558771	16385.481470
HLA B*0802	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.352496	2.793482	-1.559014	22516.254563
HLA A*3001	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.272285	2.713138	-1.559146	18719.089988
HLA A*2902	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.920985	2.361023	-1.559962	8336.524591
HLA B*2705	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.234634	2.673903	-1.560731	17164.621648
HLA A*2902	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.060775	2.500040	-1.560734	11502.035250
HLA A*3002	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.406224	2.845028	-1.561196	25481.452086
HLA A*0206	1:432-440	9	LKDALIEGL	1.577897	0.430413	-3.570353	2.008310	-1.562042	3718.369917
HLA A*0250	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.708037	2.144780	-1.563257	5105.486274
HLA B*7301	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.550842	2.987094	-1.563748	35550.197958

HLA B*1501	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.416696	1.852642	-1.564054	2610.335163
HLA A*2603	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.082700	2.518634	-1.564066	12097.624166
HLA A*6801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.105039	2.538635	-1.566404	12736.174233
HLA B*0702	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.412603	2.845028	-1.567575	25858.481907
HLA B*1509	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.232536	2.663942	-1.568594	17081.898808
HLA B*5801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.232839	2.663942	-1.568897	17093.824010
HLA B*5801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.291245	2.722320	-1.568925	19554.426172
HLA A*0203	1:229-237	9	HQALIRIGV	1.172366	0.156389	-2.897681	1.328755	-1.568926	790.097959
HLA B*1502	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.282846	2.713138	-1.569707	19179.870350
HLA A*0250	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-2.339392	0.769405	-1.569986	218.469902
HLA B*1501	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.096576	2.525744	-1.570832	12490.394248
HLA B*1801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.226700	2.655688	-1.571012	16853.884915
HLA B*1517	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.236420	2.663942	-1.572478	17235.339539
HLA A*3002	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.091863	2.518634	-1.573229	12355.578371
HLA A*3301	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.513171	1.937546	-1.575625	3259.648919
HLA A*2301	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.779851	2.203513	-1.576338	6023.535462
HLA A*0206	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-2.448215	0.871584	-1.576631	280.682322
HLA A*0203	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.293642	2.715385	-1.578257	19662.627453
HLA B*5401	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.565437	2.987094	-1.578343	36765.207737
HLA A*0219	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.291482	2.713138	-1.578344	19565.113607
HLA B*3801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.373409	2.793482	-1.579927	23627.018211
HLA B*0803	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.373526	2.793482	-1.580045	23633.410053
HLA A*2301	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.245158	2.663942	-1.581216	17585.615699
HLA A*0301	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.255312	2.673903	-1.581409	18001.639173
HLA A*6801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.256254	2.673903	-1.582351	18040.733699
HLA A*0212	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.256379	2.673903	-1.582476	18045.907154
HLA A*3201	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.246527	2.663942	-1.582586	17641.167680
HLA B*4002	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.570564	2.987094	-1.583469	37201.769752
HLA A*0212	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.213104	1.629468	-1.583636	1633.443061
HLA A*3002	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.110029	2.525744	-1.584285	12883.364608
HLA B*0801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.297525	2.713138	-1.584387	19839.249969
HLA A*3101	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-3.454579	1.870150	-1.584430	2848.258288
HLA A*6901	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.373771	1.789240	-1.584531	2364.673491
HLA B*3901	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.379323	2.793482	-1.585841	23950.940386
HLA B*1801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.181040	2.594821	-1.586220	15171.905623
HLA B*7301	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.514355	2.927757	-1.586598	32685.453973
HLA B*2705	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-2.746722	1.159900	-1.586822	558.112603
HLA A*2301	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.072273	2.485326	-1.586947	11810.630260
HLA A*0206	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.216558	1.629468	-1.587090	1646.484866
HLA B*1517	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.104727	1.517234	-1.587493	1272.702673
HLA A*0219	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.217963	1.629468	-1.588495	1651.820057
HLA A*0206	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.303493	1.714405	-1.589089	2011.376572
HLA B*7301	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.311446	2.722320	-1.589126	20485.470737
HLA B*3901	1:432-440	9	LKDALIEGL	1.577897	0.430413	-3.597860	2.008310	-1.589550	3961.506412
HLA B*0803	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.434991	2.845028	-1.589963	27226.465620
HLA A*2403	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.075699	2.485326	-1.590372	11904.156368
HLA B*0801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.825478	2.234720	-1.590759	6690.806501
HLA B*5301	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.677978	2.086183	-1.591795	4764.066355
HLA A*0203	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-2.298905	0.706599	-1.592307	199.023926
HLA A*3101	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-3.971001	2.378256	-1.592745	9354.075529
HLA A*0250	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.580810	2.987094	-1.593715	38089.888785
HLA B*1517	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.079580	2.485326	-1.594254	12011.022269
HLA A*0202	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-2.661764	1.067176	-1.594588	458.949025
HLA B*1517	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-3.564939	1.970233	-1.594707	3672.310373
HLA A*6901	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.095566	2.500040	-1.595525	12461.372208
HLA B*3501	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-2.274438	0.678719	-1.595719	188.121205
HLA A*3101	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.269808	2.673903	-1.595905	18612.657033
HLA A*0211	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.081474	2.485326	-1.596147	12063.509126
HLA B*5101	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.441227	2.845028	-1.596198	27620.198831
HLA A*3001	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.261221	2.663942	-1.597279	18248.240969
HLA A*3101	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.312797	2.715385	-1.597412	20549.293824
HLA B*3501	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.832738	2.234720	-1.598018	6803.593834
HLA A*0301	1:206-214	9	LMKITHVLR	1.064507	0.764456	-3.428260	1.828963	-1.599298	2680.775457
HLA B*5701	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.324258	2.722320	-1.601938	21098.796814
HLA A*0101	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.258150	2.655688	-1.602462	18119.667762

HLA A*6901	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.277393	2.673903	-1.603489	18940.546793
HLA B*4601	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.198492	2.594821	-1.603672	15793.999034
HLA A*6802	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-2.475540	0.871584	-1.603955	298.909399
HLA B*4402	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.260230	2.655688	-1.604541	18206.628242
HLA A*1101	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.278861	2.673903	-1.604958	19004.696594
HLA A*2501	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.105025	2.500040	-1.604984	12735.760832
HLA A*2601	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.123638	2.518634	-1.605004	13293.444139
HLA A*0206	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.269237	2.663942	-1.605296	18588.204853
HLA A*2601	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.321467	2.715385	-1.606082	20963.630755
HLA A*0301	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-2.716268	1.109528	-1.606740	520.316748
HLA A*0101	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.322658	2.715385	-1.607273	21021.209018
HLA A*0250	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.092972	2.485326	-1.607646	12387.168256
HLA B*5701	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.281706	2.673903	-1.607803	19129.612241
HLA A*2501	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.401607	2.793482	-1.608126	25212.007929
HLA A*6802	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-2.842393	1.234017	-1.608376	695.653315
HLA B*5301	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.264118	2.655688	-1.608430	18370.370788
HLA A*0212	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.373142	1.764296	-1.608845	2361.247552
HLA B*0702	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.444923	1.835915	-1.609008	2785.627149
HLA B*5301	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.127782	2.518634	-1.609148	13420.911313
HLA B*0801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.040677	2.431527	-1.609151	10981.892787
HLA A*0203	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.986132	2.376452	-1.609679	9685.712097
HLA A*0219	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.283741	2.673903	-1.609838	19219.444050
HLA B*1502	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.845957	2.234720	-1.611237	7013.851741
HLA A*2402	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-3.988744	2.376452	-1.612292	9744.154986
HLA A*2602	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.731288	2.118146	-1.613142	5386.263759
HLA B*5401	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.541416	2.927757	-1.613659	34786.912882
HLA A*3001	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.269820	2.655688	-1.614132	18613.160502
HLA A*3002	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.850862	2.235159	-1.615704	7093.528308
HLA A*0201	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-3.670929	2.055046	-1.615883	4687.371194
HLA A*0101	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.338613	2.722320	-1.616293	21807.859633
HLA B*3901	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.409037	1.792274	-1.616763	2564.702249
HLA A*3001	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.145013	2.527183	-1.617830	13964.105764
HLA A*0211	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.118050	2.500040	-1.618010	13123.523087
HLA B*3801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.293038	2.673903	-1.619135	19635.308681
HLA B*4601	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.293226	2.673903	-1.619322	19643.808508
HLA B*2705	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.332704	2.713138	-1.619566	21513.154113
HLA A*3101	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.145478	2.525744	-1.619734	13979.071542
HLA B*1509	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.413397	2.793482	-1.619915	25905.808497
HLA A*6901	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.679294	2.058588	-1.620705	4778.521159
HLA A*0250	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.549529	2.927757	-1.621772	35442.852004
HLA A*0203	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-2.234919	0.612666	-1.622254	171.758965
HLA B*5701	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.338829	2.715385	-1.623444	21818.716320
HLA A*0203	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.108784	2.485326	-1.623458	12846.477801
HLA B*5801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.338921	2.715385	-1.623536	21823.320243
HLA A*2603	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.769612	2.144780	-1.624833	5883.183789
HLA B*0801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-3.749026	2.123741	-1.625285	5610.818603
HLA B*0802	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.340800	2.715385	-1.625416	21917.974317
HLA A*6802	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.419003	2.793482	-1.625521	26242.368038
HLA A*0211	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-3.987518	2.361023	-1.626495	9716.676678
HLA B*4801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.349122	2.722320	-1.626802	22342.012455
HLA B*3901	1:229-237	9	HQALIRIGV	1.172366	0.156389	-2.956507	1.328755	-1.627752	904.705739
HLA B*3901	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.283492	2.655688	-1.627804	19208.425853
HLA A*0211	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.341012	2.713138	-1.627874	21928.648558
HLA B*0702	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.343303	2.715385	-1.627918	22044.619912
HLA B*3501	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-2.595782	0.967687	-1.628094	394.258908
HLA A*0301	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.351263	2.722320	-1.628943	22452.394811
HLA A*6802	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.342368	2.713138	-1.629229	21997.205912
HLA A*3002	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.342661	2.713138	-1.629523	22012.086249
HLA B*3901	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-2.861161	1.230828	-1.630332	726.374425
HLA B*4501	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.346056	2.715385	-1.630671	22184.835442
HLA A*2403	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.353262	2.722320	-1.630942	22555.999804
HLA B*4801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.346427	2.715385	-1.631043	22203.806314
HLA A*2301	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.450923	2.819427	-1.631496	28243.799852
HLA A*2603	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.158800	2.527183	-1.631617	14414.510787
HLA A*2501	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.117308	2.485326	-1.631982	13101.107263

HLA B*5801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.118013	2.485326	-1.632687	13122.387188
HLA A*0101	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.346265	2.713138	-1.633127	22195.519571
HLA A*6801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.836709	2.203513	-1.633196	6866.082360
HLA A*2902	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.425530	1.792274	-1.633256	2663.976180
HLA A*2301	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.159411	2.525744	-1.633666	14434.800088
HLA A*6901	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.173165	2.538635	-1.634529	14899.258624
HLA B*0803	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.153443	2.518634	-1.634809	14237.806348
HLA B*3901	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.426230	1.789240	-1.636991	2668.274365
HLA A*2603	1:23-31	9	LVRTALFNW	1.553174	0.453372	-3.643605	2.006546	-1.637059	4401.541857
HLA A*3301	1:86-94	9	RQSQRAEIY	1.602945	1.384149	-4.625603	2.987094	-1.638508	42228.206456
HLA B*0803	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.303709	2.663942	-1.639767	20123.758367
HLA B*4403	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.139858	2.500040	-1.639818	13799.341401
HLA A*3301	1:181-189	9	SVPDFALTR	1.418756	0.707454	-3.766041	2.126210	-1.639831	5835.004545
HLA A*8001	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.353727	2.713138	-1.640589	22580.173790
HLA A*0201	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.354987	2.713138	-1.641848	22645.744555
HLA A*3001	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.434223	1.792234	-1.641990	2717.837157
HLA B*0803	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.315905	2.673903	-1.642002	20696.898537
HLA A*2602	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.287301	1.645215	-1.642086	1937.763346
HLA B*4002	1:54-62	9	SEESYLALL	1.352077	0.257378	-3.251880	1.609455	-1.642425	1785.993610
HLA B*1801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-3.986630	2.343890	-1.642739	9696.826979
HLA B*4001	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.359488	2.715385	-1.644103	22881.696317
HLA A*3001	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.144722	2.500040	-1.644681	13954.741416
HLA A*0212	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.360266	2.715385	-1.644881	22922.706667
HLA B*4402	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.144999	2.500040	-1.644959	13963.652506
HLA B*5801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.171229	2.525744	-1.645484	14832.989290
HLA A*0212	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.367984	2.722320	-1.645664	23333.718552
HLA A*3001	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.241119	2.594821	-1.646298	17422.834590
HLA B*1503	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.845482	2.199112	-1.646370	7006.191207
HLA A*0301	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.360773	2.713138	-1.647635	22949.508332
HLA A*2902	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.610811	1.962632	-1.648179	4081.414702
HLA A*1101	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.493444	2.845028	-1.648416	31148.999718
HLA A*0202	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-2.613562	0.963515	-1.650047	410.735667
HLA B*4801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.363917	2.713138	-1.650779	23116.229452
HLA A*2403	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.189602	2.538635	-1.650966	15473.966627
HLA A*2601	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.373827	2.722320	-1.651507	23649.781049
HLA A*6901	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-2.951602	1.299885	-1.651717	894.543822
HLA A*0101	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.316335	2.663942	-1.652393	20717.398813
HLA A*0201	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.615759	1.962632	-1.653127	4128.181088
HLA A*2301	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.447155	2.793482	-1.653673	27999.775634
HLA B*0702	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.656969	2.003005	-1.653964	4539.089091
HLA B*1509	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.369833	2.715385	-1.654448	23433.275576
HLA A*0206	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.015491	2.361023	-1.654468	10363.124610
HLA B*0802	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.367913	2.713138	-1.654775	23329.931875
HLA B*1503	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.799803	2.144780	-1.655023	6306.716342
HLA B*4402	1:366-374	9	AELVQTRIV	1.123749	0.213984	-2.992765	1.337733	-1.655031	983.477883
HLA B*3901	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-3.692855	2.037348	-1.655507	4930.088789
HLA B*5301	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.501202	2.845028	-1.656174	31710.428035
HLA B*0702	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.330279	2.673903	-1.656376	21393.380712
HLA A*3201	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.183751	2.527183	-1.656568	15266.920294
HLA B*1509	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.330658	2.673903	-1.656754	21412.022296
HLA B*0802	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.379247	2.722320	-1.656927	23946.794443
HLA A*3001	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-3.363466	1.705831	-1.657635	2309.225483
HLA A*0301	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.407214	1.749555	-1.657658	2553.958007
HLA B*0702	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.511047	1.852642	-1.658404	3243.746394
HLA A*2602	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.037679	2.378256	-1.659424	10906.345629
HLA A*6802	1:304-312	9	VAAFDVADV	0.706341	0.208036	-2.573828	0.914377	-1.659451	374.824463
HLA A*3101	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.824670	2.164532	-1.660138	6678.366477
HLA A*6802	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.255150	2.594821	-1.660329	17994.920733
HLA B*5701	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.325592	2.663942	-1.661650	21163.729268
HLA A*6901	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.189494	2.527183	-1.662310	15470.116333
HLA A*0203	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.257290	2.594821	-1.662470	18083.825963
HLA B*0702	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.326530	2.663942	-1.662588	21209.461486
HLA A*2403	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.455021	1.792274	-1.662747	2851.156609
HLA B*2705	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-2.920541	1.257536	-1.663005	832.801366
HLA B*4402	1:54-62	9	SEESYLALL	1.352077	0.257378	-3.272504	1.609455	-1.663049	1872.852953

HLA A*8001	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.721706	2.058588	-1.663118	5268.735741
HLA A*0219	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.041908	2.378256	-1.663653	11013.068225
HLA A*0203	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-2.768257	1.104589	-1.663668	586.485405
HLA B*0803	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.042392	2.378256	-1.664137	11025.348439
HLA B*5701	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.259050	2.594821	-1.664230	18157.250410
HLA A*2602	1:23-31	9	LVRTALFNW	1.553174	0.453372	-3.671221	2.006546	-1.664675	4690.516661
HLA A*0211	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-2.782143	1.117129	-1.665014	605.539761
HLA A*3201	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.380453	2.715385	-1.665068	24013.345644
HLA B*4801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.339081	2.673903	-1.665177	21831.349918
HLA A*2603	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.260396	2.594821	-1.665576	18213.622790
HLA B*4002	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.485707	2.819427	-1.666280	30599.001203
HLA A*0212	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-2.657197	0.990658	-1.666539	454.147631
HLA B*4402	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.340457	2.673903	-1.666554	21900.669375
HLA A*6901	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.389576	2.722320	-1.667256	24523.119946
HLA A*2403	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.383178	2.715385	-1.667793	24164.514540
HLA B*5801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.325148	2.655688	-1.669460	21142.101068
HLA A*0219	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.386127	2.715385	-1.670742	24329.135565
HLA A*0216	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-2.808354	1.137355	-1.670998	643.211084
HLA A*3101	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.789903	2.118146	-1.671757	6164.566875
HLA A*1101	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.421433	1.749555	-1.671877	2638.960170
HLA A*2602	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.199404	2.527183	-1.672220	15827.186040
HLA A*0219	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.737570	2.064809	-1.672761	5464.747995
HLA B*5101	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.395102	2.722320	-1.672782	24837.147192
HLA B*4001	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.395193	2.722320	-1.672873	24842.388027
HLA B*1501	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.907945	2.234720	-1.673226	8089.941736
HLA B*4001	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.347139	2.673903	-1.673236	22240.232560
HLA A*0201	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.395623	2.722320	-1.673303	24866.994410
HLA A*0201	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.388948	2.715385	-1.673564	24487.723331
HLA A*2902	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.199418	2.525744	-1.673673	15827.699789
HLA B*4801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.034808	2.361023	-1.673785	10834.482838
HLA A*6802	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.818815	2.144780	-1.674035	6588.936631
HLA B*1501	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.338019	2.663942	-1.674077	21778.031591
HLA A*2501	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.929641	2.255532	-1.674109	8504.338503
HLA B*4501	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-3.317590	1.643417	-1.674173	2077.735678
HLA B*5101	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.493818	2.819427	-1.674391	31175.804754
HLA A*6901	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.389938	2.715385	-1.674553	24543.559233
HLA B*1801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-3.874545	2.199112	-1.675433	7491.091728
HLA A*8001	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.161149	2.485326	-1.675823	14492.703007
HLA A*0202	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-2.780489	1.104589	-1.675900	603.237912
HLA B*0803	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.389143	2.713138	-1.676005	24498.721297
HLA B*1801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.214835	2.538635	-1.676200	16399.670592
HLA B*0802	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.350476	2.673903	-1.676572	22411.740897
HLA A*3101	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.398945	2.722320	-1.676626	25057.945973
HLA A*3101	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-2.403091	0.726109	-1.676982	252.982717
HLA B*0801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.177070	2.500040	-1.677029	15033.825426
HLA A*2402	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-3.912555	2.235159	-1.677396	8176.267344
HLA B*3901	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-3.803196	2.123741	-1.679455	6356.176590
HLA A*2402	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.474296	2.793482	-1.680814	29805.458159
HLA A*0250	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-2.743165	1.062125	-1.681039	553.560011
HLA B*4801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.345323	2.663942	-1.681381	22147.421566
HLA A*0216	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.394989	2.713138	-1.681851	24830.698451
HLA B*0802	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.347480	2.663942	-1.683538	22257.685397
HLA B*1801	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.357757	2.673903	-1.683853	22790.646606
HLA B*4801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.372808	1.688566	-1.684242	2359.434328
HLA A*0212	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.397703	2.713138	-1.684564	24986.336873
HLA A*3301	1:2-10	9	TATETVRVR	1.064509	0.662041	-3.411744	1.726550	-1.685193	2580.735877
HLA A*3301	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.613432	2.927757	-1.685676	41061.263018
HLA A*2402	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.211894	2.525744	-1.686149	16288.967979
HLA B*3801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.402691	2.715385	-1.687306	25274.964113
HLA B*5101	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.480870	2.793482	-1.687388	30260.051378
HLA A*0201	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.452080	1.764296	-1.687783	2831.910461
HLA B*4403	1:377-385	9	GDAWELLKF	1.384021	0.916265	-3.988213	2.300286	-1.687927	9732.248722
HLA B*0801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.410994	2.722320	-1.688674	25762.833551
HLA A*6801	1:35-43	9	RHTGGTFVF	1.667665	1.260092	-4.616653	2.927757	-1.688897	41366.944896
HLA A*0201	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.108862	1.419915	-1.688947	1284.878463

HLA B*0801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.405066	2.715385	-1.689681	25413.581681
HLA A*2501	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.208534	2.518634	-1.689900	16163.440394
HLA A*0206	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.693414	2.003005	-1.690409	4936.440631
HLA A*6801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-2.867175	1.176703	-1.690472	736.504198
HLA A*0219	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.413381	2.722320	-1.691061	25904.827483
HLA B*4402	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.355010	2.663942	-1.691068	22646.969697
HLA B*4001	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.404681	2.713138	-1.691542	25391.044196
HLA B*1501	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.764317	2.072193	-1.692124	5811.880508
HLA B*0702	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-2.378962	0.686428	-1.692533	239.310438
HLA A*0301	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.348450	2.655688	-1.692762	22307.470989
HLA A*0211	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-2.894269	1.200757	-1.693512	783.915926
HLA B*1501	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.486405	1.792274	-1.694131	3064.823674
HLA B*0801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-3.469903	1.775750	-1.694153	2950.548182
HLA A*0206	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-2.995170	1.300706	-1.694465	988.941200
HLA B*4801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.682447	1.987904	-1.694543	4813.339803
HLA A*0219	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.233293	2.538635	-1.694657	17111.681140
HLA A*6802	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.180086	2.485326	-1.694760	15138.618392
HLA A*6802	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.417145	2.722320	-1.694825	26130.311041
HLA A*2501	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.417490	2.722320	-1.695170	26151.099532
HLA B*5101	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.222870	2.527183	-1.695687	16705.918697
HLA B*0702	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.418578	2.722320	-1.696258	26216.684352
HLA A*8001	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.370183	2.673903	-1.696280	23452.172133
HLA B*1509	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.409495	2.713138	-1.696356	25674.066171
HLA A*0203	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.419478	2.722320	-1.697158	26271.061310
HLA A*0219	1:227-235	9	ALHQALIRI	1.220562	0.336437	-3.254737	1.556999	-1.697738	1797.781366
HLA B*1501	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-2.942119	1.241782	-1.700337	875.223760
HLA A*3201	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.422682	2.722320	-1.700362	26465.634809
HLA A*0301	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.364970	2.663942	-1.701028	23172.322594
HLA B*3501	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.261886	2.560573	-1.701313	18276.200398
HLA A*2402	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.296825	2.594821	-1.702005	19807.291950
HLA B*5801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.416612	1.714405	-1.702207	2609.826834
HLA B*0801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.366551	2.663942	-1.702609	23256.843441
HLA A*2402	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.064191	2.361023	-1.703168	11592.866786
HLA B*1502	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.065201	2.361023	-1.704178	11619.866111
HLA A*2301	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.231592	2.527183	-1.704408	17044.789880
HLA B*1501	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.849429	2.144780	-1.704649	7070.158017
HLA A*1101	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.265683	2.560573	-1.705110	18436.678360
HLA B*0801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.597400	1.892220	-1.705180	3957.308102
HLA A*0206	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.605665	1.900474	-1.705192	4033.344820
HLA A*0203	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.418352	2.713138	-1.705214	26203.072269
HLA B*5401	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.525200	2.819427	-1.705773	33511.953450
HLA A*3002	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-3.567406	1.861442	-1.705964	3693.229864
HLA A*2603	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.379959	2.673903	-1.706056	23986.080132
HLA A*2601	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.909764	2.203513	-1.706250	8123.887398
HLA B*4001	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.370622	2.663942	-1.706681	23475.909511
HLA A*0212	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.245639	2.538635	-1.707004	17605.129445
HLA A*1101	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.363431	2.655688	-1.707742	23090.357300
HLA A*3001	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.051941	2.343890	-1.708050	11270.433754
HLA A*0216	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.696050	1.987904	-1.708146	4966.495433
HLA A*0216	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.423589	2.715385	-1.708204	26520.958547
HLA B*3901	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.431448	2.722320	-1.709128	27005.252609
HLA B*4601	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.364883	2.655688	-1.709194	23167.684750
HLA A*0211	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.424757	2.715385	-1.709372	26592.361792
HLA A*2602	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.431758	2.722320	-1.709438	27024.544092
HLA A*0206	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.431768	2.722320	-1.709448	27025.128897
HLA A*3001	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-2.633345	0.923460	-1.709885	429.877863
HLA B*1503	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-3.747790	2.037348	-1.710442	5594.875143
HLA A*0203	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.230048	2.518634	-1.711414	16984.315168
HLA A*0206	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.230191	2.518634	-1.711558	16989.920972
HLA A*6901	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.376405	2.663942	-1.712463	23790.551482
HLA B*5801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.548916	1.835915	-1.713001	3539.287903
HLA A*0101	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.387266	2.673903	-1.713363	24393.054078
HLA B*4501	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.213787	2.500040	-1.713747	16360.148992
HLA A*1101	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.436309	2.722320	-1.713989	27309.222039
HLA B*0803	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.436601	2.722320	-1.714281	27327.547928

HLA B*4001	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.370005	2.655688	-1.714316	23442.531717
HLA A*6802	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-1.642708	-0.072551	-1.715259	43.924641
HLA B*3501	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.241067	2.525744	-1.715323	17420.761090
HLA B*4601	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.379663	2.663942	-1.715722	23969.735687
HLA A*2902	1:21-29	9	VGLVRTALF	1.226065	1.008655	-3.950983	2.234720	-1.716263	8932.710518
HLA B*1517	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.608316	1.891829	-1.716486	4058.032973
HLA B*5401	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.561784	2.845028	-1.716755	36457.222188
HLA A*0216	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.439166	2.722320	-1.716846	27489.465924
HLA A*3101	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.381400	2.663942	-1.717458	24065.756300
HLA B*3801	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.440649	2.722320	-1.718329	27583.465415
HLA A*2402	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.096609	2.378256	-1.718353	12491.340287
HLA A*6801	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.512271	2.793482	-1.718789	32528.986191
HLA A*6901	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.374943	2.655688	-1.719255	23710.631979
HLA A*3001	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.837508	2.118146	-1.719362	6878.723195
HLA A*0201	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.384943	2.663942	-1.721001	24262.890483
HLA A*1101	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.206546	2.485326	-1.721220	16089.633134
HLA A*0206	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.247011	2.525744	-1.721267	17660.838612
HLA B*3901	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.221682	2.500040	-1.721641	16660.250385
HLA A*0201	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-2.497512	0.775701	-1.721811	314.421297
HLA A*2601	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.386371	2.663942	-1.722429	24342.827681
HLA A*2603	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.511775	1.789240	-1.722535	3249.190934
HLA A*3101	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.378270	2.655688	-1.722582	23892.962447
HLA B*4601	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.283165	2.560573	-1.722592	19193.987035
HLA B*2705	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.051610	1.328755	-1.722855	1126.185157
HLA A*0250	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.542461	2.819427	-1.723034	34870.759805
HLA A*0219	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.143414	1.419915	-1.723499	1391.276906
HLA A*1101	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.249323	2.525744	-1.723579	17755.103780
HLA A*6901	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.318471	2.594821	-1.723650	20819.529383
HLA B*3901	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.497782	1.773509	-1.724273	3146.166483
HLA A*3001	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.263274	2.538635	-1.724639	18334.727392
HLA B*4403	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.570080	2.845028	-1.725051	37160.333811
HLA B*4801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.380791	2.655688	-1.725103	24032.059906
HLA B*1502	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.928738	2.203513	-1.725225	8486.689950
HLA A*3201	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.326833	1.601532	-1.725301	2122.429001
HLA B*4801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.320289	2.594821	-1.725469	20906.888815
HLA B*1503	1:94-102	9	YRDVLARLL	1.616307	0.425031	-3.766845	2.041338	-1.725507	5845.810359
HLA A*0212	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.322176	2.594821	-1.727356	20997.908846
HLA B*0702	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.253881	2.525744	-1.728137	17942.428160
HLA B*5301	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.402167	2.673903	-1.728263	25244.490648
HLA B*4801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-3.761934	2.032901	-1.729033	5780.085982
HLA A*0101	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.324025	2.594821	-1.729205	21087.499766
HLA A*2501	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.105866	2.376452	-1.729414	12760.450595
HLA A*6802	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.445280	2.715385	-1.729895	27879.158584
HLA B*0801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.522230	1.792234	-1.729997	3328.361126
HLA B*1517	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.385755	2.655688	-1.730067	24308.348818
HLA A*0211	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.190126	1.459786	-1.730340	1549.266168
HLA B*4403	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-2.952889	1.222401	-1.730488	897.199739
HLA A*0212	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.030930	1.299885	-1.731045	1073.815410
HLA A*0216	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.109611	2.378256	-1.731356	12870.964412
HLA B*5101	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.251008	2.518634	-1.732374	17824.107627
HLA A*2601	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.258242	2.525744	-1.732497	18123.491156
HLA B*0803	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.327319	2.594821	-1.732499	21248.049467
HLA A*6901	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-2.688022	0.954860	-1.733162	487.553520
HLA A*2602	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.507758	1.773509	-1.734249	3219.271563
HLA B*0802	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.389982	2.655688	-1.734294	24546.082143
HLA B*3901	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.449948	2.715385	-1.734563	28180.460712
HLA A*2501	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.938183	2.203513	-1.734670	8673.277979
HLA A*0212	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.398706	2.663942	-1.734764	25044.122595
HLA A*3301	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-3.499234	1.764418	-1.734815	3156.702701
HLA A*3101	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.329772	2.594821	-1.734951	21368.396376
HLA A*0301	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.330366	2.594821	-1.735546	21397.663366
HLA B*3901	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.112252	2.376452	-1.735800	12949.467519
HLA A*6802	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.409713	2.673903	-1.735810	25686.986549
HLA A*2501	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.399841	2.663942	-1.735899	25109.647868
HLA A*0219	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.391789	2.655688	-1.736101	24648.411579

HLA B*2705	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.332063	2.594821	-1.737242	21481.404793
HLA B*4402	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.426315	1.688566	-1.737749	2668.794078
HLA A*0201	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.394101	2.655688	-1.738413	24779.973092
HLA B*4402	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.266059	2.527183	-1.738875	18452.643731
HLA B*0802	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.333808	2.594821	-1.738988	21567.924090
HLA B*0802	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.117317	2.378256	-1.739062	13101.390768
HLA A*2601	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-3.995177	2.255532	-1.739646	9889.562352
HLA A*0202	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.462062	2.722320	-1.739742	28977.574672
HLA B*3901	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.414161	2.673903	-1.740258	25951.396517
HLA A*2601	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.084655	2.343890	-1.740764	12152.198637
HLA A*2403	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.397395	2.655688	-1.741707	24968.635442
HLA B*5401	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-2.732489	0.990658	-1.741831	540.117998
HLA A*0203	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.594736	1.852642	-1.742093	3933.105068
HLA B*1502	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.406443	2.663942	-1.742501	25494.275531
HLA A*0203	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.490376	1.747156	-1.743220	3092.972961
HLA B*1503	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.451610	1.708081	-1.743529	2828.848054
HLA A*2501	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.399725	2.655688	-1.744037	25102.992570
HLA A*3101	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.271568	2.527183	-1.744385	18688.228654
HLA A*0216	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-2.469732	0.725139	-1.744593	294.938620
HLA A*6901	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-2.357276	0.612666	-1.744610	227.654319
HLA A*3101	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.088517	2.343890	-1.744627	12260.760615
HLA A*8001	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.339621	2.594821	-1.744800	21858.531017
HLA B*1501	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.949066	2.203513	-1.745553	8893.364250
HLA A*0203	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.409748	2.663942	-1.745807	25689.071090
HLA B*7301	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.591079	2.845028	-1.746051	39001.319782
HLA B*4403	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.539675	2.793482	-1.746193	34647.740753
HLA B*4002	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-2.595133	0.848752	-1.746381	393.670668
HLA B*3901	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.461216	2.713138	-1.748078	28921.194024
HLA B*0801	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.404058	2.655688	-1.748370	25354.669152
HLA A*2603	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.404187	2.655688	-1.748499	25362.214401
HLA B*0702	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.462945	2.713138	-1.749807	29036.578477
HLA B*7301	1:478-486	9	QRLRAARQL	1.551442	0.535207	-3.838429	2.086649	-1.751780	6893.326220
HLA B*4002	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-2.933868	1.181912	-1.751956	858.751894
HLA B*0803	1:206-214	9	LMKITHVLR	1.064507	0.764456	-3.581729	1.828963	-1.752766	3817.058353
HLA A*0219	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.417699	2.663942	-1.753757	26163.693799
HLA B*3501	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.009344	2.255532	-1.753813	10217.495792
HLA B*1501	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-2.544243	0.790220	-1.754024	350.141197
HLA A*1101	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.467212	2.713138	-1.754074	29323.250116
HLA B*5301	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.548131	2.793482	-1.754649	35328.948992
HLA B*1509	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.273330	2.518634	-1.754697	18764.208625
HLA B*5101	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.470478	2.715385	-1.755093	29544.584653
HLA B*0802	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.281051	2.525744	-1.755306	19100.760566
HLA A*0216	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.011177	2.255532	-1.755646	10260.701792
HLA B*5701	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.411358	2.655688	-1.755670	25784.445592
HLA B*5401	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.550154	2.793482	-1.756672	35493.892065
HLA A*0219	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.062004	1.305053	-1.756951	1153.463671
HLA A*1101	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.420904	2.663942	-1.756962	26357.472093
HLA A*3201	1:227-235	9	ALHQALIRI	1.220562	0.336437	-3.314390	1.556999	-1.757392	2062.482626
HLA A*3101	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.257612	2.500040	-1.757572	18097.233846
HLA B*0702	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.413982	2.655688	-1.758294	25940.728752
HLA A*3001	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-3.770703	2.012396	-1.758307	5897.970240
HLA B*1503	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.059092	2.300286	-1.758806	11457.568515
HLA B*3901	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.923964	2.164532	-1.759432	8393.907568
HLA B*0801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.285935	2.525744	-1.760191	19316.802519
HLA A*0216	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.424437	2.663942	-1.760496	26572.803792
HLA A*0206	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.287977	2.527183	-1.760794	19407.828346
HLA A*2902	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-3.825854	2.064809	-1.761045	6696.600452
HLA A*0202	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.508378	1.747156	-1.761222	3223.872647
HLA A*6901	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.246556	2.485326	-1.761229	17642.312959
HLA A*2301	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.483783	2.722320	-1.761463	30463.726135
HLA B*7301	1:25-33	9	RTALFNWAY	1.425350	1.394077	-4.580984	2.819427	-1.761557	38105.140431
HLA B*1503	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.471961	1.710232	-1.761729	2964.564201
HLA A*3001	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.653797	1.891829	-1.761967	4506.059294
HLA B*4801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.663294	1.900474	-1.762820	4605.677459
HLA A*0250	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.123863	2.361023	-1.762840	13300.349874

HLA B*1502	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.510154	1.747156	-1.762998	3237.084886
HLA B*4402	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.323809	2.560573	-1.763236	21077.006922
HLA B*0702	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.139915	2.376452	-1.763463	13801.133187
HLA A*6901	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.535463	1.771882	-1.763580	3431.332001
HLA A*0201	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.200858	1.437023	-1.763836	1588.029202
HLA A*0203	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.419821	2.655688	-1.764132	26291.819542
HLA B*4001	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.358988	2.594821	-1.764167	22855.344778
HLA A*6802	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.072276	1.307776	-1.764500	1181.070628
HLA A*0211	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.486922	2.722320	-1.764602	30684.703733
HLA B*5101	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.438626	2.673903	-1.764723	27455.282753
HLA B*5801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.304748	2.538635	-1.766112	20171.935291
HLA A*0216	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.729596	1.962632	-1.766964	5365.324422
HLA B*1801	1:54-62	9	SEESYLALL	1.352077	0.257378	-3.376520	1.609455	-1.767065	2379.688326
HLA B*1503	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.853597	2.086183	-1.767414	7138.337980
HLA A*0301	1:181-189	9	SVPDFALTR	1.418756	0.707454	-3.893844	2.126210	-1.767634	7831.478948
HLA A*0206	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-3.353420	1.585411	-1.768009	2256.420016
HLA B*3801	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.481184	2.713138	-1.768046	30281.995603
HLA A*3101	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.328853	2.560573	-1.768280	21323.244291
HLA A*0219	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.363447	2.594821	-1.768627	23091.231730
HLA B*5801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.329260	2.560573	-1.768687	21343.210288
HLA B*4002	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.484718	2.715385	-1.769333	30529.389342
HLA A*2902	1:311-319	9	DVNSSPARF	1.154757	1.048756	-3.972979	2.203513	-1.769466	9396.781720
HLA B*4001	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.288872	2.518634	-1.770238	19447.872391
HLA A*0201	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.365188	2.594821	-1.770368	23183.983979
HLA A*6802	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.426514	2.655688	-1.770826	26700.188383
HLA B*0801	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.401208	1.629468	-1.771741	2518.885744
HLA A*0216	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.258059	2.485326	-1.772732	18115.845175
HLA B*1503	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-3.764025	1.990887	-1.773138	5807.983054
HLA A*0212	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.429775	2.655688	-1.774087	26901.432745
HLA A*2301	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.368947	2.594821	-1.774127	23385.531454
HLA B*1503	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.629113	1.854767	-1.774347	4257.093734
HLA A*6802	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.438645	2.663942	-1.774703	27456.471019
HLA A*0101	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.274907	2.500040	-1.774866	18832.447150
HLA B*1509	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.260316	2.485326	-1.774990	18210.272953
HLA B*2705	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.302267	2.527183	-1.775083	20057.024739
HLA A*2902	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.312248	1.536595	-1.775652	2052.331772
HLA B*2705	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.295500	2.518634	-1.776866	19746.948493
HLA B*0801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.541205	1.764296	-1.776908	3477.001531
HLA B*3501	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.155713	2.378256	-1.777457	14312.407214
HLA B*3501	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.566866	1.789240	-1.777626	3688.637330
HLA B*1502	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-3.622455	1.843794	-1.778661	4192.323352
HLA A*6802	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.679143	1.900474	-1.778669	4776.866964
HLA B*4002	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.572236	2.793482	-1.778755	37345.341387
HLA A*0202	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.278955	2.500040	-1.778914	19008.809571
HLA B*4403	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.434839	2.655688	-1.779150	27216.893312
HLA B*3901	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.571612	1.792234	-1.779378	3729.167724
HLA B*4801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.306585	2.527183	-1.779402	20257.454103
HLA A*0216	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.435607	2.655688	-1.779919	27265.083528
HLA A*3001	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-1.477591	-0.303590	-1.781181	30.032475
HLA B*5301	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.497405	2.715385	-1.782021	31434.411674
HLA B*0702	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.342659	2.560573	-1.782086	22011.967166
HLA B*4001	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.282160	2.500040	-1.782119	19149.596064
HLA B*4001	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.308354	2.525744	-1.782610	20340.144121
HLA A*0212	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.282747	2.500040	-1.782707	19175.512884
HLA A*6801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.038497	2.255532	-1.782965	10926.897708
HLA B*4403	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.472731	1.688566	-1.784165	2969.829323
HLA A*0206	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-3.817166	2.032901	-1.784265	6563.961004
HLA A*3001	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.019466	2.235159	-1.784307	10458.419283
HLA B*4601	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.272047	2.485326	-1.786721	18708.864693
HLA B*3801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.305495	2.518634	-1.786861	20206.667842
HLA A*0101	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.348121	2.560573	-1.787548	22290.582054
HLA A*0101	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.273192	2.485326	-1.787865	18758.220356
HLA B*5401	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-2.900975	1.112802	-1.788173	796.113370
HLA A*6802	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.314319	2.525744	-1.788575	20621.458012
HLA A*2601	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.349376	2.560573	-1.788803	22355.069992

HLA B*3801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.315264	2.525744	-1.789519	20666.353854
HLA A*8001	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.308222	2.518634	-1.789589	20333.982931
HLA B*5401	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.512005	2.722320	-1.789685	32509.106730
HLA A*3001	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.275635	2.485326	-1.790309	18864.056898
HLA B*2705	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.316354	2.525744	-1.790610	20718.295463
HLA A*0202	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.506225	2.715385	-1.790841	32079.331039
HLA A*3101	1:118-126	9	EARHVAAGR	0.989892	0.619354	-3.400466	1.609246	-1.791220	2514.583325
HLA A*0202	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.455192	2.663942	-1.791250	28522.798870
HLA B*4002	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.636810	2.845028	-1.791781	43332.094304
HLA A*2603	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.455742	2.663942	-1.791800	28558.929146
HLA A*0250	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.507334	2.715385	-1.791949	32161.349244
HLA A*6801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.317778	2.525744	-1.792033	20786.329635
HLA A*1101	1:206-214	9	LMKITHVLR	1.064507	0.764456	-3.621050	1.828963	-1.792087	4178.782624
HLA B*5301	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.136179	2.343890	-1.792289	13682.928762
HLA B*1501	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.310001	1.517234	-1.792767	2041.744812
HLA B*1503	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-3.916982	2.123741	-1.793241	8260.027879
HLA B*5101	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.457340	2.663942	-1.793398	28664.183063
HLA B*2705	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.353986	2.560573	-1.793413	22593.614975
HLA B*5401	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.506608	2.713138	-1.793470	32107.631451
HLA B*5101	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.450141	2.655688	-1.794452	28192.964645
HLA A*2902	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.321647	2.527183	-1.794464	20972.365215
HLA B*0802	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.321666	2.527183	-1.794483	20973.272900
HLA A*0250	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.331885	1.536595	-1.795289	2147.259654
HLA A*6901	1:60-68	9	ALLDALRWL	1.537707	0.516755	-3.850233	2.054462	-1.795771	7083.251206
HLA B*0803	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.322547	2.525744	-1.796803	21015.864744
HLA B*4402	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.323506	2.525744	-1.797761	21062.302923
HLA A*6901	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.323760	2.525744	-1.798015	21074.612549
HLA B*5701	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.358711	2.560573	-1.798137	22840.759338
HLA A*3001	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-3.963417	2.164532	-1.798884	9192.142212
HLA A*3301	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.592585	2.793482	-1.799104	39136.800949
HLA A*2601	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.299363	2.500040	-1.799322	19923.358363
HLA B*4402	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.394251	2.594821	-1.799431	24788.554220
HLA B*2705	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.338317	2.538635	-1.799682	21792.999458
HLA A*0203	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.565701	1.764296	-1.801404	3678.752858
HLA B*0803	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.458289	2.655688	-1.802600	28726.899876
HLA B*0801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.179607	2.376452	-1.803155	15121.920366
HLA A*0301	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.328950	2.525744	-1.803205	21327.974427
HLA B*4402	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.235428	2.431527	-1.803902	17196.036601
HLA B*5101	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.180533	2.376452	-1.804081	15154.187059
HLA A*6901	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.364991	2.560573	-1.804418	23173.450859
HLA A*6901	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.323059	2.518634	-1.804426	21040.664548
HLA B*0802	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.304567	2.500040	-1.804526	20163.534190
HLA B*1517	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.569032	1.764296	-1.804736	3707.081911
HLA B*5801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.008517	2.203513	-1.805004	10198.057323
HLA A*0211	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-2.185792	0.380458	-1.805334	153.388105
HLA B*4601	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.166506	2.361023	-1.805483	14672.570952
HLA A*0206	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-2.773182	0.967578	-1.805603	593.173485
HLA B*4601	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.923814	2.118146	-1.805668	8391.001824
HLA A*2301	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.521401	2.715385	-1.806016	33220.076395
HLA B*4501	1:169-177	9	DLVRGPVTF	1.778828	1.066200	-4.651367	2.845028	-1.806339	44809.189516
HLA A*3201	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.345603	2.538635	-1.806967	22161.684153
HLA B*1801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.367775	2.560573	-1.807202	23322.486535
HLA B*5401	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.335035	2.527183	-1.807851	21628.917172
HLA B*3501	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-3.655470	1.846931	-1.808539	4523.449388
HLA A*2402	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.336358	2.527183	-1.809174	21694.894251
HLA B*5701	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.645287	1.835915	-1.809372	4418.624207
HLA A*3201	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.012911	2.203513	-1.809398	10301.749512
HLA B*0802	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.371074	2.560573	-1.810500	23500.306576
HLA B*7301	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.474646	2.663942	-1.810704	29829.493234
HLA B*4801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.329967	2.518634	-1.811333	21377.993385
HLA A*0219	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.045619	1.234017	-1.811602	1110.755858
HLA B*7301	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.525148	2.713138	-1.812010	33507.965176
HLA B*7301	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.527808	2.715385	-1.812423	33713.797385
HLA A*0201	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.298895	2.485326	-1.813569	19901.921055
HLA A*0219	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.299854	2.485326	-1.814527	19945.897783

HLA A*3002	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-3.959362	2.144780	-1.814582	9106.710351
HLA A*0250	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.191632	2.376452	-1.815180	15546.463477
HLA A*0202	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.333820	2.518634	-1.815186	21568.507499
HLA B*0801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.014302	2.199112	-1.815190	10334.795344
HLA B*1501	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.050667	2.235159	-1.815509	11237.435441
HLA A*0206	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.460979	1.645215	-1.815764	2890.542552
HLA B*7301	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.609429	2.793482	-1.815947	40684.481114
HLA B*1509	1:94-102	9	YRDVLARLL	1.616307	0.425031	-3.857375	2.041338	-1.816037	7200.705988
HLA B*1502	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.708079	1.891829	-1.816250	5105.983460
HLA B*1801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.902753	2.086183	-1.816570	7993.795466
HLA A*8001	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.342570	2.525744	-1.816825	22007.442504
HLA A*6901	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.193633	2.376452	-1.817181	15618.286030
HLA B*4801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.377765	2.560573	-1.817192	23865.188073
HLA B*1503	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.710044	1.892220	-1.817824	5129.128424
HLA A*0212	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.670535	1.852642	-1.817892	4683.112959
HLA A*0216	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.412713	2.594821	-1.817893	25865.057644
HLA B*4601	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.344069	2.525744	-1.818324	22083.532633
HLA A*2301	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.592048	1.773509	-1.818539	3908.838591
HLA A*1101	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.415455	2.594821	-1.820635	26028.869118
HLA A*0101	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.339520	2.518634	-1.820886	21853.446763
HLA A*3201	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.339602	2.518634	-1.820969	21857.585020
HLA A*3201	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.165435	2.343890	-1.821544	14636.419657
HLA A*2301	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-3.910910	2.089268	-1.821642	8145.363007
HLA B*3501	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-3.535825	1.713159	-1.822666	3434.191913
HLA A*6802	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.361335	2.538635	-1.822700	22979.200400
HLA B*1801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.486750	2.663942	-1.822809	30672.588064
HLA A*0301	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.530994	1.708081	-1.822913	3396.205962
HLA A*0206	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-3.666884	1.843794	-1.823090	4643.907211
HLA A*3101	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.341912	2.518634	-1.823278	21974.131549
HLA A*8001	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.323482	2.500040	-1.823442	21061.163506
HLA A*0211	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.200447	2.376452	-1.823995	15865.248490
HLA B*4501	1:100-108	9	RLLAAGEAY	1.333942	1.459540	-4.617525	2.793482	-1.824043	41450.054579
HLA A*0202	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.600158	1.776041	-1.824118	3982.521780
HLA A*2601	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.351761	2.527183	-1.824577	22478.160156
HLA A*0219	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.324819	2.500040	-1.824779	21126.094432
HLA A*0211	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.716650	1.891829	-1.824821	5207.752366
HLA A*2602	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.060046	2.235159	-1.824888	11482.761748
HLA A*0201	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-2.815548	0.990658	-1.824890	653.954666
HLA B*4001	1:366-374	9	AELVQTRIV	1.123749	0.213984	-3.163159	1.337733	-1.825425	1455.990858
HLA B*5101	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.364312	2.538635	-1.825676	23137.248451
HLA A*0301	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.353008	2.527183	-1.825825	22542.824904
HLA A*0219	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.362512	1.536595	-1.825917	2304.159032
HLA B*3501	1:462-470	9	PPLFESLEL	1.313352	0.107023	-3.246852	1.420375	-1.826477	1765.436100
HLA B*4402	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.127322	2.300286	-1.827035	13406.688149
HLA A*0216	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.327375	2.500040	-1.827335	21250.808436
HLA A*3301	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.619687	1.792234	-1.827453	4165.691258
HLA A*0206	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.483839	2.655688	-1.828151	30467.681721
HLA B*3801	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.423195	2.594821	-1.828374	26496.865622
HLA A*0211	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.423312	2.594821	-1.828491	26504.033847
HLA A*0216	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.664543	1.835915	-1.828629	4618.951973
HLA B*1501	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.729229	1.900474	-1.828756	5360.798305
HLA B*4002	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.551631	2.722320	-1.829312	35614.877128
HLA B*4001	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.389900	2.560573	-1.829327	24541.434878
HLA A*2501	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.621590	1.792234	-1.829356	4183.985413
HLA A*0211	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-2.897883	1.067176	-1.830707	790.465638
HLA A*3101	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.370359	2.538635	-1.831724	23461.689587
HLA A*0203	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.331962	2.500040	-1.831921	21476.408257
HLA B*5301	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.426911	2.594821	-1.832091	26724.610761
HLA A*0206	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.160128	1.327486	-1.832641	1445.865225
HLA A*6901	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.212002	2.378256	-1.833746	16293.022073
HLA B*0801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.394479	2.560573	-1.833906	24801.565656
HLA A*3001	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.266390	2.431527	-1.834863	18466.724673
HLA A*1101	1:376-384	9	LGDAWELLK	0.881918	0.032559	-2.750650	0.914477	-1.836173	563.183819
HLA A*1101	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.336217	2.500040	-1.836176	21687.853375
HLA B*0801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.321603	2.485326	-1.836277	20970.209621

HLA A*0301	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.355034	2.518634	-1.836400	22648.194907
HLA A*0211	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.500857	2.663942	-1.836915	31685.220224
HLA A*3002	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.198022	2.361023	-1.836999	15776.919519
HLA B*0802	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.268697	2.431527	-1.837171	18565.090407
HLA B*0801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.376303	2.538635	-1.837668	23785.017843
HLA B*5701	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.323264	2.485326	-1.837938	21050.569885
HLA A*3001	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-3.551543	1.713576	-1.837966	3560.759289
HLA B*4002	1:62-70	9	LDALRWLGL	1.379202	0.313002	-3.530181	1.692204	-1.837977	3389.854816
HLA A*0216	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.039364	1.200757	-1.838607	1094.874355
HLA B*3901	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.357252	2.518634	-1.838618	22764.153619
HLA A*3002	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.801894	1.962632	-1.839262	6337.155148
HLA A*0201	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.400358	2.560573	-1.839784	25139.550550
HLA B*5301	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.503998	2.663942	-1.840056	31915.230946
HLA A*2402	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.562815	2.722320	-1.840495	36543.908849
HLA B*4801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.379142	2.538635	-1.840506	23940.965425
HLA A*0250	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.485837	1.645215	-1.840622	3060.813853
HLA A*0201	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-2.958105	1.117129	-1.840976	908.040031
HLA B*1517	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.146473	1.305053	-1.841420	1401.111203
HLA B*1501	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.733487	1.891829	-1.841657	5413.607117
HLA B*5701	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.076845	2.234720	-1.842125	11935.625170
HLA A*2301	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.498113	2.655688	-1.842424	31485.640434
HLA A*2403	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.404469	2.560573	-1.843896	25378.684559
HLA B*1801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.369706	2.525744	-1.843962	23426.430919
HLA A*0212	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.205212	2.361023	-1.844189	16040.268519
HLA B*4402	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.363435	2.518634	-1.844802	23090.607134
HLA A*6802	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.363576	2.518634	-1.844943	23098.103408
HLA A*2402	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.560559	2.715385	-1.845175	36354.610279
HLA A*2403	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.080548	2.235159	-1.845389	12037.823185
HLA B*1503	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.698639	1.852642	-1.845997	4996.192613
HLA A*0203	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.010867	2.164532	-1.846335	10253.377185
HLA A*6802	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.223115	2.376452	-1.846663	16715.320568
HLA B*1501	1:23-31	9	LVRTALFNW	1.553174	0.453372	-3.853268	2.006546	-1.846722	7132.933561
HLA A*0216	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-2.914766	1.067986	-1.846780	821.800488
HLA A*0101	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.374252	2.527183	-1.847069	23672.950018
HLA B*5801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.278741	2.431527	-1.847215	18999.453839
HLA B*3901	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.373512	2.525744	-1.847768	23632.642941
HLA A*0216	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.208966	2.361023	-1.847943	16179.537810
HLA B*4801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.348166	2.500040	-1.848126	22292.873373
HLA A*0212	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.836653	1.987904	-1.848749	6865.190944
HLA A*0301	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.349101	2.500040	-1.849061	22340.924671
HLA A*0201	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.349550	2.500040	-1.849509	22364.021229
HLA A*0250	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.562754	2.713138	-1.849616	36538.769050
HLA B*3801	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.389228	2.538635	-1.850593	24503.493035
HLA B*0702	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.390393	2.538635	-1.851758	24569.331674
HLA B*5401	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.567173	2.715385	-1.851788	36912.485864
HLA A*2603	1:460-468	9	VSPPLFESL	1.613644	0.458549	-3.924171	2.072193	-1.851978	8397.904609
HLA B*4002	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.565634	2.713138	-1.852496	36781.918772
HLA B*4801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-3.865011	2.012396	-1.852615	7328.429342
HLA B*4001	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.391392	2.538635	-1.852756	24625.886543
HLA A*6901	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-2.737202	0.883995	-1.853207	546.011407
HLA B*0801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-3.570874	1.717294	-1.853580	3722.838345
HLA B*4001	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.153894	2.300286	-1.853608	14252.602822
HLA A*2501	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.379959	2.525744	-1.854215	23986.080132
HLA A*0202	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-2.630183	0.775701	-1.854482	426.758986
HLA B*4402	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-3.077224	1.222401	-1.854823	1194.603780
HLA A*0202	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.543489	1.688566	-1.854922	3495.333194
HLA A*6901	1:204-212	9	DALMKITHV	0.852595	-0.031547	-2.676928	0.821048	-1.855880	475.256459
HLA A*2603	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.578261	2.722320	-1.855941	37866.966320
HLA B*1502	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.648243	1.792274	-1.855969	4448.798336
HLA A*2403	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.055145	2.199112	-1.856034	11353.906884
HLA B*0802	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.394824	2.538635	-1.856189	24821.297038
HLA B*2705	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.356824	2.500040	-1.856783	22741.751067
HLA B*4001	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.343733	2.485326	-1.858406	22066.455106
HLA B*5801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.236756	2.378256	-1.858500	17248.678200
HLA B*4402	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.397348	2.538635	-1.858712	24965.934037

HLA B*4402	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.944922	2.086183	-1.858739	8808.898153
HLA B*0803	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.386559	2.527183	-1.859376	24353.365321
HLA A*6801	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.575089	2.715385	-1.859704	37591.418036
HLA B*5101	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.360261	2.500040	-1.860221	22922.458650
HLA A*0250	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.583150	2.722320	-1.860830	38295.680543
HLA B*4403	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.534844	2.673903	-1.860941	34264.498517
HLA A*3002	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.095777	2.234720	-1.861057	12467.441003
HLA B*4801	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.388110	2.525744	-1.862365	24440.475087
HLA B*3901	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.347980	2.485326	-1.862654	22283.347853
HLA A*3101	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.098038	2.235159	-1.862879	12532.494606
HLA A*3301	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.458651	2.594821	-1.863830	28750.842887
HLA A*0203	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.424867	2.560573	-1.864294	26599.124153
HLA A*2501	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.640579	1.776041	-1.864538	4370.978794
HLA B*4002	1:205-213	9	ALMKITHVL	1.662500	0.455646	-3.983082	2.118146	-1.864936	9617.936915
HLA A*3201	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.100157	2.235159	-1.864998	12593.799123
HLA A*3001	1:60-68	9	ALLDALRWL	1.537707	0.516755	-3.920069	2.054462	-1.865607	8318.954260
HLA A*0201	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.391688	2.525744	-1.865943	24642.678403
HLA A*8001	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.393704	2.527183	-1.866520	24757.327828
HLA B*0803	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.427398	2.560573	-1.866825	26754.555001
HLA A*0201	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.394592	2.527183	-1.867409	24808.006831
HLA A*0211	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.030103	1.162401	-1.867702	1071.772510
HLA B*1501	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-3.729178	1.861442	-1.867736	5360.160314
HLA B*4001	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.395372	2.527183	-1.868189	24852.604114
HLA B*5701	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.406948	2.538635	-1.868312	25523.945842
HLA B*3501	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.660606	1.792234	-1.868372	4577.261344
HLA A*0301	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.353929	2.485326	-1.868603	22590.681670
HLA A*0216	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.871749	2.003005	-1.868744	7443.020718
HLA B*1517	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.300847	2.431527	-1.869321	19991.593904
HLA A*0219	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.245860	2.376452	-1.869408	17614.084451
HLA B*3901	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.397026	2.527183	-1.869843	24947.437271
HLA A*0206	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.832536	1.962632	-1.869904	6800.429195
HLA A*2601	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.301851	2.431527	-1.870324	20037.828320
HLA B*0801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-3.425093	1.554677	-1.870416	2661.296931
HLA A*0206	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-2.938708	1.067986	-1.870721	868.375670
HLA A*3301	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.593384	2.722320	-1.871064	39208.853951
HLA B*2705	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.834078	1.962632	-1.871446	6824.606027
HLA A*2301	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.172333	2.300286	-1.872047	14870.752348
HLA A*3101	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.357992	2.485326	-1.872665	22802.979428
HLA A*2402	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.528560	2.655688	-1.872871	33772.212063
HLA B*1509	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.252307	2.378256	-1.874051	17877.511295
HLA A*0212	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.435377	2.560573	-1.874803	27250.632253
HLA A*0201	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.393596	2.518634	-1.874962	24751.167613
HLA A*0216	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.639479	1.764296	-1.875183	4359.926225
HLA B*3801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.435828	2.560573	-1.875255	27278.952155
HLA A*0206	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.651447	1.776041	-1.875407	4481.747833
HLA B*4403	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.539508	2.663942	-1.875566	34634.435038
HLA A*6802	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-3.934170	2.058588	-1.875582	8593.505226
HLA B*4002	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.375664	2.500040	-1.875624	23750.044169
HLA B*0702	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.307569	2.431527	-1.876043	20303.424639
HLA B*1503	1:23-31	9	LVRTALFNW	1.553174	0.453372	-3.882604	2.006546	-1.876058	7631.393514
HLA A*0212	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.394773	2.518634	-1.876139	24818.343044
HLA A*2301	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.237597	2.361023	-1.876574	17282.116781
HLA B*1509	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.437656	2.560573	-1.877082	27394.008326
HLA B*0803	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.362420	2.485326	-1.877094	23036.705730
HLA A*6802	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.377166	2.500040	-1.877125	23832.288226
HLA A*0211	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.533230	2.655688	-1.877542	34137.387649
HLA A*2501	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.238572	2.361023	-1.877549	17320.960519
HLA A*2403	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.113709	2.234720	-1.878989	12992.974656
HLA B*0702	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.779941	1.900474	-1.879467	6024.773882
HLA B*1517	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.732213	1.852642	-1.879571	5397.756805
HLA A*6802	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.653224	1.773509	-1.879715	4500.115161
HLA A*0250	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-2.587460	0.707098	-1.880361	386.776108
HLA B*5801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.883520	2.003005	-1.880515	7647.511658
HLA B*4002	1:319-327	9	FDQKKADAL	1.490473	0.285277	-3.656706	1.775750	-1.880955	4536.339655
HLA A*2603	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.595798	1.714405	-1.881393	3942.734339

HLA A*3301	1:50-58	9	AQRDSEESY	1.389559	1.325826	-4.596866	2.715385	-1.881481	39524.472740
HLA A*2402	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.420164	2.538635	-1.881528	26312.594176
HLA A*3301	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.555555	2.673903	-1.881652	35938.098139
HLA B*5701	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.629099	1.747156	-1.881943	4256.955554
HLA B*5401	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.556124	2.673903	-1.882220	35985.178864
HLA B*2705	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.260923	2.378256	-1.882667	18235.707713
HLA A*6802	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-2.889726	1.006851	-1.882874	775.756786
HLA B*1801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.259511	2.376452	-1.883059	18176.513448
HLA B*4002	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.547104	2.663942	-1.883162	35245.525712
HLA A*0212	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.368536	2.485326	-1.883210	23363.402132
HLA A*0203	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.244622	2.361023	-1.883599	17563.938010
HLA B*5101	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-3.730700	1.846931	-1.883769	5378.983911
HLA A*6901	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.227701	2.343890	-1.883811	16892.771385
HLA B*1501	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.221210	1.337377	-1.883833	1664.216117
HLA A*3101	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.633441	1.749555	-1.883886	4299.727812
HLA A*0203	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.409678	2.525744	-1.883933	25684.902177
HLA A*0219	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.444685	2.560573	-1.884112	27841.026427
HLA B*4801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.369622	2.485326	-1.884295	23421.868925
HLA A*0216	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.260798	2.376452	-1.884346	18230.479845
HLA A*2301	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.262819	2.378256	-1.884563	18315.494851
HLA A*6802	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.445764	2.560573	-1.885191	27910.245473
HLA B*1801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.370723	2.485326	-1.885397	23481.371235
HLA A*0212	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.141390	2.255532	-1.885859	13848.101040
HLA A*0211	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.823759	1.937546	-1.886213	6664.363041
HLA A*0250	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.481638	2.594821	-1.886817	30313.629807
HLA B*0801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.890381	2.003005	-1.887376	7769.277683
HLA B*1501	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.052598	2.164532	-1.888066	11287.518794
HLA B*1509	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.388838	2.500040	-1.888798	24481.497757
HLA A*0206	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.145464	2.255532	-1.889933	13978.617798
HLA B*3901	1:319-327	9	FDQKKADAL	1.490473	0.285277	-3.665704	1.775750	-1.889954	4631.312563
HLA B*4801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.268274	2.378256	-1.890019	18547.020892
HLA B*1503	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.604458	1.714405	-1.890053	4022.144945
HLA B*0803	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.429313	2.538635	-1.890677	26872.777864
HLA B*3501	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.664191	1.773509	-1.890682	4615.205291
HLA B*5101	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.486102	2.594821	-1.891281	30626.824095
HLA A*0219	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.418799	2.527183	-1.891615	26230.019702
HLA A*3301	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.147555	2.255532	-1.892024	14046.084355
HLA A*3002	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.269129	2.376452	-1.892677	18583.579663
HLA B*3901	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.431747	2.538635	-1.893111	27023.813103
HLA B*2705	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.378888	2.485326	-1.893562	23926.981570
HLA B*4402	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.270283	2.376452	-1.893831	18633.008018
HLA A*0212	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.421118	2.527183	-1.893934	26370.451068
HLA B*4402	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.379320	2.485326	-1.893994	23950.810814
HLA A*0202	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.550429	2.655688	-1.894740	35516.365285
HLA A*2601	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.273295	2.378256	-1.895039	18762.686002
HLA A*3002	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.098968	2.203513	-1.895454	12559.371950
HLA A*3001	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.272010	2.376452	-1.895558	18707.245357
HLA A*0203	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.032969	1.137355	-1.895614	1078.869673
HLA B*1509	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.434519	2.538635	-1.895884	27196.875986
HLA B*4403	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.982278	2.086183	-1.896096	9600.158432
HLA A*6802	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.423364	2.527183	-1.896180	26507.188480
HLA B*4002	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.570406	2.673903	-1.896503	37188.287947
HLA B*1502	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.660977	1.764296	-1.896680	4581.175488
HLA A*2402	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.100194	2.203513	-1.896681	12594.889267
HLA A*3101	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.132326	2.234720	-1.897606	13562.067778
HLA B*5401	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.553603	2.655688	-1.897914	35776.896804
HLA B*0702	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.383958	2.485326	-1.898632	24207.955018
HLA B*0803	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.399159	2.500040	-1.899119	25070.285035
HLA A*0219	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.425006	2.525744	-1.899262	26607.615508
HLA A*0212	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.425455	2.525744	-1.899710	26635.123069
HLA A*1101	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.427238	2.527183	-1.900055	26744.714547
HLA A*2301	1:375-383	9	VLGDAWELL	1.509402	0.401696	-3.811236	1.911098	-1.900138	6474.942143
HLA B*1501	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.672546	1.771882	-1.900663	4704.850115
HLA A*0203	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.427891	2.527183	-1.900708	26784.967500
HLA B*4402	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.261945	2.361023	-1.900922	18278.672371

HLA B*1501	1:281-289	9	LNYLALLGW	1.664731	0.421452	-3.987541	2.086183	-1.901359	9717.202354
HLA A*3101	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.839246	1.937546	-1.901700	6906.316106
HLA A*0211	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.904863	2.003005	-1.901858	8032.724451
HLA A*0219	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.420561	2.518634	-1.901927	26336.662026
HLA B*7301	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-2.464812	0.562720	-1.902092	291.616319
HLA B*1503	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-3.714254	1.811844	-1.902410	5179.094677
HLA B*5401	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.566828	2.663942	-1.902886	36883.142742
HLA A*0201	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.280501	2.376452	-1.904049	19076.595943
HLA A*0250	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.404225	2.500040	-1.904184	25364.409805
HLA B*4601	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.336123	2.431527	-1.904596	21683.160728
HLA B*1503	1:60-68	9	ALLDALRWL	1.537707	0.516755	-3.959145	2.054462	-1.904683	9102.178980
HLA B*3501	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.140173	2.235159	-1.905015	13809.348518
HLA A*2602	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.465683	2.560573	-1.905109	29220.160024
HLA A*0211	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.423876	2.518634	-1.905242	26538.468329
HLA A*3002	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.433450	2.527183	-1.906267	27130.013213
HLA A*2501	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.434526	2.527183	-1.907343	27197.317386
HLA B*1509	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.910962	2.003005	-1.907957	8146.332506
HLA B*0802	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.393603	2.485326	-1.908277	24751.569319
HLA B*3901	1:210-218	9	THVLRGEDL	1.116170	0.447749	-3.472492	1.563919	-1.908573	2968.190997
HLA B*3501	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.208919	2.300286	-1.908633	16177.787315
HLA B*1509	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.436175	2.527183	-1.908992	27300.802165
HLA A*0216	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.469724	2.560573	-1.909151	29493.322806
HLA A*3001	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.033117	2.123741	-1.909376	10792.363309
HLA B*1801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.340998	2.431527	-1.909471	21927.936780
HLA B*4001	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.033554	2.123741	-1.909813	10803.228475
HLA A*3001	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.036293	2.126210	-1.910083	10871.589875
HLA B*5301	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.288456	2.378256	-1.910201	19429.258986
HLA B*3901	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-3.943827	2.032901	-1.910926	8786.718816
HLA A*2301	1:23-31	9	LVRTALFNW	1.553174	0.453372	-3.917846	2.006546	-1.911300	8276.488646
HLA A*0219	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.272473	2.361023	-1.911450	18727.193197
HLA A*0216	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.540970	1.629468	-1.911502	3475.121020
HLA A*0250	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.575498	2.663942	-1.911556	37626.820276
HLA A*2403	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.676018	1.764296	-1.911722	4742.620031
HLA B*4403	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.437498	2.525744	-1.911754	27384.080823
HLA B*3901	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.472642	2.560573	-1.912069	29692.158117
HLA B*5301	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.273102	2.361023	-1.912080	18754.364516
HLA B*5301	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.437900	2.525744	-1.912156	27409.425312
HLA B*5401	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.430917	2.518634	-1.912284	26972.255219
HLA B*2705	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.274709	2.361023	-1.913687	18823.891052
HLA B*5101	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.474608	2.560573	-1.914035	29826.911358
HLA B*4501	1:383-391	9	LKFFNDDQY	1.359636	1.362684	-4.637289	2.722320	-1.914969	43379.942755
HLA B*1509	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.346629	2.431527	-1.915103	22214.139048
HLA B*3801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.347017	2.431527	-1.915491	22233.976946
HLA A*0250	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.572032	2.655688	-1.916344	37327.768551
HLA B*1501	1:375-383	9	VLGDAWELL	1.509402	0.401696	-3.827499	1.911098	-1.916401	6722.008036
HLA A*3001	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.277872	2.361023	-1.916849	18961.461448
HLA A*2501	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.477712	2.560573	-1.917139	30040.831769
HLA B*3801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.444683	2.527183	-1.917500	27840.875810
HLA B*4801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.753415	1.835915	-1.917500	5667.807170
HLA B*3901	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.818594	1.900474	-1.918121	6585.586814
HLA A*6901	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.563417	1.645215	-1.918202	3659.459230
HLA B*1517	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-2.969077	1.050133	-1.918944	931.273168
HLA A*3201	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.574779	2.655688	-1.919090	37564.583385
HLA A*0101	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.155962	2.235159	-1.920803	14320.616992
HLA A*0301	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-2.781598	0.860662	-1.920936	604.780229
HLA A*8001	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.352928	2.431527	-1.921402	22538.678843
HLA B*7301	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.595339	2.673903	-1.921436	39385.731858
HLA A*0216	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.441335	2.518634	-1.922701	27627.073108
HLA A*3301	1:364-372	9	AAAELVQTR	0.986953	0.803779	-3.713671	1.790732	-1.922939	5172.150790
HLA B*3501	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-3.926154	2.003005	-1.923149	8436.336664
HLA B*3501	1:59-67	9	LALLDALRW	1.480034	0.393544	-3.797435	1.873578	-1.923857	6272.418358
HLA B*1509	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.449713	2.525744	-1.923969	28165.219518
HLA B*3501	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-3.642181	1.717294	-1.924887	4387.135502
HLA A*6901	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.554564	1.629468	-1.925096	3585.618283
HLA A*0206	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.160022	2.234720	-1.925302	14455.117948

HLA B*5801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.070666	2.144780	-1.925886	11767.007387
HLA A*2402	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.103089	2.177014	-1.926075	12679.114363
HLA A*2402	1:375-383	9	VLGDAWELL	1.509402	0.401696	-3.837362	1.911098	-1.926264	6876.416367
HLA A*0202	1:54-62	9	SEESYLALL	1.352077	0.257378	-3.536041	1.609455	-1.926586	3435.901570
HLA A*0301	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.358198	2.431527	-1.926672	22813.837833
HLA A*2603	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.452711	2.525744	-1.926967	28360.317158
HLA A*0216	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.453376	2.525744	-1.927632	28403.770019
HLA A*3101	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.359166	2.431527	-1.927640	22864.743721
HLA B*1509	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.305060	2.376452	-1.928608	20186.454529
HLA A*2602	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.592759	2.663942	-1.928817	39152.471791
HLA A*0206	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.777817	1.848352	-1.929465	5995.381417
HLA A*0212	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.234743	1.305053	-1.929690	1716.891131
HLA A*2301	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.468340	2.538635	-1.929704	29399.494122
HLA B*1502	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.455528	2.525744	-1.929784	28544.873048
HLA B*3801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.429862	2.500040	-1.929822	26906.818033
HLA B*0702	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.273967	2.343890	-1.930077	18791.738631
HLA A*0202	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.043062	1.112802	-1.930260	1104.237197
HLA B*4501	1:378-386	9	DAWELLKFF	1.666410	1.046728	-4.643673	2.713138	-1.930534	44022.279348
HLA A*2301	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.129746	2.199112	-1.930634	13481.747096
HLA A*8001	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.292349	2.361023	-1.931327	19604.209456
HLA B*0801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-3.986921	2.055046	-1.931875	9703.334047
HLA A*6802	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.136165	2.203513	-1.932652	13682.484631
HLA A*0301	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.311204	2.378256	-1.932948	20474.059031
HLA A*2403	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.110128	2.177014	-1.933114	12886.292239
HLA B*4001	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-2.982089	1.048747	-1.933341	959.596241
HLA B*1502	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-2.953899	1.020365	-1.933534	899.289281
HLA A*2403	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.233826	2.300286	-1.933540	17132.707960
HLA A*3001	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.079275	2.144780	-1.934495	12002.578060
HLA B*0802	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.311740	2.376452	-1.935288	20499.328437
HLA A*0203	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.191124	2.255532	-1.935593	15528.307484
HLA B*5101	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.314277	2.378256	-1.936021	20619.450034
HLA A*3001	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.644610	1.708081	-1.936530	4411.745138
HLA B*4601	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.316641	2.378256	-1.938385	20731.974186
HLA A*0211	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.465812	2.527183	-1.938628	29228.855598
HLA A*6901	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.142697	2.203513	-1.939183	13889.817428
HLA A*0216	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.466486	2.527183	-1.939303	29274.272684
HLA B*3901	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.004152	2.064809	-1.939343	10096.064249
HLA A*6802	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.244864	1.305053	-1.939811	1757.374574
HLA A*0201	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.195687	2.255532	-1.940155	15692.307942
HLA B*1517	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.240870	2.300286	-1.940583	17412.846360
HLA A*0202	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.833232	1.891829	-1.941402	6811.327631
HLA A*0250	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-2.717292	0.775701	-1.941591	521.545473
HLA B*3501	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-3.496607	1.554677	-1.941930	3137.667776
HLA A*3001	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.247580	1.305053	-1.942527	1768.399336
HLA A*3101	1:325-333	9	DALNAEHIR	1.176166	0.604409	-3.723896	1.780575	-1.943322	5295.367878
HLA A*3002	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.375244	2.431527	-1.943717	23727.056467
HLA A*0216	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.088903	2.144780	-1.944123	12271.643456
HLA B*4601	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.179579	2.234720	-1.944859	15120.938702
HLA A*1101	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.463899	2.518634	-1.945266	29100.424944
HLA A*1101	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.003884	2.058588	-1.945296	10089.839650
HLA A*3001	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.108688	1.162617	-1.946071	1284.364189
HLA A*0250	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.800926	1.854767	-1.946160	6323.046155
HLA A*0201	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.378075	2.431527	-1.946548	23882.236418
HLA A*0212	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.378460	2.431527	-1.946934	23903.434662
HLA B*5801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.065098	2.118146	-1.946952	11617.100504
HLA A*0101	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.323607	2.376452	-1.947155	21067.203116
HLA B*3501	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.071324	2.123741	-1.947583	11784.845191
HLA B*4001	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.379177	2.431527	-1.947650	23942.908273
HLA B*1801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.248130	2.300286	-1.947843	17706.375772
HLA B*0801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.724728	1.776041	-1.948687	5305.518758
HLA A*0211	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.474528	2.525744	-1.948784	29821.425612
HLA B*5701	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.380542	2.431527	-1.949015	24018.282714
HLA A*0203	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.722543	1.773509	-1.949034	5278.892685
HLA B*1801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.739041	1.789240	-1.949801	5483.286232
HLA A*3001	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.184828	2.234720	-1.950108	15304.794490

HLA B*4601	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.294217	2.343890	-1.950327	19688.706027
HLA A*0203	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.382271	2.431527	-1.950745	24114.106435
HLA A*0202	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.477261	2.525744	-1.951516	30009.644596
HLA B*0803	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.383077	2.431527	-1.951551	24158.893918
HLA B*4501	1:236-244	9	GVAERIPKF	1.580848	1.093055	-4.625626	2.673903	-1.951723	42230.491017
HLA B*5401	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.546789	2.594821	-1.951969	35219.984603
HLA A*6801	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.471183	2.518634	-1.952549	29592.573463
HLA A*2602	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-3.814168	1.861442	-1.952726	6518.805892
HLA B*4501	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.608487	2.655688	-1.952798	40596.317267
HLA A*3301	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.608496	2.655688	-1.952808	40597.195763
HLA B*0702	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.313849	2.361023	-1.952827	20599.158118
HLA B*2705	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.071272	2.118146	-1.953126	11783.442671
HLA A*0216	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.117985	2.164532	-1.953452	13121.535327
HLA A*0211	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.514042	2.560573	-1.953469	32661.944749
HLA A*2602	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-2.944699	0.990658	-1.954041	880.438112
HLA A*0206	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.385589	2.431527	-1.954062	24299.013723
HLA B*5101	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.480541	2.525744	-1.954796	30237.141562
HLA B*4002	1:188-196	9	TRASGDPLY	1.277550	1.378138	-4.611226	2.655688	-1.955538	40853.205389
HLA A*0203	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.810616	1.854767	-1.955849	6465.701162
HLA A*0211	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-2.681806	0.725139	-1.956667	480.624117
HLA A*6901	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.388276	2.431527	-1.956750	24449.864529
HLA A*8001	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.074961	2.118146	-1.956815	11883.951882
HLA B*2705	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.388594	2.431527	-1.957067	24467.727643
HLA A*3101	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.102046	2.144780	-1.957266	12648.695795
HLA A*2501	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.746893	1.789240	-1.957653	5583.324838
HLA A*3101	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.258379	1.300706	-1.957673	1812.919734
HLA B*2705	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.334288	2.376452	-1.957836	21591.739966
HLA A*2902	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.122411	2.164532	-1.957879	13255.956913
HLA A*0219	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.395302	1.437023	-1.958279	2484.859646
HLA B*4801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.390057	2.431527	-1.958531	24550.331842
HLA A*0101	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.337041	2.378256	-1.958786	21729.074938
HLA A*6901	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-3.513537	1.554677	-1.958860	3262.401037
HLA A*0201	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.320127	2.361023	-1.959104	20899.086099
HLA B*0702	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-3.971607	2.012396	-1.959211	9367.140609
HLA A*0211	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.032116	2.072193	-1.959923	10767.519729
HLA A*3301	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.498867	2.538635	-1.960231	31540.365095
HLA A*0203	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.105124	2.144780	-1.960344	12738.654921
HLA A*0216	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.078126	1.117129	-1.960997	1197.088026
HLA A*1101	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.339414	2.378256	-1.961159	21848.127298
HLA A*3201	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.590633	1.629468	-1.961166	3896.129175
HLA A*3201	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.015636	2.054462	-1.961174	10366.601121
HLA B*1801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.339677	2.378256	-1.961422	21861.369255
HLA B*1509	1:51-59	9	QRDSEESYL	1.503495	0.502197	-3.967345	2.005692	-1.961653	9275.665392
HLA A*0101	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.393241	2.431527	-1.961714	24730.956807
HLA B*1501	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.924946	1.962632	-1.962314	8412.910472
HLA A*0206	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.523748	2.560573	-1.963175	33400.099636
HLA A*0212	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.339790	2.376452	-1.963338	21867.046836
HLA B*4801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.088466	2.123741	-1.964725	12259.301456
HLA B*1503	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.653679	1.688566	-1.965113	4504.840594
HLA A*3201	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.342097	2.376452	-1.965645	21983.524887
HLA B*2705	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-3.731053	1.764418	-1.966634	5383.350638
HLA A*3201	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.858470	1.891829	-1.966640	7218.881929
HLA A*0211	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-2.644139	0.677348	-1.966790	440.695499
HLA A*3201	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.021853	2.055046	-1.966807	10516.061703
HLA B*1517	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.085797	2.118146	-1.967651	12184.191311
HLA A*3301	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.347313	2.378256	-1.969058	22249.137815
HLA A*1101	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.204756	2.235159	-1.969597	16023.442791
HLA B*4801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.346481	2.376452	-1.970029	22206.569249
HLA B*0801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.314089	2.343890	-1.970199	20610.528049
HLA B*0702	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.742199	1.771882	-1.970316	5523.299900
HLA B*5101	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.456531	2.485326	-1.971205	28610.888571
HLA B*5701	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.349548	2.378256	-1.971292	22363.900243
HLA A*6802	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-2.935996	0.963515	-1.972481	862.971277
HLA A*0203	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.044793	2.072193	-1.972601	11086.475389
HLA B*1503	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-2.762976	0.790220	-1.972756	579.396099

HLA B*3801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.351209	2.378256	-1.972953	22449.601291
HLA B*5701	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.045348	2.072193	-1.973155	11100.638907
HLA B*0802	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.317475	2.343890	-1.973584	20771.828421
HLA A*0301	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.351049	2.376452	-1.974597	22441.344220
HLA B*0702	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-2.765579	0.790220	-1.975359	582.879520
HLA A*3301	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.640275	2.663942	-1.976333	43679.249734
HLA A*0101	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.337798	2.361023	-1.976775	21766.959633
HLA B*4501	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.640731	2.663942	-1.976789	43725.115979
HLA A*0212	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.211582	1.234017	-1.977565	1627.726875
HLA B*4001	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.338726	2.361023	-1.977703	21813.523318
HLA A*2301	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.538383	2.560573	-1.977810	34544.801734
HLA B*7301	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-3.979135	2.001284	-1.977851	9530.919235
HLA B*3501	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.096012	2.118146	-1.977866	12474.187575
HLA A*2603	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.339635	2.361023	-1.978612	21859.240542
HLA A*2603	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.410418	2.431527	-1.978891	25728.709522
HLA A*3301	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.506068	2.525744	-1.980323	32067.705589
HLA A*2402	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.281615	2.300286	-1.981328	19125.576592
HLA B*0803	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.358128	2.376452	-1.981676	22810.135523
HLA A*3001	1:57-65	9	SYLALLDAL	1.498520	0.489384	-3.969976	1.987904	-1.982072	9332.037963
HLA A*8001	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.358981	2.376452	-1.982529	22854.973846
HLA A*3301	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.326433	2.343890	-1.982543	21204.757633
HLA B*5301	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.835816	1.852642	-1.983174	6851.981855
HLA A*0301	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.344466	2.361023	-1.983443	22103.732205
HLA B*4001	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.359909	2.376452	-1.983457	22903.865001
HLA A*0250	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.831991	1.848352	-1.983639	6791.899369
HLA A*0219	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.146101	1.162401	-1.983701	1399.914097
HLA B*1501	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.284077	2.300286	-1.983790	19234.318237
HLA B*3501	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-3.413055	1.429220	-1.983835	2588.538161
HLA A*3101	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.345469	2.361023	-1.984446	22154.851348
HLA A*3001	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.501691	1.517234	-1.984457	3174.616310
HLA A*0219	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.416116	2.431527	-1.984589	26068.467746
HLA B*4002	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-3.796603	1.811844	-1.984759	6260.417540
HLA A*0216	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.630664	1.645215	-1.985449	4272.320970
HLA B*3801	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.470863	2.485326	-1.985537	29570.808884
HLA A*0219	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-3.415371	1.429823	-1.985548	2602.382706
HLA A*0211	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.838316	1.852642	-1.985674	6891.536430
HLA B*5301	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.546371	2.560573	-1.985798	35186.085482
HLA A*0201	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.839232	1.852642	-1.986590	6906.091935
HLA A*2501	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.418199	2.431527	-1.986673	26193.859767
HLA B*1509	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.762799	1.776041	-1.986758	5791.604666
HLA B*4403	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.547391	2.560573	-1.986818	35268.795666
HLA A*0201	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.523443	1.536595	-1.986847	3337.665236
HLA A*3301	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.514216	2.527183	-1.987033	32675.022981
HLA B*5101	1:59-67	9	LALLDALRW	1.480034	0.393544	-3.861153	1.873578	-1.987575	7263.618908
HLA B*0801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.074265	2.086649	-1.987616	11864.937015
HLA A*0202	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.836155	1.848352	-1.987803	6857.321794
HLA B*1509	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.107205	2.118146	-1.989059	12799.859921
HLA A*0211	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.881415	1.892220	-1.989195	7610.531874
HLA A*0206	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.333933	2.343890	-1.990042	21574.109021
HLA B*5401	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.366812	2.376452	-1.990359	23270.813315
HLA B*3501	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.766577	1.776041	-1.990536	5842.206199
HLA A*3201	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.329145	1.338560	-1.990585	2133.757519
HLA A*6802	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.422438	2.431527	-1.990911	26450.748677
HLA A*3301	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.509609	2.518634	-1.990975	32330.212683
HLA B*4002	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-3.018322	1.027215	-1.991108	1043.091234
HLA B*0702	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-3.982570	1.990887	-1.991683	9606.600631
HLA B*4002	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-2.839010	0.846543	-1.992467	690.255062
HLA B*4001	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.371019	2.378256	-1.992764	23497.382675
HLA A*0206	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.931337	1.937546	-1.993791	8537.620896
HLA B*5401	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.532664	2.538635	-1.994029	34092.908896
HLA A*2902	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.120344	2.126210	-1.994134	13192.999226
HLA B*1801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.812293	1.817618	-1.994675	6490.724270
HLA A*3001	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.295000	2.300286	-1.994713	19724.207063
HLA A*2403	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.339543	2.343890	-1.995653	21854.629042
HLA A*2603	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.481274	2.485326	-1.995948	30288.221488

HLA B*0702	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.161732	2.164532	-1.997200	14512.160228
HLA A*2402	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.003927	2.006546	-1.997381	10090.822226
HLA A*3201	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.558414	2.560573	-1.997841	36175.489265
HLA A*6802	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-3.427668	1.429220	-1.998449	2677.123268
HLA A*3001	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.254020	2.255532	-1.998488	17948.156001
HLA B*1517	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.032125	2.032901	-1.999224	10767.752736
HLA B*5101	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.198915	2.199112	-1.999803	15809.386406
HLA A*0216	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.891654	1.891829	-1.999825	7792.091879
HLA B*3801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.086840	2.086649	-2.000191	12213.492803
HLA A*2902	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.255763	2.255532	-2.000232	18020.347167
HLA A*0203	1:435-443	9	ALIEGLALK	0.478643	0.243793	-2.722837	0.722436	-2.000401	528.246909
HLA B*4801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.165858	2.164532	-2.001325	14650.679252
HLA A*0301	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.119803	2.118146	-2.001657	13176.593722
HLA B*5401	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.562745	2.560573	-2.002171	36537.978375
HLA A*6801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-2.862998	0.860662	-2.002336	729.453886
HLA A*6801	1:260-268	9	KRDPQSNLF	1.481443	1.182499	-4.666930	2.663942	-2.002988	46444.049297
HLA B*1801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.206758	2.203513	-2.003244	16097.468924
HLA B*5301	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.489072	2.485326	-2.003745	30836.971061
HLA A*6901	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.896743	1.892220	-2.004523	7883.935259
HLA B*1502	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.382795	2.378256	-2.004540	24143.215375
HLA B*0801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.365940	2.361023	-2.004917	23224.154030
HLA B*3901	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-3.435398	1.429220	-2.006178	2725.198707
HLA A*3101	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.382936	2.376452	-2.006484	24151.053374
HLA B*1502	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.241643	2.235159	-2.006484	17443.866273
HLA A*0202	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.367556	2.361023	-2.006534	23310.755484
HLA A*2301	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.078927	2.072193	-2.006734	11992.971879
HLA A*2601	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.368052	2.361023	-2.007029	23337.379592
HLA A*2601	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.242503	2.235159	-2.007344	17478.439684
HLA A*6801	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.534910	2.527183	-2.007727	34269.689190
HLA A*0212	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.074973	1.067176	-2.007797	1188.428554
HLA A*1101	1:364-372	9	AAAELVQTR	0.986953	0.803779	-3.798920	1.790732	-2.008188	6293.900774
HLA A*6802	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-3.112800	1.104589	-2.008211	1296.581398
HLA A*0202	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-3.855364	1.846931	-2.008433	7167.437580
HLA A*0216	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.439986	2.431527	-2.008460	27541.416473
HLA B*1501	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.192710	1.183813	-2.008898	1558.513148
HLA B*4402	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.352809	2.343890	-2.008918	22532.461181
HLA B*1517	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.067743	2.058588	-2.009155	11688.082456
HLA A*0250	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.535251	2.525744	-2.009506	34296.582044
HLA A*0250	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.570145	2.560573	-2.009572	37165.963169
HLA A*2402	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.064797	2.055046	-2.009751	11609.058844
HLA A*6802	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.354597	2.343890	-2.010706	22625.416863
HLA B*4001	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.175528	2.164532	-2.010996	14980.566634
HLA A*2603	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.387764	2.376452	-2.011312	24421.046435
HLA B*7301	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.606593	2.594821	-2.011772	40419.687642
HLA A*2403	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.135700	2.123741	-2.011959	13667.836374
HLA A*0216	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.339939	1.327486	-2.012452	2187.452336
HLA A*0211	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.868018	1.854767	-2.013252	7379.352318
HLA B*5801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.313690	2.300286	-2.013403	20591.581649
HLA B*2705	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.019128	2.005692	-2.013436	10450.275096
HLA B*3901	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-3.860815	1.846931	-2.013884	7257.962578
HLA A*3201	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.445602	2.431527	-2.014075	27899.829016
HLA B*3901	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.790523	1.776041	-2.014482	6173.377466
HLA B*1801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.779118	1.764296	-2.014822	6013.377000
HLA B*4801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.134036	2.118146	-2.015891	13615.585935
HLA A*3001	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.978618	1.962632	-2.015986	9519.582516
HLA B*4002	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.543293	2.527183	-2.016110	34937.604811
HLA A*0301	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.074862	2.058588	-2.016274	11881.251972
HLA B*4601	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.916812	1.900474	-2.016339	8256.811125
HLA B*1509	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.181026	2.164532	-2.016494	15171.413161
HLA B*5101	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.448623	2.431527	-2.017096	28094.608168
HLA B*3501	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.007986	1.990887	-2.017100	10185.596441
HLA B*5401	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-3.864231	1.846931	-2.017300	7315.278686
HLA B*1502	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.072630	2.055046	-2.017584	11820.346173
HLA A*2902	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.396002	2.378256	-2.017746	24888.662803
HLA A*0250	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.536517	2.518634	-2.017884	34396.734432

HLA A*3101	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.141949	2.123741	-2.018209	13865.942696
HLA A*2501	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.396709	2.378256	-2.018453	24929.223935
HLA B*1501	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.073551	2.055046	-2.018505	11845.439902
HLA A*8001	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.253280	2.234720	-2.018560	17917.596324
HLA A*0203	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.981193	1.962632	-2.018561	9576.194056
HLA A*0206	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-2.982920	0.963515	-2.019405	961.435725
HLA A*6801	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.519479	2.500040	-2.019438	33073.392744
HLA B*5301	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.319852	2.300286	-2.019566	20885.862061
HLA B*7301	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.196735	2.177014	-2.019721	15730.216222
HLA A*0206	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.074778	2.055046	-2.019732	11878.938252
HLA A*6801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-3.487007	1.466619	-2.020388	3069.071186
HLA A*0101	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.085233	2.064809	-2.020423	12168.381947
HLA B*4801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.365416	2.343890	-2.021526	23196.153182
HLA A*6901	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.382851	2.361023	-2.021829	24146.350270
HLA A*0212	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.366774	2.343890	-2.022884	23268.799122
HLA B*3801	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.367002	2.343890	-2.023111	23281.012844
HLA A*0203	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.265751	1.241782	-2.023969	1843.958999
HLA A*0301	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-3.894234	1.870150	-2.024084	7838.515101
HLA B*3801	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.400564	2.376452	-2.024112	25151.521591
HLA B*1503	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.962378	1.937546	-2.024832	9170.188486
HLA B*5401	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.525263	2.500040	-2.025223	33516.848798
HLA A*8001	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.404093	2.378256	-2.025838	25356.726724
HLA B*3901	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-3.989689	1.962632	-2.027057	9765.369395
HLA B*4002	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.622057	2.594821	-2.027237	41884.878821
HLA A*6801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.882444	1.854767	-2.027677	7628.586650
HLA A*3301	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-3.341856	1.313812	-2.028044	2197.130123
HLA A*0202	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.459710	2.431527	-2.028184	28821.076564
HLA B*1509	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.029710	2.001284	-2.028426	10708.035530
HLA B*0801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.193370	2.164532	-2.028838	15608.825658
HLA B*4801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.920821	1.891829	-2.028991	8333.368211
HLA A*0206	1:54-62	9	SEESYLALL	1.352077	0.257378	-3.638643	1.609455	-2.029188	4351.537434
HLA B*0802	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.264101	2.234720	-2.029382	18369.675129
HLA A*2402	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.590078	2.560573	-2.029505	38911.540336
HLA B*4402	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.408010	2.378256	-2.029754	25586.435149
HLA B*4501	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.625067	2.594821	-2.030246	42176.151985
HLA A*2403	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.085496	2.055046	-2.030450	12175.757096
HLA B*4403	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.557785	2.527183	-2.030601	36123.078225
HLA B*5301	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.567214	1.536595	-2.030618	3691.591870
HLA B*4002	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.549515	2.518634	-2.030881	35441.701571
HLA B*4501	1:428-436	9	IEAALKDAL	1.293005	0.395561	-3.720494	1.688566	-2.031928	5254.048560
HLA A*3001	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.235529	2.203513	-2.032016	17200.037299
HLA B*4501	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.592682	2.560573	-2.032109	39145.482667
HLA A*0206	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.033469	2.001284	-2.032185	10801.124686
HLA A*6901	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.020204	1.987904	-2.032300	10476.200152
HLA A*2602	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.464170	2.431527	-2.032643	29118.535036
HLA B*5801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.104917	2.072193	-2.032724	12732.591870
HLA B*0702	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.039803	2.006546	-2.033257	10959.814185
HLA B*1801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.288813	2.255532	-2.033282	19445.242298
HLA A*3201	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-3.877924	1.843794	-2.034130	7549.595348
HLA A*1101	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.410721	2.376452	-2.034269	25746.671230
HLA A*0201	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.172228	1.137355	-2.034873	1486.714784
HLA B*4403	1:354-362	9	HIALDEAAF	1.481866	1.112955	-4.630132	2.594821	-2.035312	42670.962913
HLA B*3901	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.396479	2.361023	-2.035456	24916.010733
HLA B*4001	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.871430	1.835915	-2.035515	7437.546567
HLA B*1501	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.890291	1.854767	-2.035525	7767.680672
HLA A*0202	1:435-443	9	ALIEGLALK	0.478643	0.243793	-2.758704	0.722436	-2.036268	573.725566
HLA B*4002	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.562679	2.525744	-2.036934	36532.444135
HLA A*0203	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-2.763102	0.725139	-2.037964	579.565385
HLA A*0250	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.565554	2.527183	-2.038371	36775.153867
HLA B*5401	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.564199	2.525744	-2.038454	36660.538981
HLA B*3901	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-3.803313	1.764802	-2.038512	6357.896133
HLA B*4403	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.415122	2.376452	-2.038670	26008.881309
HLA B*4402	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.273951	2.235159	-2.038792	18791.027016
HLA A*0201	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.382795	2.343890	-2.038905	24143.215375
HLA A*2601	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.340234	2.300286	-2.039948	21889.416649

HLA A*0202	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.600879	2.560573	-2.040306	39891.374945
HLA B*5701	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.243926	2.203513	-2.040413	17535.834906
HLA B*0702	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.094997	2.054462	-2.040535	12445.068540
HLA A*1101	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.472167	2.431527	-2.040641	29659.728320
HLA A*6901	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.044183	2.003005	-2.041178	11070.892434
HLA B*1501	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.642923	1.601532	-2.041392	4394.641834
HLA B*2705	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.385551	2.343890	-2.041661	24296.910534
HLA A*0211	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.206790	2.164532	-2.042258	16098.688167
HLA A*0202	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.569718	2.527183	-2.042534	37129.387578
HLA B*1502	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.220300	2.177014	-2.043286	16607.338084
HLA A*3201	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.480541	1.437023	-2.043519	3023.717261
HLA B*1503	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.617652	1.573351	-2.044301	4146.220789
HLA B*5101	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-2.967865	0.923460	-2.044404	928.677141
HLA B*1503	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.032421	1.987904	-2.044517	10775.095034
HLA A*0203	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.936431	1.891829	-2.044601	8638.345099
HLA A*0203	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.945321	1.900474	-2.044847	8817.003257
HLA B*2705	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.280015	2.235159	-2.044856	19055.245031
HLA A*0206	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-3.045332	1.000328	-2.045004	1110.022994
HLA A*2902	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.818726	1.773509	-2.045217	6587.582245
HLA A*8001	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.345786	2.300286	-2.045500	22171.037722
HLA A*8001	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.281093	2.235159	-2.045934	19102.620651
HLA B*4501	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.572204	2.525744	-2.046459	37342.513016
HLA A*6801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.281828	2.235159	-2.046670	19134.994430
HLA B*5701	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.761403	1.714405	-2.046999	5773.023366
HLA B*1801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.408433	2.361023	-2.047410	25611.362844
HLA A*3002	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.426387	2.378256	-2.048132	26692.389489
HLA B*1501	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.896875	1.848352	-2.048523	7886.324089
HLA B*4403	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.567253	2.518634	-2.048620	36919.276032
HLA A*1101	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.166859	2.118146	-2.048713	14684.482331
HLA B*4002	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.609415	2.560573	-2.048842	40683.160544
HLA A*0201	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.036819	1.987904	-2.048915	10884.772218
HLA A*0206	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.386487	1.337377	-2.049110	2434.930645
HLA B*4402	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.226216	2.177014	-2.049202	16835.112781
HLA B*4403	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.481255	2.431527	-2.049728	30286.910669
HLA B*7301	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.610331	2.560573	-2.049758	40769.086800
HLA B*5801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-3.951416	1.900474	-2.050942	8941.606741
HLA B*0801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-3.943056	1.891829	-2.051227	8771.141104
HLA B*4001	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.395656	2.343890	-2.051766	24868.877869
HLA A*0203	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.168905	1.117129	-2.051777	1475.385424
HLA B*0702	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-3.769086	1.717294	-2.051792	5876.058776
HLA B*3801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.093315	2.041338	-2.051977	12396.956049
HLA A*3002	1:93-101	9	IYRDVLARL	1.447955	0.489591	-3.989571	1.937546	-2.052025	9762.728274
HLA B*0802	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.170693	2.118146	-2.052547	14814.704748
HLA A*6901	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.352863	2.300286	-2.052576	22535.265012
HLA A*1101	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-3.763010	1.710050	-2.052961	5794.425227
HLA B*4403	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-3.696407	1.643417	-2.052990	4970.581077
HLA A*0203	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.086065	2.032901	-2.053164	12191.707953
HLA B*0801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-3.818045	1.764802	-2.053243	6577.255302
HLA B*0801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.309564	2.255532	-2.054032	20396.892669
HLA A*6901	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.180401	2.126210	-2.054191	15149.596736
HLA B*1517	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-3.767869	1.713159	-2.054710	5859.615214
HLA A*0203	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.398948	2.343890	-2.055057	25058.081534
HLA A*6801	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.615739	2.560573	-2.055166	41279.981894
HLA B*7301	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.593885	2.538635	-2.055249	39254.060604
HLA B*3501	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-2.578983	0.523691	-2.055292	379.299873
HLA B*4601	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.291287	2.235159	-2.056129	19556.330436
HLA B*3901	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-3.118979	1.062587	-2.056392	1315.161031
HLA A*2501	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.129074	2.072193	-2.056882	13460.903884
HLA A*3002	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.221494	2.164532	-2.056961	16653.041537
HLA B*3901	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.488856	2.431527	-2.057329	30821.627017
HLA A*0206	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.593937	1.536595	-2.057341	3925.877312
HLA A*1101	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.418900	2.361023	-2.057877	26236.122176
HLA B*4402	1:415-423	9	AALTSVTDW	1.150326	0.497710	-3.706289	1.648036	-2.058253	5084.978208
HLA A*3301	1:124-132	9	AGRNPKLGY	1.255901	1.304672	-4.619304	2.560573	-2.058731	41620.152472
HLA B*1509	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.145563	2.086649	-2.058914	13981.794315

HLA B*1509	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.402881	2.343890	-2.058990	25286.042055
HLA B*4601	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.359434	2.300286	-2.059148	22878.849383
HLA A*0201	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.223721	2.164532	-2.059188	16738.667289
HLA B*4601	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-3.895427	1.835915	-2.059512	7860.086722
HLA B*0802	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.258644	2.199112	-2.059532	18140.264792
HLA B*4002	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-2.965539	0.905846	-2.059693	923.716637
HLA A*0301	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.295380	2.235159	-2.060222	19741.500975
HLA B*1501	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.316676	2.255532	-2.061144	20733.656620
HLA B*1501	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.238426	2.177014	-2.061412	17315.151815
HLA B*7301	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.588883	2.527183	-2.061699	38804.539600
HLA A*2403	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.916681	1.854767	-2.061914	8254.310072
HLA A*6802	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.707642	1.645215	-2.062427	5100.848202
HLA B*0801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-3.754829	1.692204	-2.062625	5686.295909
HLA B*1502	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.075304	2.012396	-2.062908	11893.342055
HLA A*3301	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.563416	2.500040	-2.063376	36594.554726
HLA A*0301	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.363743	2.300286	-2.063457	23106.977143
HLA B*3801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.425222	2.361023	-2.064199	26620.861675
HLA B*0802	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.425624	2.361023	-2.064601	26645.499790
HLA A*2602	1:112-120	9	STPEEVEAR	0.994604	0.605580	-3.665103	1.600184	-2.064918	4624.902952
HLA B*1517	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.320832	2.255532	-2.065301	20933.032160
HLA A*6901	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.841742	1.776041	-2.065701	6946.109181
HLA B*3901	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.409683	2.343890	-2.065792	25685.180083
HLA A*3301	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.776407	1.710232	-2.066176	5975.952358
HLA A*2403	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.211076	2.144780	-2.066296	16258.330542
HLA B*0803	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.410651	2.343890	-2.066760	25742.492970
HLA B*4402	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-3.115563	1.048747	-2.066816	1304.856583
HLA B*4002	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.605639	2.538635	-2.067004	40331.006660
HLA A*2402	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.156723	2.089268	-2.067455	14345.740240
HLA A*0101	1:53-61	9	DSEESYLAL	1.497889	0.291351	-3.856797	1.789240	-2.067557	7191.129427
HLA B*1501	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.122378	2.054462	-2.067916	13254.952965
HLA A*0219	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.212697	2.144780	-2.067917	16319.133433
HLA A*6801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-3.393704	1.325261	-2.068444	2475.735325
HLA A*6801	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.446833	2.378256	-2.068577	27979.031153
HLA A*0203	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.006229	1.937546	-2.068683	10144.462718
HLA B*5301	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.500540	2.431527	-2.069013	31662.087846
HLA B*5801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.843071	1.773509	-2.069562	6967.410745
HLA A*0206	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.234099	2.164532	-2.069566	17143.462916
HLA B*3501	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.918236	1.848352	-2.069884	8283.924615
HLA A*0216	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.414151	2.343890	-2.070261	25950.834946
HLA A*0202	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.112421	2.041338	-2.071083	12954.512474
HLA A*3001	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.373339	1.300706	-2.072633	2362.320819
HLA B*1503	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.822391	1.749555	-2.072836	6643.412923
HLA B*2705	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.781054	1.708081	-2.072974	6040.242960
HLA B*1503	1:364-372	9	AAAELVQTR	0.986953	0.803779	-3.864189	1.790732	-2.073457	7314.566374
HLA A*3301	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.277158	2.203513	-2.073644	18930.302938
HLA B*5701	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.928414	1.854767	-2.073647	8480.356451
HLA B*3901	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.329257	2.255532	-2.073726	21343.094824
HLA A*3301	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-3.540575	1.466619	-2.073956	3471.964052
HLA B*1509	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.435496	2.361023	-2.074474	27258.151858
HLA B*1509	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.273586	2.199112	-2.074475	18775.276727
HLA A*0219	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.418385	2.343890	-2.074495	26205.056924
HLA B*0702	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.866890	1.792274	-2.074616	7360.214867
HLA B*7301	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.593297	2.518634	-2.074664	39201.006460
HLA A*2902	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.192882	2.118146	-2.074736	15591.271597
HLA B*7301	1:3-11	9	ATETVRVRF	1.431229	1.094515	-4.600578	2.525744	-2.074834	39863.761094
HLA A*6802	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-3.839801	1.764802	-2.074999	6915.139264
HLA B*4501	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-2.656943	0.581735	-2.075208	453.882364
HLA B*4402	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-3.887120	1.811844	-2.075275	7711.157235
HLA B*2705	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.310649	2.234720	-2.075930	20447.935787
HLA A*0206	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.823091	1.747156	-2.075935	6654.131718
HLA A*2602	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.275085	2.199112	-2.075974	18840.191732
HLA A*2403	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.141428	2.064809	-2.076618	13849.299759
HLA B*1503	1:233-241	9	IRIGVAERI	1.016372	0.381644	-3.474663	1.398016	-2.076647	2983.065351
HLA B*3901	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.221667	2.144780	-2.076888	16659.709613
HLA A*2603	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.455768	2.378256	-2.077512	28560.628703

HLA A*3002	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.150252	2.072193	-2.078060	14133.589749
HLA B*5401	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.563814	2.485326	-2.078487	36628.027375
HLA B*5701	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.223481	2.144780	-2.078701	16729.433295
HLA B*3501	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.243457	2.164532	-2.078924	17516.871782
HLA B*4601	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.223707	2.144780	-2.078927	16738.123972
HLA B*1517	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.852028	1.771882	-2.080145	7112.587968
HLA A*0201	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.083621	2.003005	-2.080616	12123.306536
HLA A*0216	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.315985	2.235159	-2.080827	20700.705796
HLA B*1509	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.094593	2.012396	-2.082198	12433.493778
HLA A*0211	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.513793	2.431527	-2.082266	32643.220183
HLA A*0206	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.219636	1.137355	-2.082280	1658.194875
HLA B*4403	1:415-423	9	AALTSVTDW	1.150326	0.497710	-3.730545	1.648036	-2.082509	5377.063673
HLA A*0201	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.411344	1.328755	-2.082589	2578.363514
HLA A*3001	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.281723	2.199112	-2.082611	19130.336678
HLA A*3301	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.858658	1.776041	-2.082617	7222.006874
HLA A*0101	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.383009	2.300286	-2.082722	24155.104004
HLA B*4801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.383183	2.300286	-2.082896	24164.775996
HLA A*0202	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.729060	1.645215	-2.083845	5358.710617
HLA B*4801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.170773	2.086649	-2.084124	14817.429960
HLA A*0203	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.384567	2.300286	-2.084280	24241.898042
HLA A*0211	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.428361	2.343890	-2.084471	26813.963925
HLA A*0101	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.340058	2.255532	-2.084526	21880.537002
HLA B*5801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.340215	2.255532	-2.084684	21888.469315
HLA A*6802	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.446114	2.361023	-2.085091	27932.752252
HLA B*2705	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.385833	2.300286	-2.085547	24312.688886
HLA B*5701	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.386037	2.300286	-2.085751	24324.134598
HLA A*0250	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.098221	2.012396	-2.085825	12537.784076
HLA A*0201	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.386444	2.300286	-2.086157	24346.910475
HLA A*3301	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.572145	2.485326	-2.086819	37337.462886
HLA A*2403	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.342624	2.255532	-2.087092	22010.181004
HLA B*0801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.290707	2.203513	-2.087194	19530.215885
HLA A*0203	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.090416	2.003005	-2.087411	12314.472040
HLA A*0250	1:58-66	9	YLALLDALR	0.982293	0.674716	-3.744854	1.657009	-2.087845	5557.168213
HLA A*8001	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.344080	2.255532	-2.088549	22084.129988
HLA B*1501	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.287740	2.199112	-2.088628	19397.226829
HLA B*1503	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-3.740662	1.651959	-2.088703	5503.792621
HLA A*6901	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.251246	1.162401	-2.088845	1783.386767
HLA A*0206	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.324053	2.235159	-2.088895	21088.868783
HLA A*6801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-3.900935	1.811844	-2.089090	7960.393393
HLA A*0211	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-3.882820	1.792234	-2.090586	7635.192678
HLA B*0803	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.451896	2.361023	-2.090873	28307.128216
HLA B*1503	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.863484	1.771882	-2.091601	7302.704704
HLA B*4601	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.157160	2.064809	-2.092351	14360.182754
HLA A*3101	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.349442	2.255532	-2.093910	22358.456525
HLA A*6802	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.258496	2.164532	-2.093963	18134.083226
HLA A*1101	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.394425	2.300286	-2.094139	24798.479853
HLA A*3101	1:112-120	9	STPEEVEAR	0.994604	0.605580	-3.694598	1.600184	-2.094414	4949.918618
HLA B*5101	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.329972	2.234720	-2.095252	21378.224691
HLA A*3301	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.526992	2.431527	-2.095466	33650.568148
HLA B*3801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.101463	2.005692	-2.095771	12631.737019
HLA B*4403	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.634481	2.538635	-2.095846	43100.403898
HLA A*2902	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.273398	2.177014	-2.096384	18767.152712
HLA B*1509	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.151761	2.055046	-2.096715	14182.763154
HLA A*2402	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.870504	1.773509	-2.096995	7421.710347
HLA A*3101	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.103676	2.006546	-2.097131	12696.274116
HLA A*0301	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.331910	2.234720	-2.097190	21473.852339
HLA B*4801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.332652	2.235159	-2.097494	21510.593823
HLA A*0101	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.301080	2.203513	-2.097567	20002.303850
HLA A*3101	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.301146	2.203513	-2.097632	20005.333966
HLA A*0216	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.187995	2.089268	-2.098726	15416.813125
HLA A*2603	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-3.953511	1.854767	-2.098745	8984.859824
HLA A*3101	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.399340	2.300286	-2.099054	25080.730525
HLA B*0801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.436742	1.337377	-2.099365	2733.644778
HLA A*0301	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.355398	2.255532	-2.099866	22667.194126
HLA A*0101	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.334638	2.234720	-2.099918	21609.151511

HLA A*3002	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.103202	2.003005	-2.100197	12682.407236
HLA B*5101	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.444417	2.343890	-2.100527	27823.861398
HLA A*0203	1:327-335	9	LNAEHIRML	1.465570	0.426650	-3.992813	1.892220	-2.100594	9835.886102
HLA A*0202	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.815103	1.714405	-2.100699	6532.856889
HLA B*4403	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.586080	2.485326	-2.100753	38554.901637
HLA B*0801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.134140	2.032901	-2.101239	13618.827308
HLA A*6802	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-3.056525	0.955018	-2.101507	1139.003141
HLA B*4002	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.478083	2.376452	-2.101631	30066.520523
HLA B*4601	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.278795	2.177014	-2.101781	19001.818040
HLA A*6802	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.849100	1.747156	-2.101944	7064.805217
HLA B*4001	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-3.688339	1.585411	-2.102928	4879.092263
HLA B*4601	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.267743	2.164532	-2.103211	18524.358513
HLA B*1503	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-3.847512	1.743756	-2.103756	7039.015809
HLA B*1503	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.015646	1.911098	-2.104548	10366.825452
HLA B*1503	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.005867	1.900474	-2.105393	10136.014653
HLA A*2403	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.112181	2.006546	-2.105636	12947.366034
HLA A*3001	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-2.999592	0.893488	-2.106104	999.061449
HLA A*3002	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.094137	1.987904	-2.106233	12420.451441
HLA A*2501	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.251438	2.144780	-2.106658	17841.762404
HLA A*2603	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.224816	2.118146	-2.106670	16780.918845
HLA A*3001	1:435-443	9	ALIEGLALK	0.478643	0.243793	-2.829109	0.722436	-2.106672	674.697142
HLA A*6802	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.110151	2.003005	-2.107146	12886.989392
HLA A*3001	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.284300	2.177014	-2.107286	19244.206053
HLA B*0801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.407737	2.300286	-2.107451	25570.383492
HLA B*4403	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.468570	2.361023	-2.107547	29415.084959
HLA B*7301	1:233-241	9	IRIGVAERI	1.016372	0.381644	-3.505667	1.398016	-2.107651	3203.808666
HLA A*2603	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.193981	2.086183	-2.107798	15630.796030
HLA A*2902	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.194216	2.086183	-2.108033	15639.254405
HLA B*1509	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.312076	2.203513	-2.108562	20515.193144
HLA A*2602	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.855937	1.747156	-2.108781	7176.904938
HLA A*1101	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.819426	1.710232	-2.109195	6598.210961
HLA A*2902	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.253989	2.144780	-2.109209	17946.893777
HLA B*1501	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.233018	2.123741	-2.109277	17100.853608
HLA B*4801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.344764	2.234720	-2.110044	22118.923923
HLA A*0219	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.313636	2.203513	-2.110122	20589.019650
HLA A*6901	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.345723	2.235159	-2.110564	22167.799501
HLA A*3001	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.197280	2.086649	-2.110631	15749.971522
HLA B*5801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.234813	2.123741	-2.111072	17171.680360
HLA A*0212	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.411374	2.300286	-2.111088	25785.422047
HLA B*0702	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.101846	0.990658	-2.111189	1264.289373
HLA B*1503	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.114197	2.003005	-2.111192	13007.603320
HLA A*2301	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.288311	2.177014	-2.111297	19422.743251
HLA B*4601	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.366976	2.255532	-2.111444	23279.627461
HLA A*6802	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-3.434435	1.322784	-2.111651	2719.160767
HLA A*0206	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.237954	2.126210	-2.111744	17296.333765
HLA A*2902	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.201203	2.089268	-2.111935	15892.909589
HLA A*0202	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.274806	1.162401	-2.112406	1882.808609
HLA A*0206	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.412720	2.300286	-2.112434	25865.477429
HLA A*0212	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.449857	1.337377	-2.112480	2817.454460
HLA A*2403	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.167028	2.054462	-2.112566	14690.203228
HLA B*5101	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.120179	2.006546	-2.113633	13188.004086
HLA B*4801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.369293	2.255532	-2.113761	23404.136281
HLA A*2602	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.475163	2.361023	-2.114140	29865.016705
HLA B*0801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.292387	2.177014	-2.115373	19605.906436
HLA A*1101	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.261078	2.144780	-2.116298	18242.219984
HLA A*0202	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.351422	2.234720	-2.116703	22460.655948
HLA A*0212	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.281302	2.164532	-2.116770	19111.820398
HLA B*0801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.934457	1.817618	-2.116839	8599.178867
HLA B*4501	1:440-448	9	LALKPRKAF	1.407943	1.119240	-4.644166	2.527183	-2.116983	44072.320454
HLA B*5101	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.478074	2.361023	-2.117051	30065.869904
HLA A*3201	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.417699	2.300286	-2.117413	26163.693799
HLA B*5401	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.495876	2.378256	-2.117620	31323.899491
HLA B*7301	1:103-111	9	AAGEAYHAF	1.364634	1.135406	-4.617673	2.500040	-2.117633	41464.184119
HLA B*7301	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-2.418461	0.299836	-2.118625	262.096477
HLA B*4001	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.374370	2.255532	-2.118838	23679.354286

HLA A*6801	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.550367	2.431527	-2.118841	35511.370006
HLA B*4402	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.317954	2.199112	-2.118842	20794.765227
HLA A*2301	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.263850	2.144780	-2.119070	18359.044770
HLA B*4801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.264092	2.144780	-2.119312	18369.277622
HLA B*4501	1:275-283	9	FIPEGLLNY	1.273574	1.265061	-4.658747	2.538635	-2.120111	45577.113943
HLA A*3002	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.185034	2.064809	-2.120225	15312.082382
HLA B*3501	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.297401	2.177014	-2.120387	19833.562393
HLA B*0802	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.376451	2.255532	-2.120920	23793.125707
HLA A*0211	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.210583	2.089268	-2.121314	16239.870319
HLA B*4402	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.356427	2.234720	-2.121707	22720.968440
HLA B*1503	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.180636	2.058588	-2.122048	15157.794717
HLA A*2501	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.248367	2.126210	-2.122157	17716.053158
HLA B*5401	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.554326	2.431527	-2.122800	35836.559603
HLA A*0211	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-2.735872	0.612666	-2.123206	544.342079
HLA B*4001	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.268037	2.144780	-2.123257	18536.889590
HLA A*0212	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.015096	1.891829	-2.123267	10353.710245
HLA A*0216	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.131626	2.008310	-2.123315	13540.221346
HLA B*0801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.196199	2.072193	-2.124006	15710.825674
HLA B*1503	1:321-329	9	QKKADALNA	1.204390	-0.265678	-3.062812	0.938712	-2.124100	1155.612268
HLA A*0206	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.016562	1.892220	-2.124342	10388.721059
HLA A*2603	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.137166	2.012396	-2.124770	13714.053823
HLA B*0702	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-2.349969	0.225072	-2.124897	223.856132
HLA A*2603	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.360726	2.235159	-2.125568	22947.025381
HLA B*4501	1:33-41	9	YARHTGGTF	1.316740	1.201894	-4.644366	2.518634	-2.125732	44092.591356
HLA B*1801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.190776	2.064809	-2.125967	15515.879509
HLA A*0202	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.212791	2.086183	-2.126608	16322.665203
HLA B*4001	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.244833	2.118146	-2.126688	17572.491799
HLA A*0301	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.330232	2.203513	-2.126719	21391.066121
HLA B*1801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.185326	2.058588	-2.126737	15322.357575
HLA A*0219	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.243939	1.117129	-2.126810	1753.632725
HLA A*6901	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.325973	2.199112	-2.126861	21182.285333
HLA B*1509	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.362155	2.235159	-2.126996	23022.627293
HLA B*4601	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.330592	2.203513	-2.127078	21408.779115
HLA A*0216	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.427508	2.300286	-2.127222	26761.358607
HLA A*2402	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.664059	1.536595	-2.127464	4613.807308
HLA A*3101	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.116063	1.987904	-2.128159	13063.597029
HLA B*4402	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.331971	2.203513	-2.128458	21476.873002
HLA B*1517	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-3.977119	1.848352	-2.128767	9486.782226
HLA B*1801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.364850	2.234720	-2.130130	23165.930132
HLA A*0250	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.256600	2.126210	-2.130390	18055.086365
HLA B*3901	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.307562	2.177014	-2.130548	20303.095123
HLA A*6901	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.365531	2.234720	-2.130811	23202.302939
HLA A*2501	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.431122	2.300286	-2.130835	26984.952978
HLA A*3101	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.907123	1.776041	-2.131083	8074.638238
HLA A*0202	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.254908	2.123741	-2.131167	17984.896422
HLA A*3001	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.134318	2.003005	-2.131313	13624.427862
HLA B*4001	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.366588	2.235159	-2.131430	23258.856599
HLA A*3002	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.432040	2.300286	-2.131754	27042.093762
HLA A*0206	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.255632	2.123741	-2.131891	18014.888661
HLA A*2501	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.120057	1.987904	-2.132153	13184.294634
HLA A*0212	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.221710	2.089268	-2.132441	16661.331982
HLA A*0206	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.342781	1.210192	-2.132590	2201.818293
HLA B*7301	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.618007	2.485326	-2.132681	41496.049320
HLA A*3201	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.256546	2.123741	-2.132805	18052.839957
HLA A*3002	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-3.985789	1.852707	-2.133081	9678.064918
HLA A*6901	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-2.902309	0.768573	-2.133737	798.563443
HLA A*0203	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.142485	2.008310	-2.134175	13883.056261
HLA A*0201	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.369354	2.235159	-2.134195	23407.428471
HLA B*2705	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.143044	2.008310	-2.134734	13900.942953
HLA A*6802	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.435426	2.300286	-2.135140	27253.728310
HLA B*1509	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.168804	2.032901	-2.135903	14750.407370
HLA B*0702	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.391540	2.255532	-2.136008	24634.281042
HLA A*2403	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.436780	1.300706	-2.136074	2733.881408
HLA B*0803	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.370843	2.234720	-2.136123	23487.850741
HLA A*0219	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.988880	1.852642	-2.136238	9747.212924

HLA A*2602	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.736005	1.599646	-2.136360	5445.094011
HLA B*1503	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.465213	1.328755	-2.136458	2918.859153
HLA A*3002	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.313669	2.177014	-2.136655	20590.579090
HLA A*0219	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.051107	0.914377	-2.136730	1124.882109
HLA B*1503	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.393720	2.255532	-2.138189	24758.265387
HLA A*2602	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.315215	2.177014	-2.138200	20664.006131
HLA A*0201	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.373559	2.234720	-2.138839	23635.200079
HLA A*2603	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.130028	1.990887	-2.139141	13490.502108
HLA A*3001	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.849509	1.710232	-2.139277	7071.458595
HLA A*0219	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.439852	2.300286	-2.139566	27532.925010
HLA A*1101	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.374391	2.234720	-2.139671	23680.507238
HLA B*5401	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.338785	2.199112	-2.139673	21816.473736
HLA B*1502	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.050930	1.911098	-2.139833	11244.246352
HLA A*2403	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.266070	2.126210	-2.139860	18453.142871
HLA B*5701	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.395668	2.255532	-2.140136	24869.550568
HLA A*2402	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.285012	2.144780	-2.140232	19275.776955
HLA A*0203	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.128228	1.987904	-2.140324	13434.713477
HLA B*0802	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.343855	2.203513	-2.140341	22072.663588
HLA A*0101	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.199695	2.058588	-2.141107	15837.806894
HLA B*1509	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.441434	2.300286	-2.141147	27633.351116
HLA B*5801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-3.994275	1.852642	-2.141632	9869.039126
HLA A*0203	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.345972	2.203513	-2.142458	22180.515233
HLA B*4001	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.151540	2.008310	-2.143230	14175.552633
HLA B*4002	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.629101	2.485326	-2.143775	42569.742124
HLA B*4501	1:290-298	9	SIADDHDLF	1.324197	1.161129	-4.629146	2.485326	-2.143819	42574.118003
HLA A*2902	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.055845	1.911098	-2.144748	11372.225813
HLA B*4801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.718177	1.573351	-2.144826	5226.097288
HLA B*0802	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.269165	2.123741	-2.145424	18585.087750
HLA A*2402	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.344621	2.199112	-2.145509	22111.625811
HLA B*2705	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-3.825366	1.679828	-2.145538	6689.069294
HLA A*0216	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.000835	1.854767	-2.146068	10019.236610
HLA B*0702	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.196686	1.050133	-2.146553	1572.844540
HLA B*5801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.323602	2.177014	-2.146588	21066.975174
HLA A*2501	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.382088	2.235159	-2.146929	24103.933119
HLA A*0202	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.491111	2.343890	-2.147221	30982.115326
HLA B*1502	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.202030	2.054462	-2.147568	15923.202989
HLA B*2705	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.312628	2.164532	-2.148095	20541.291186
HLA A*6901	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.220718	2.072193	-2.148526	16623.337993
HLA B*0802	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.448825	2.300286	-2.148539	28107.682238
HLA B*3901	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.448978	2.300286	-2.148691	28117.567840
HLA B*0702	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.449095	2.300286	-2.148809	28125.174515
HLA A*3001	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.001544	1.852707	-2.148837	10035.619283
HLA B*1502	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.920783	1.771882	-2.148901	8332.646921
HLA B*3501	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.293820	2.144780	-2.149040	19670.713435
HLA B*1509	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.405158	2.255532	-2.149626	25418.944148
HLA B*7301	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-3.037583	0.887847	-2.149736	1090.393801
HLA A*0201	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.222043	2.072193	-2.149851	16674.136205
HLA A*8001	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.354848	2.203513	-2.151335	22638.517561
HLA A*0219	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.386200	2.234720	-2.151480	24333.216063
HLA A*0250	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.583159	2.431527	-2.151633	38296.509254
HLA A*0212	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.386824	2.235159	-2.151666	24368.257510
HLA A*3001	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.927766	1.776041	-2.151725	8467.703630
HLA B*5301	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.386984	2.235159	-2.151826	24377.223570
HLA A*0203	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.387031	2.235159	-2.151873	24379.861275
HLA A*0212	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.052406	1.900474	-2.151932	11282.512638
HLA A*2501	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.216766	2.064809	-2.151957	16472.761155
HLA B*5801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.351176	2.199112	-2.152064	22447.901057
HLA A*2301	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.408409	2.255532	-2.152878	25609.977335
HLA B*0801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.388143	2.235159	-2.152984	24442.326241
HLA A*6901	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.753279	1.599646	-2.153633	5666.029041
HLA B*4402	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.298601	2.144780	-2.153821	19888.467207
HLA A*2403	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.358313	2.203513	-2.154800	22819.886231
HLA A*6901	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.187999	2.032901	-2.155098	15416.979932
HLA B*1501	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.047575	1.892220	-2.155355	11157.715601
HLA A*2601	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.390325	2.234720	-2.155605	24565.477373

HLA A*2902	1:58-66	9	YLALLDALR	0.982293	0.674716	-3.812791	1.657009	-2.155782	6498.172729
HLA A*2601	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.273953	2.118146	-2.155807	18791.128673
HLA A*3201	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.188793	2.032901	-2.155892	15445.196325
HLA B*0803	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.948352	1.792274	-2.156078	8878.750188
HLA A*3201	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.391664	2.234720	-2.156945	24641.345298
HLA B*4801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.165313	2.008310	-2.157002	14632.302803
HLA A*0301	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.321572	2.164532	-2.157040	20968.734868
HLA B*1503	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.758683	1.601532	-2.157151	5736.970433
HLA B*5701	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.281349	2.123741	-2.157608	19113.888366
HLA B*0702	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.392381	2.234720	-2.157661	24682.037478
HLA A*2403	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.803088	1.645215	-2.157873	6354.595021
HLA A*2601	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.284455	2.126210	-2.158245	19251.078475
HLA A*6802	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.126629	0.967578	-2.159051	1338.532299
HLA B*3901	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-3.713948	1.554677	-2.159271	5175.453575
HLA B*0802	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.160985	2.001284	-2.159701	14487.215772
HLA A*8001	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.324723	2.164532	-2.160190	21121.409068
HLA A*0250	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.232811	2.072193	-2.160618	17092.714338
HLA B*1503	1:463-471	9	PLFESLELL	1.291656	0.202256	-3.655559	1.493912	-2.161647	4524.379396
HLA A*0202	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.250961	2.089268	-2.161692	17822.179202
HLA B*1503	1:434-442	9	DALIEGLAL	1.463983	0.353635	-3.979379	1.817618	-2.161761	9536.283111
HLA B*7301	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-3.089437	0.927578	-2.161859	1228.673546
HLA A*6802	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-2.414815	0.252948	-2.161867	259.905088
HLA B*4402	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.418070	2.255532	-2.162539	26186.067103
HLA A*0206	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.248762	2.086183	-2.162579	17732.161914
HLA B*5701	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.936257	1.773509	-2.162748	8634.887587
HLA B*0802	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.398365	2.235159	-2.163207	25024.484839
HLA A*3001	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.252509	2.089268	-2.163241	17885.830750
HLA A*2601	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.362561	2.199112	-2.163450	23044.184505
HLA B*0801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.133778	1.970233	-2.163545	13607.485876
HLA B*1503	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.016440	1.852707	-2.163733	10385.798975
HLA B*1517	1:364-372	9	AAAELVQTR	0.986953	0.803779	-3.954592	1.790732	-2.163860	9007.246933
HLA A*2501	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.363527	2.199112	-2.164415	23095.479435
HLA B*5301	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.367953	2.203513	-2.164440	23332.077583
HLA A*3001	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.251290	2.086183	-2.165107	17835.682557
HLA B*0702	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.310231	2.144780	-2.165451	20428.254715
HLA B*0702	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.369323	2.203513	-2.165810	23405.782318
HLA B*0803	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.369720	2.203513	-2.166207	23427.191337
HLA B*4001	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.401006	2.234720	-2.166286	25177.115190
HLA B*2705	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.422118	2.255532	-2.166587	26431.294831
HLA A*0206	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-3.554047	1.386690	-2.167357	3581.353306
HLA A*2403	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.200738	2.032901	-2.167837	15875.894886
HLA B*1503	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.011910	1.843794	-2.168116	10278.035305
HLA B*4601	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.240386	2.072193	-2.168193	17393.451646
HLA A*2402	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.423848	2.255532	-2.168316	26536.745543
HLA A*2403	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.159458	1.990887	-2.168571	14436.361986
HLA A*2501	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.286870	2.118146	-2.168725	19358.439028
HLA B*3801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.404009	2.235159	-2.168850	25351.788830
HLA A*0301	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.367965	2.199112	-2.168853	23332.708712
HLA A*3001	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.241474	2.072193	-2.169281	17437.073001
HLA B*0801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-2.990434	0.821048	-2.169386	978.214078
HLA A*2603	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.945495	1.776041	-2.169454	8820.533690
HLA A*0211	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.295664	2.126210	-2.169454	19754.427925
HLA B*4403	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.404946	2.235159	-2.169787	25406.570930
HLA B*4501	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.934490	1.764296	-2.170193	8599.830180
HLA A*0203	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.946261	1.776041	-2.170220	8836.103520
HLA B*4002	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.158377	1.987904	-2.170473	14400.481056
HLA A*3001	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.225915	2.055046	-2.170869	16823.459076
HLA B*5301	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.944489	1.773509	-2.170980	8800.133966
HLA A*0203	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.295462	2.123741	-2.171722	19745.239306
HLA A*0219	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.406978	2.235159	-2.171820	25525.740968
HLA B*0801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.026702	1.854767	-2.171936	10634.142183
HLA B*0801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.160130	1.987904	-2.172226	14458.715622
HLA A*6802	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.235321	1.062125	-2.173195	1719.177547
HLA A*0212	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.407944	2.234720	-2.173224	25582.559689
HLA A*2301	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.174509	2.001284	-2.173225	14945.435142

HLA B*4801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.377248	2.203513	-2.173735	23836.801204
HLA A*3002	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-3.947262	1.773509	-2.173753	8856.490800
HLA B*0803	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.409091	2.235159	-2.173932	25650.187539
HLA A*0216	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.408992	2.234720	-2.174272	25644.360085
HLA A*3101	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-3.705030	1.530697	-2.174333	5070.254651
HLA B*0801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.747997	1.573351	-2.174646	5597.539331
HLA B*3501	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.819882	1.645215	-2.174667	6605.139540
HLA A*1101	1:112-120	9	STPEEVEAR	0.994604	0.605580	-3.775218	1.600184	-2.175034	5959.616132
HLA A*8001	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.352506	2.177014	-2.175491	22516.741810
HLA B*3501	1:409-417	9	VLDAALAAL	1.329115	0.442767	-3.947534	1.771882	-2.175652	8862.050410
HLA B*1501	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-3.951806	1.776041	-2.175765	8949.640282
HLA B*0801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-3.919542	1.743756	-2.175786	8308.879331
HLA B*5101	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.476084	2.300286	-2.175797	29928.417948
HLA A*0206	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.226233	1.050133	-2.176100	1683.576761
HLA A*6802	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.088174	1.911098	-2.177077	12251.080352
HLA A*0250	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.521046	2.343890	-2.177155	33192.950219
HLA A*2301	1:283-291	9	YLALLGWSI	1.492210	0.300064	-3.969850	1.792274	-2.177576	9329.312155
HLA A*0216	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.714324	1.536595	-2.177729	5179.935295
HLA B*1517	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.190476	2.012396	-2.178080	15505.139012
HLA B*3801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.478837	2.300286	-2.178551	30118.778635
HLA A*3001	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.237160	2.058588	-2.178571	17264.735581
HLA B*0702	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.413747	2.235159	-2.178589	25926.698901
HLA A*2902	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.185194	2.006546	-2.178648	15317.716311
HLA A*0101	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.355701	2.177014	-2.178687	22683.018531
HLA B*3901	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.191185	2.012396	-2.178790	15530.491804
HLA B*0801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.243609	2.064809	-2.178800	17523.032547
HLA B*1801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-3.896292	1.717294	-2.178997	7875.750477
HLA A*6901	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.343568	2.164532	-2.179036	22058.100293
HLA A*6802	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-2.967296	0.787998	-2.179299	927.462119
HLA A*0203	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.356394	2.177014	-2.179380	22719.247654
HLA A*0101	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.324363	2.144780	-2.179584	21103.933836
HLA A*3002	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.303723	2.123741	-2.179982	20124.411582
HLA A*0203	1:58-66	9	YLALLDALR	0.982293	0.674716	-3.837090	1.657009	-2.180081	6872.102446
HLA A*0202	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.480386	2.300286	-2.180099	30226.347236
HLA A*0219	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.183361	2.003005	-2.180356	15253.216119
HLA B*4002	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.612549	2.431527	-2.181022	40977.824442
HLA B*1517	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.346230	2.164532	-2.181698	22193.718515
HLA A*0212	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.017803	1.835915	-2.181888	10418.438047
HLA B*3901	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.417091	2.235159	-2.181932	26127.059915
HLA A*0211	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.417215	2.235159	-2.182056	26134.552247
HLA A*3001	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.827617	1.645215	-2.182401	6723.826548
HLA B*7301	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.223805	2.041338	-2.182468	16741.927562
HLA A*0203	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.381768	2.199112	-2.182657	24086.205295
HLA B*0803	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.483175	2.300286	-2.182888	30421.071431
HLA B*4001	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-2.590833	0.407915	-2.182919	389.792519
HLA B*2705	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.306747	2.123741	-2.183006	20265.017265
HLA B*3501	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.255469	2.072193	-2.183277	18008.165276
HLA A*3101	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.520938	1.337377	-2.183562	3318.472509
HLA B*4601	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.382748	2.199112	-2.183636	24140.603274
HLA B*3801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.221047	2.037348	-2.183699	16635.933020
HLA A*6802	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.418543	2.234720	-2.183823	26214.556998
HLA A*0203	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.418775	2.234720	-2.184055	26228.600725
HLA A*0219	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.383218	2.199112	-2.184106	24166.737007
HLA A*8001	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.310706	2.126210	-2.184496	20450.590865
HLA A*0212	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.622027	1.437023	-2.185005	4188.197623
HLA A*3101	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.384163	2.199112	-2.185051	24219.351425
HLA B*5401	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.529079	2.343890	-2.185188	33812.613778
HLA A*2902	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.384390	2.199112	-2.185279	24232.064089
HLA A*2301	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.240929	2.055046	-2.185883	17415.201559
HLA B*3901	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.385161	2.199112	-2.186049	24275.100692
HLA A*8001	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.385326	2.199112	-2.186214	24284.295225
HLA A*2603	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.421092	2.234720	-2.186372	26368.881842
HLA A*0201	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.389952	2.203513	-2.186438	24544.355913
HLA B*4801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.386103	2.199112	-2.186991	24327.819422
HLA A*6802	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.422866	2.235159	-2.187707	26476.804905

HLA A*0301	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.364836	2.177014	-2.187822	23165.178193
HLA B*2705	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.391843	2.203513	-2.188330	24651.478709
HLA A*0202	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.059932	0.871584	-2.188347	1147.973004
HLA B*5101	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.443912	2.255532	-2.188381	27791.517550
HLA B*5301	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.089062	1.900474	-2.188589	12276.158686
HLA B*1801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.365801	2.177014	-2.188787	23216.742447
HLA A*2602	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.209552	1.020365	-2.189187	1620.136398
HLA B*4001	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.388366	2.199112	-2.189254	24454.891345
HLA B*4001	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.230873	2.041338	-2.189535	17016.596833
HLA A*0250	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.177845	1.987904	-2.189941	15060.688736
HLA B*4002	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-3.775754	1.585411	-2.190343	5966.971584
HLA A*3001	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.374232	1.183813	-2.190419	2367.182174
HLA A*0216	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.317461	2.126210	-2.191251	20771.154192
HLA A*2402	1:224-232	9	RQLALHQAL	1.264243	0.500053	-3.956359	1.764296	-2.192062	9043.965183
HLA B*0702	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.162334	1.970233	-2.192101	14532.272502
HLA B*0801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.247218	2.054462	-2.192756	17669.248414
HLA A*0201	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.391979	2.199112	-2.192867	24659.214905
HLA B*7301	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.624397	2.431527	-2.192871	42111.174122
HLA B*3801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.357996	2.164532	-2.193464	22803.226153
HLA A*0219	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.358215	2.164532	-2.193682	22814.701792
HLA B*3801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.282958	2.089268	-2.193690	19184.851523
HLA B*1517	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.392811	2.199112	-2.193699	24706.485035
HLA A*6802	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.319913	2.126210	-2.193704	20888.800013
HLA A*0250	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.358492	2.164532	-2.193960	22829.270592
HLA A*0212	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.049117	1.854767	-2.194350	11197.383423
HLA B*0801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.094908	1.900474	-2.194434	12442.510398
HLA A*2301	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.538763	2.343890	-2.194873	34575.090139
HLA B*1509	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-3.959728	1.764802	-2.194926	9114.399137
HLA B*4001	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.284291	2.089268	-2.195022	19243.789621
HLA B*3901	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.429829	2.234720	-2.195110	26904.780230
HLA A*6901	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.372359	2.177014	-2.195345	23569.951900
HLA A*0212	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.399260	2.203513	-2.195747	25076.117694
HLA B*5301	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.430584	2.234720	-2.195864	26951.542974
HLA B*5301	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.198924	2.003005	-2.195919	15809.728518
HLA B*0802	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.373019	2.177014	-2.196005	23605.809691
HLA A*0216	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.048656	1.852642	-2.196014	11185.516701
HLA B*1509	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.341308	2.144780	-2.196528	21943.601230
HLA B*1517	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.373862	2.177014	-2.196848	23651.700267
HLA A*0101	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.396002	2.199112	-2.196890	24888.662803
HLA A*0101	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.315128	2.118146	-2.196982	20659.870316
HLA B*5101	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.433152	2.235159	-2.197993	27111.379778
HLA B*4001	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.375098	2.177014	-2.198084	23719.099436
HLA B*1517	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.041890	1.843794	-2.198096	11012.591600
HLA B*1509	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.376076	2.177014	-2.199062	23772.539710
HLA A*0211	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.499402	2.300286	-2.199116	31579.292710
HLA A*2602	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.271676	2.072193	-2.199484	18692.879890
HLA B*0803	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.455345	2.255532	-2.199813	28532.830470
HLA B*1503	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.170063	1.970233	-2.199831	14793.241207
HLA A*0206	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.047129	1.846931	-2.200198	11146.252712
HLA A*0202	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-3.965075	1.764802	-2.200274	9227.317643
HLA B*3501	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.947699	1.747156	-2.200543	8865.407035
HLA A*2601	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.377652	2.177014	-2.200638	23858.991692
HLA B*4001	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.404326	2.203513	-2.200812	25370.310893
HLA B*0702	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.378357	2.177014	-2.201343	23897.745482
HLA A*0206	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.402313	1.200757	-2.201555	2525.298533
HLA B*3901	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-2.991811	0.790220	-2.201591	981.320128
HLA B*4801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-3.948794	1.747156	-2.201638	8887.784996
HLA A*0216	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.274286	2.072193	-2.202094	18805.569644
HLA B*5701	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.320402	2.118146	-2.202256	20912.318510
HLA B*1509	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.239975	2.037348	-2.202627	17376.992526
HLA B*1509	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.437371	2.234720	-2.202651	27376.082170
HLA A*3101	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.291924	2.089268	-2.202656	19585.022607
HLA B*3801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.320926	2.118146	-2.202780	20937.562465
HLA B*0803	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.320994	2.118146	-2.202848	20940.847550
HLA A*3101	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.776337	1.573351	-2.202985	5974.982559

HLA B*4002	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.367528	2.164532	-2.202996	23309.242230
HLA A*0201	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.380373	2.177014	-2.203359	24008.929126
HLA B*4801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.380648	2.177014	-2.203634	24024.130557
HLA B*5401	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.564974	2.361023	-2.203951	36726.046156
HLA A*0206	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-3.917254	1.713159	-2.204095	8265.213062
HLA A*0219	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.381317	2.177014	-2.204303	24061.199973
HLA A*6802	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.174560	1.970233	-2.204328	14947.214017
HLA B*2705	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.269155	2.064809	-2.204346	18584.685582
HLA A*0211	1:435-443	9	ALIEGLALK	0.478643	0.243793	-2.927045	0.722436	-2.204608	845.366052
HLA B*3801	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.460720	2.255532	-2.205189	28888.199703
HLA B*3801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.329189	2.123741	-2.205449	21339.746637
HLA A*3301	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.583277	2.376452	-2.206825	38306.869648
HLA B*4002	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.585701	2.378256	-2.207446	38521.335240
HLA A*3101	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.262361	2.054462	-2.207898	18296.183503
HLA B*1503	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.449801	1.241782	-2.208019	2817.088673
HLA B*5301	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.331778	2.123741	-2.208038	21467.347740
HLA B*4002	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.569100	2.361023	-2.208077	37076.597417
HLA A*0216	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.449993	1.241782	-2.208211	2818.338641
HLA B*5701	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.385478	2.177014	-2.208464	24292.836124
HLA B*5801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.273469	2.064809	-2.208660	18770.198806
HLA A*6901	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.263791	2.055046	-2.208745	18356.561928
HLA A*6802	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.197073	1.987904	-2.209169	15742.475213
HLA B*1502	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.509566	2.300286	-2.209280	32327.064585
HLA B*7301	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.585762	2.376452	-2.209310	38526.753921
HLA B*1501	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.335641	2.126210	-2.209431	21659.126841
HLA A*0211	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.412977	2.203513	-2.209463	25880.734228
HLA B*5301	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.465081	2.255532	-2.209550	29179.720110
HLA A*2501	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.444518	2.234720	-2.209799	27830.334683
HLA A*1101	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.465535	2.255532	-2.210003	29210.202818
HLA A*2402	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.553908	2.343890	-2.210018	35802.067030
HLA B*0801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.094084	0.883995	-2.210089	1241.891884
HLA B*1517	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.336677	2.126210	-2.210467	21710.862033
HLA A*2902	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.198511	1.987904	-2.210607	15794.682599
HLA A*2501	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.243565	2.032901	-2.210664	17521.231484
HLA B*3801	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.414440	2.203513	-2.210927	25968.108803
HLA A*0301	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.355776	2.144780	-2.210996	22686.945675
HLA A*3002	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.549743	1.338560	-2.211183	3546.034122
HLA A*0203	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.337401	2.126210	-2.211191	21747.067822
HLA B*4402	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.375888	2.164532	-2.211355	23762.253391
HLA B*0803	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.388558	2.177014	-2.211544	24465.742209
HLA B*3901	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.415801	2.203513	-2.212287	26049.576906
HLA A*0212	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.220638	2.008310	-2.212328	16620.280640
HLA A*3001	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.245545	2.032901	-2.212644	17601.320185
HLA B*0801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.357712	2.144780	-2.212932	22788.304123
HLA A*6901	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.124352	1.911098	-2.213254	13315.324609
HLA A*6901	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.337048	2.123741	-2.213308	21729.427596
HLA A*6901	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.300380	2.086649	-2.213731	19970.083176
HLA B*0802	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.378279	2.164532	-2.213747	23893.479486
HLA A*0212	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.413031	2.199112	-2.213919	25883.954702
HLA B*5701	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.413106	2.199112	-2.213994	25888.436028
HLA B*3501	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.300446	2.086183	-2.214263	19973.108411
HLA A*0201	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.069524	1.854767	-2.214758	11736.110134
HLA A*2602	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.515104	2.300286	-2.214818	32741.909747
HLA A*0101	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.379628	2.164532	-2.215096	23967.790662
HLA B*3901	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.063585	1.848352	-2.215233	11576.697313
HLA A*2601	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.280860	2.064809	-2.216051	19092.392427
HLA A*2301	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.281149	2.064809	-2.216340	19105.101045
HLA A*2603	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.342755	2.126210	-2.216545	22016.850082
HLA A*0216	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.420081	2.203513	-2.216568	26307.612461
HLA A*0201	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.340392	2.123741	-2.216651	21897.352181
HLA B*5701	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.381298	2.164532	-2.216766	24060.158649
HLA A*2602	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.207871	1.990887	-2.216984	16138.800431
HLA B*4501	1:267-275	9	LFAHRDRGF	1.188229	1.243298	-4.649342	2.431527	-2.217815	44600.716195
HLA A*3301	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.088532	1.870150	-2.218382	12261.158597
HLA B*1501	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.047580	1.828963	-2.218617	11157.836326

HLA A*3101	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.291276	2.072193	-2.219083	19555.801455
HLA A*6802	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.418592	2.199112	-2.219480	26217.535342
HLA B*1502	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.475015	2.255532	-2.219483	29854.839754
HLA A*0301	1:58-66	9	YLALLDALR	0.982293	0.674716	-3.876552	1.657009	-2.219543	7525.780983
HLA A*0201	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.461369	1.241782	-2.219588	2893.139545
HLA A*8001	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.364424	2.144780	-2.219645	23143.257388
HLA A*6901	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.189968	1.970233	-2.219735	15487.031280
HLA A*6901	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.306197	2.086183	-2.220015	20239.379725
HLA B*0803	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.384564	2.164532	-2.220032	24241.766896
HLA B*2705	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.365007	2.144780	-2.220227	23174.328436
HLA B*7301	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.599115	2.378256	-2.220859	39729.631989
HLA B*5101	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.307088	2.086183	-2.220905	20280.920068
HLA B*4402	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.339064	2.118146	-2.220918	21830.523198
HLA A*3001	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-2.332851	0.111406	-2.221445	215.204153
HLA B*3501	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.228147	2.006546	-2.221602	16910.144036
HLA A*0211	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-3.669731	1.448126	-2.221605	4674.456358
HLA A*2603	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.277195	2.054462	-2.222733	18931.941583
HLA A*3201	1:112-120	9	STPEEVEAR	0.994604	0.605580	-3.823185	1.600184	-2.223001	6655.571799
HLA A*2602	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.193483	1.970233	-2.223250	15612.879401
HLA A*3001	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.289032	2.064809	-2.224223	19455.028044
HLA B*0802	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.079068	1.854767	-2.224301	11996.865350
HLA B*2705	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.350558	2.126210	-2.224348	22415.984875
HLA A*0202	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.459532	2.235159	-2.224373	28809.229169
HLA B*1517	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.279723	2.055046	-2.224677	19042.466559
HLA A*0301	1:232-240	9	LIRIGVAER	0.803790	0.789705	-3.818317	1.593495	-2.224822	6581.384135
HLA B*5701	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.826517	1.601532	-2.224985	6706.824507
HLA B*1509	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.017328	1.792234	-2.225094	10407.059021
HLA A*0101	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.348880	2.123741	-2.225140	22329.566538
HLA B*5301	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.402561	2.177014	-2.225547	25267.444820
HLA A*0101	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.267374	2.041338	-2.226036	18508.631480
HLA A*0216	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.126885	1.900474	-2.226411	13393.204596
HLA A*2602	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.164025	1.937546	-2.226479	14588.987834
HLA B*3801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.461209	2.234720	-2.226489	28920.724646
HLA B*1801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.233189	2.006546	-2.226644	17107.608443
HLA B*1517	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-3.936816	1.710050	-2.226766	8646.012628
HLA B*1501	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.217526	0.990658	-2.226868	1650.158767
HLA B*2705	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.426301	2.199112	-2.227189	26687.047118
HLA B*1801	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.462393	2.235159	-2.227235	28999.687035
HLA A*0211	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.340070	1.112802	-2.227268	2188.115133
HLA B*2705	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.316758	2.089268	-2.227490	20737.582829
HLA B*5801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.353791	2.126210	-2.227581	22583.472249
HLA B*2705	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-3.879808	1.651959	-2.227849	7582.422174
HLA A*6901	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.229435	2.001284	-2.228151	16960.350559
HLA A*2403	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.314451	2.086183	-2.228268	20627.706308
HLA B*4501	1:177-185	9	FAAGSVPDF	1.283549	1.092903	-4.604805	2.376452	-2.228353	40253.624862
HLA A*3201	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.528278	1.299885	-2.228393	3375.032936
HLA A*2902	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.102210	1.873578	-2.228632	12653.486665
HLA B*4001	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.300937	2.072193	-2.228744	19995.704114
HLA A*6802	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.352501	2.123741	-2.228760	22516.498185
HLA B*5701	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.231883	2.003005	-2.228878	17056.227809
HLA A*2902	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.858907	1.629468	-2.229439	7226.149508
HLA B*5101	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.301773	2.072193	-2.229581	20034.251359
HLA B*1509	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.353582	2.123741	-2.229841	22572.601373
HLA B*1503	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.356058	2.126210	-2.229848	22701.678520
HLA A*0211	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.875184	1.645215	-2.229969	7502.122908
HLA A*2501	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.285104	2.054462	-2.230641	19279.844297
HLA A*3002	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.022939	1.792274	-2.230664	10542.378093
HLA A*2601	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.395661	2.164532	-2.231128	24869.146947
HLA A*3101	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.408456	2.177014	-2.231442	25612.748428
HLA A*2603	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-3.981043	1.749555	-2.231487	9572.879037
HLA A*2403	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.067508	1.835915	-2.231593	11681.761043
HLA B*4001	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.318382	2.086649	-2.231732	20815.249832
HLA A*6802	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.287465	2.055046	-2.232419	19384.953102
HLA B*7301	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.594164	2.361023	-2.233141	39279.339594
HLA B*3901	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.236378	2.003005	-2.233373	17233.661278

HLA A*3301	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.292037	2.058588	-2.233448	19590.109002
HLA B*0801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.274914	2.041338	-2.233576	18832.752796
HLA A*2301	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.948216	1.714405	-2.233811	8875.964708
HLA A*3101	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.298951	2.064809	-2.234142	19904.505236
HLA A*0202	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-3.947379	1.713159	-2.234220	8858.886756
HLA A*2402	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.237270	2.003005	-2.234265	17269.125954
HLA B*2705	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.288926	2.054462	-2.234464	19450.292391
HLA B*0802	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.379417	2.144780	-2.234637	23956.123824
HLA A*0216	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.563436	1.328755	-2.234681	3659.617612
HLA B*1501	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.236528	2.001284	-2.235244	17239.629172
HLA B*1501	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.949809	1.714405	-2.235404	8908.580681
HLA B*4001	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.223448	1.987904	-2.235544	16728.166281
HLA A*2601	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.380439	2.144780	-2.235659	24012.566200
HLA A*6901	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.243971	2.008310	-2.235661	17537.637470
HLA B*3901	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.053623	1.817618	-2.236005	11314.174220
HLA A*2501	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.097624	1.861442	-2.236182	12520.567589
HLA A*2603	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.224299	1.987904	-2.236395	16760.958485
HLA A*2902	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.174372	1.937546	-2.236826	14940.746395
HLA B*1503	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.269794	2.032901	-2.236893	18612.052888
HLA B*4601	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.363219	2.126210	-2.237009	23079.117572
HLA A*3201	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.243555	2.006546	-2.237009	17520.852336
HLA A*2601	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.092573	1.854767	-2.237806	12375.781248
HLA B*1501	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.241116	2.003005	-2.238111	17422.740335
HLA A*8001	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.303206	2.064809	-2.238397	20100.474246
HLA B*1517	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.176036	1.937546	-2.238490	14998.082198
HLA B*1801	1:465-473	9	FESLELLGR	0.858673	0.563144	-3.660343	1.421817	-2.238526	4574.488787
HLA A*3201	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.812124	1.573351	-2.238773	6488.196547
HLA A*6801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-3.734206	1.495432	-2.238774	5422.576366
HLA A*3002	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.494840	2.255532	-2.239308	31249.257225
HLA B*4601	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.298063	2.058588	-2.239475	19863.843344
HLA A*0301	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.363428	2.123741	-2.239688	23090.232384
HLA A*3101	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-3.672283	1.432365	-2.239917	4702.000275
HLA A*3002	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.092615	1.852642	-2.239972	12376.986435
HLA A*0206	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.124261	0.883995	-2.240266	1331.252923
HLA A*3001	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.281638	2.041338	-2.240300	19126.611293
HLA A*3001	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.210648	1.970233	-2.240416	16242.330471
HLA B*1801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.358631	2.118146	-2.240485	22836.558481
HLA A*3002	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.012455	1.771882	-2.240573	10290.943307
HLA B*4001	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.569549	1.328755	-2.240794	3711.496616
HLA A*0212	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.417824	2.177014	-2.240810	26171.196637
HLA A*6802	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.417859	2.177014	-2.240845	26173.320472
HLA A*0211	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.476166	2.234720	-2.241446	29934.085314
HLA A*3201	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.418519	2.177014	-2.241505	26213.138858
HLA A*0301	1:226-234	9	LALHQALIR	1.054870	0.655362	-3.952059	1.710232	-2.241828	8954.870799
HLA B*5101	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.445360	2.203513	-2.241846	27884.287043
HLA B*1501	1:227-235	9	ALHQALIRI	1.220562	0.336437	-3.798873	1.556999	-2.241874	6293.219824
HLA A*3201	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.013780	1.771882	-2.241898	10322.390753
HLA A*1101	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.445747	2.203513	-2.242234	27909.188554
HLA B*4801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.331527	2.089268	-2.242259	21454.924787
HLA B*4501	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.542936	2.300286	-2.242650	34908.887317
HLA B*0702	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.091248	1.848352	-2.242896	12338.078092
HLA A*2301	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.816447	1.573351	-2.243096	6553.103841
HLA A*0201	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.369318	2.126210	-2.243108	23405.529074
HLA A*3201	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.095923	1.852642	-2.243281	12471.623448
HLA A*0206	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.333108	2.089268	-2.243840	21533.181440
HLA B*4601	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.367728	2.123741	-2.243987	23319.963230
HLA B*3801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.443125	2.199112	-2.244013	27741.196238
HLA A*0206	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.421357	2.177014	-2.244343	26385.006528
HLA A*6901	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.309223	2.064809	-2.244414	20380.898928
HLA A*0219	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.080712	1.835915	-2.244797	12042.382679
HLA B*5801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.037082	1.792274	-2.244808	10891.369383
HLA A*0101	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.371109	2.126210	-2.244899	23502.213664
HLA A*0206	1:435-443	9	ALIEGLALK	0.478643	0.243793	-2.967555	0.722436	-2.245118	928.014205
HLA B*1801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.410185	2.164532	-2.245653	25714.933454
HLA A*8001	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.331879	2.086183	-2.245697	21472.342167

HLA B*0801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.332056	2.086183	-2.245873	21481.056159
HLA A*3001	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.237292	1.990887	-2.246405	17269.966791
HLA A*0206	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.287810	2.041338	-2.246472	19400.375189
HLA A*3001	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.284103	2.037348	-2.246755	19235.462882
HLA A*0216	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.314174	1.067176	-2.246998	2061.456363
HLA B*4001	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-3.469860	1.222401	-2.247460	2950.260878
HLA B*7301	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-3.000631	0.752921	-2.247710	1001.453235
HLA A*0201	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.337102	2.089268	-2.247834	21732.131502
HLA A*0250	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.256621	2.008310	-2.248310	18055.965471
HLA B*1501	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.119905	0.871584	-2.248320	1317.967282
HLA B*4801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.239932	1.990887	-2.249045	17375.300471
HLA B*4801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-3.635856	1.386690	-2.249166	4323.706789
HLA A*0101	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.587936	1.338560	-2.249377	3872.007043
HLA B*4501	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.628201	2.378256	-2.249946	42481.629464
HLA B*4601	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.336320	2.086183	-2.250137	21693.016461
HLA B*4801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.377166	2.126210	-2.250956	23832.288226
HLA B*1502	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.242385	1.990887	-2.251498	17473.712502
HLA B*3501	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.377720	2.126210	-2.251510	23862.735147
HLA B*4402	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.338197	2.086649	-2.251548	21786.987504
HLA B*0803	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.375535	2.123741	-2.251794	23742.978540
HLA A*3101	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.243926	1.990887	-2.253040	17535.834906
HLA B*5401	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-3.015188	0.761813	-2.253375	1035.590559
HLA B*1501	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.223852	1.970233	-2.253620	16743.739100
HLA B*0702	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.018113	1.764296	-2.253816	10425.880566
HLA B*4601	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.115804	1.861442	-2.254362	13055.825354
HLA B*1501	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.304654	1.050133	-2.254521	2016.759136
HLA A*0211	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.103122	1.848352	-2.254770	12680.074696
HLA B*1503	1:227-235	9	ALHQALIRI	1.220562	0.336437	-3.812049	1.556999	-2.255050	6487.073430
HLA B*1509	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.243130	1.987904	-2.255226	17503.704491
HLA B*1502	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.419760	2.164532	-2.255227	26288.121671
HLA B*5801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.313838	2.058588	-2.255249	20598.600930
HLA B*2705	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.047904	1.792274	-2.255630	11166.169483
HLA A*0301	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.320623	2.064809	-2.255814	20922.955747
HLA A*0219	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.264311	2.008310	-2.256000	18378.521892
HLA B*1801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.400975	2.144780	-2.256196	25175.344582
HLA B*0801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.964559	1.708081	-2.256478	9216.342048
HLA A*6901	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.103488	1.846931	-2.256557	12690.780470
HLA B*3501	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.244723	1.987904	-2.256819	17568.024301
HLA B*0702	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.290026	2.032901	-2.257125	19499.599580
HLA A*3101	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.069449	1.811844	-2.257605	11734.078596
HLA A*0301	1:314-322	9	SSPARFDQK	0.878945	0.297758	-3.434454	1.176703	-2.257750	2719.278452
HLA A*0211	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.299605	2.041338	-2.258267	19934.463122
HLA B*5801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.347595	2.089268	-2.258327	22263.586348
HLA A*3301	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.619534	2.361023	-2.258511	41642.224043
HLA A*6802	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.795344	1.536595	-2.258749	6242.290498
HLA A*2601	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.313354	2.054462	-2.258892	20575.657870
HLA A*0206	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.265476	2.006546	-2.258930	18427.903295
HLA B*3801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.262722	2.003005	-2.259717	18311.432824
HLA B*5101	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.404643	2.144780	-2.259863	25388.846487
HLA A*6802	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.314599	2.054462	-2.260137	20634.737903
HLA A*3002	1:289-297	9	WSIADDHDL	1.275539	0.438866	-3.974647	1.714405	-2.260243	9432.944365
HLA A*0212	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.384179	2.123741	-2.260438	24220.268610
HLA B*5101	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.424990	2.164532	-2.260457	26606.607918
HLA B*4801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.315684	2.055046	-2.260639	20686.376227
HLA A*0202	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-3.328670	1.067986	-2.260684	2131.427028
HLA A*0202	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.470993	1.210192	-2.260801	2957.963918
HLA A*0201	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.269395	2.008310	-2.261084	18594.943603
HLA A*2301	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.115922	1.854767	-2.261155	13059.357360
HLA A*3101	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.316241	2.055046	-2.261195	20712.916145
HLA B*4402	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.326330	2.064809	-2.261521	21199.710757
HLA A*0101	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.333750	2.072193	-2.261557	21565.007286
HLA A*0202	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.176010	0.914377	-2.261634	1499.720511
HLA A*3001	1:235-243	9	IGVAERIPK	0.603044	0.187675	-3.052371	0.790719	-2.261653	1128.160870
HLA A*2403	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.348436	2.086649	-2.261787	22306.746915
HLA B*5801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.348627	2.086649	-2.261977	22316.523897

HLA B*4402	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.274547	2.012396	-2.262152	18816.865737
HLA B*1503	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.051438	1.789240	-2.262198	11257.393339
HLA B*5101	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.265474	2.003005	-2.262469	18427.803603
HLA A*0301	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.317350	2.054462	-2.262888	20765.873491
HLA B*4801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.327820	2.064809	-2.263010	21272.547842
HLA A*1101	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.462478	2.199112	-2.263366	29005.335448
HLA B*3801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.408233	2.144780	-2.263453	25599.588408
HLA A*0201	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.564300	1.300706	-2.263594	3666.910579
HLA A*0206	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.254485	1.990887	-2.263598	17967.391613
HLA B*3801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.440644	2.177014	-2.263630	27583.166969
HLA A*1101	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.428370	2.164532	-2.263838	26814.544174
HLA B*0802	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.350518	2.086649	-2.263869	22413.923414
HLA B*4403	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.608000	2.343890	-2.264110	40550.881046
HLA B*4801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.336362	2.072193	-2.264170	21695.128986
HLA A*8001	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.056766	1.792274	-2.264492	11396.368216
HLA B*1501	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.353765	2.089268	-2.264497	22582.128374
HLA B*0702	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.319697	2.055046	-2.264651	20878.406039
HLA B*4402	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.255636	1.990887	-2.264749	18015.083580
HLA A*0201	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.297746	2.032901	-2.264845	19849.341380
HLA B*5401	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.565378	2.300286	-2.265092	36760.235681
HLA B*0802	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.337297	2.072193	-2.265105	21741.891872
HLA A*2301	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.351371	2.086183	-2.265188	22457.982895
HLA B*0801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.391963	2.126210	-2.265753	24658.281097
HLA B*0702	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.352482	2.086649	-2.265833	22515.523712
HLA B*1509	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.352120	2.086183	-2.265938	22496.773325
HLA B*7301	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.610124	2.343890	-2.266234	40749.682470
HLA A*6901	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.013583	1.747156	-2.266427	10317.701007
HLA B*4402	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.273116	2.006546	-2.266571	18754.973280
HLA A*2601	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.267912	2.001284	-2.266629	18531.575378
HLA A*0301	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.352879	2.086183	-2.266696	22536.118422
HLA A*0101	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.353084	2.086183	-2.266901	22546.727776
HLA A*2602	1:221-229	9	STPRQLALH	0.899770	-0.287449	-2.879721	0.612321	-2.267401	758.091237
HLA A*6802	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.594900	1.327486	-2.267414	3934.594786
HLA B*2705	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.353734	2.086183	-2.267552	22580.540261
HLA B*1502	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.353925	2.086183	-2.267742	22590.437246
HLA A*0203	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.353960	2.086183	-2.267777	22592.270496
HLA B*0801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.305382	2.037348	-2.268034	20201.421363
HLA B*0803	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.160069	1.891829	-2.268239	14456.682044
HLA A*0201	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.607193	1.338560	-2.268633	4047.552752
HLA B*1801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.130310	1.861442	-2.268868	13499.262806
HLA A*2601	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.301923	2.032901	-2.269022	20041.189077
HLA A*3001	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.538916	1.269415	-2.269501	3458.728587
HLA B*1501	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.113380	1.843794	-2.269586	12983.137705
HLA A*0202	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.474164	2.203513	-2.270651	29796.429850
HLA B*7301	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.308143	2.037348	-2.270794	20330.243119
HLA B*4402	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.325559	2.054462	-2.271097	21162.126420
HLA A*2301	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.395045	2.123741	-2.271305	24833.922612
HLA A*0201	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.312649	2.041338	-2.271311	20542.291345
HLA B*5101	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.448348	2.177014	-2.271334	28076.831114
HLA A*0211	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.283903	2.012396	-2.271507	19226.619669
HLA A*0206	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.284072	2.012396	-2.271677	19234.110127
HLA B*4801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.313091	2.041338	-2.271753	20563.194699
HLA B*4403	1:368-376	9	LVQTRIVVL	1.986473	0.391783	-4.650044	2.378256	-2.271789	44672.918769
HLA A*1101	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.448846	2.177014	-2.271832	28109.050807
HLA A*2601	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.358377	2.086183	-2.272194	22823.219707
HLA B*4402	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.145807	1.873578	-2.272229	13989.663084
HLA A*2402	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.337384	2.064809	-2.272575	21746.244293
HLA B*0702	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.337415	2.064809	-2.272605	21747.773729
HLA B*5701	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.399427	2.126210	-2.273217	25085.751334
HLA B*0803	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.399493	2.126210	-2.273283	25089.551534
HLA B*0702	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.399512	2.126210	-2.273302	25090.637411
HLA B*3801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.338303	2.064809	-2.273494	21792.292083
HLA A*3101	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-3.665403	1.391860	-2.273544	4628.106648
HLA A*2301	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.328024	2.054462	-2.273562	21282.562343
HLA A*6801	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.392256	2.118146	-2.274111	24674.961557

HLA A*0206	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.049897	1.775750	-2.274146	11217.512927
HLA A*2501	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.439042	2.164532	-2.274509	27481.585161
HLA A*2601	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.398541	2.123741	-2.274801	25034.640376
HLA A*0202	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-3.860307	1.585411	-2.274896	7249.486341
HLA B*3501	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.067208	1.792274	-2.274933	11673.674623
HLA A*0203	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.287613	2.012396	-2.275217	19391.561066
HLA A*0211	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.312698	2.037348	-2.275350	20544.625240
HLA A*3101	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.186552	1.911098	-2.275454	15365.688486
HLA A*2501	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.213003	1.937546	-2.275457	16330.614481
HLA B*0803	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.317200	2.041338	-2.275862	20758.684907
HLA B*0803	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.288691	2.012396	-2.276296	19439.772844
HLA A*2501	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.453374	2.177014	-2.276360	28403.616358
HLA A*6802	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.048459	1.771882	-2.276576	11180.434814
HLA B*3901	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.331673	2.055046	-2.276627	21462.122257
HLA A*0250	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.511885	2.235159	-2.276727	32500.138563
HLA B*3901	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.511113	1.234017	-2.277096	3244.237784
HLA A*3002	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.366407	2.089268	-2.277139	23249.169873
HLA A*2902	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.332295	2.055046	-2.277249	21492.912864
HLA A*2402	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.403710	2.126210	-2.277500	25334.376716
HLA B*3901	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.403753	2.126210	-2.277543	25336.843847
HLA A*1101	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-3.926370	1.648791	-2.277579	8440.536557
HLA B*3801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.285926	2.008310	-2.277615	19316.384517
HLA A*2402	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.363865	2.086183	-2.277683	23113.478379
HLA B*0801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.290214	2.012396	-2.277818	19508.040660
HLA A*2402	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.907396	1.629468	-2.277928	8079.707044
HLA A*3001	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.286309	2.008310	-2.277998	19333.425447
HLA A*8001	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.319347	2.041338	-2.278009	20861.583291
HLA B*4001	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.404347	2.126210	-2.278137	25371.546178
HLA A*6901	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.319869	2.041338	-2.278531	20886.653007
HLA B*1502	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.241591	1.962632	-2.278959	17441.790270
HLA A*0301	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.368449	2.089268	-2.279181	23358.726044
HLA B*2705	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.334365	2.055046	-2.279319	21595.595004
HLA A*0202	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.456670	2.177014	-2.279656	28620.022151
HLA A*0216	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.478819	2.199112	-2.279707	30117.475149
HLA A*0202	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.285428	2.005692	-2.279736	19294.243322
HLA B*1503	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.055836	1.776041	-2.279796	11371.979726
HLA A*2501	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.797308	1.517234	-2.280074	6270.586239
HLA B*4601	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.217889	1.937546	-2.280343	16515.413637
HLA A*0250	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.580958	2.300286	-2.280671	38102.872908
HLA A*6801	1:465-473	9	FESLELLGR	0.858673	0.563144	-3.702657	1.421817	-2.280840	5042.626389
HLA A*0301	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.367547	2.086649	-2.280898	23310.251055
HLA B*3801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.336019	2.055046	-2.280973	21677.999988
HLA A*0216	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.458646	2.177014	-2.281632	28750.531811
HLA A*3201	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.990060	1.708081	-2.281979	9773.720035
HLA B*1801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.408299	2.126210	-2.282089	25603.466447
HLA A*0211	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.405895	2.123741	-2.282154	25462.160136
HLA B*2705	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.111251	1.828963	-2.282288	12919.658373
HLA B*1517	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.881937	1.599646	-2.282291	7619.677578
HLA B*1509	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.046838	1.764296	-2.282541	11138.778021
HLA B*1501	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.315621	2.032901	-2.282720	20683.354851
HLA B*3901	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.928348	1.645215	-2.283133	8479.071970
HLA B*4402	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.406990	2.123741	-2.283249	25526.431434
HLA B*4001	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.338232	2.054462	-2.283770	21788.755553
HLA B*0803	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.290470	2.006546	-2.283924	19519.547513
HLA A*3001	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.289692	2.005692	-2.284000	19484.625657
HLA B*3901	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.138778	1.854767	-2.284011	13765.043757
HLA A*8001	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.407982	2.123741	-2.284241	25584.774166
HLA A*0206	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.370996	2.086649	-2.284347	23496.111527
HLA B*0803	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.349186	2.064809	-2.284376	22345.276124
HLA B*0702	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.176769	1.892220	-2.284549	15023.418619
HLA A*0212	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.929875	1.645215	-2.284660	8508.940500
HLA B*4002	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.628871	2.343890	-2.284980	42547.178942
HLA A*2902	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.326605	2.041338	-2.285267	21213.133510
HLA B*1501	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-3.993617	1.708081	-2.285536	9854.101128
HLA A*3001	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.286875	2.001284	-2.285591	19358.648483

HLA B*1501	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.298106	2.012396	-2.285710	19865.777740
HLA B*4801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.371929	2.086183	-2.285746	23546.628965
HLA A*6801	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.646797	2.361023	-2.285775	44340.168623
HLA A*0201	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.371997	2.086183	-2.285814	23550.323410
HLA B*1509	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.178042	1.892220	-2.285822	15067.534330
HLA A*3201	1:415-423	9	AALTSVTDW	1.150326	0.497710	-3.934147	1.648036	-2.286110	8593.040339
HLA B*4801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.289654	2.003005	-2.286649	19482.939175
HLA A*0219	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.249302	1.962632	-2.286670	17754.239323
HLA A*3001	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.030509	1.743756	-2.286753	10727.749612
HLA B*2705	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.299633	2.012396	-2.287237	19935.757283
HLA B*3901	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.342196	2.054462	-2.287734	21988.520449
HLA A*0301	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.342812	2.055046	-2.287766	22019.708877
HLA B*2705	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-3.160819	0.872828	-2.287990	1448.166714
HLA A*0203	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.295037	2.006546	-2.288491	19725.914429
HLA B*5801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.343061	2.054462	-2.288598	22032.339662
HLA A*6901	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.251271	1.962632	-2.288639	17834.910661
HLA B*4501	1:159-167	9	RMPDDDLAW	1.804469	0.556554	-4.649680	2.361023	-2.288657	44635.474762
HLA B*1509	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.377974	2.089268	-2.288706	23876.681454
HLA A*0301	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.361248	2.072193	-2.289055	22974.601208
HLA B*4601	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.343674	2.054462	-2.289212	22063.470881
HLA B*1503	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.162879	1.873578	-2.289300	14550.523325
HLA B*3901	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.378989	2.089268	-2.289721	23932.548237
HLA B*0702	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.348486	2.058588	-2.289897	22309.281277
HLA B*1503	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.379508	2.089268	-2.290240	23961.178756
HLA B*4601	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.323628	2.032901	-2.290727	21068.228882
HLA B*4001	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.005698	1.714405	-2.291294	10132.067323
HLA B*1801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.183596	1.892220	-2.291377	15261.470172
HLA A*0202	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.282325	0.990658	-2.291667	1915.686891
HLA B*4002	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.356634	2.064809	-2.291824	22731.787792
HLA B*5801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.347017	2.055046	-2.291971	22233.976946
HLA A*6901	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.381465	2.089268	-2.292197	24069.401982
HLA A*3301	1:112-120	9	STPEEVEAR	0.994604	0.605580	-3.892420	1.600184	-2.292236	7805.846323
HLA B*4001	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.357089	2.064809	-2.292280	22755.657748
HLA B*4402	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.381599	2.089268	-2.292331	24076.825256
HLA A*2603	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.469392	2.177014	-2.292378	29470.834043
HLA B*5301	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.110043	1.817618	-2.292425	12883.782801
HLA B*4402	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.418716	2.126210	-2.292506	26225.053620
HLA A*1101	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.417053	2.123741	-2.293312	26124.798501
HLA A*0206	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-3.678086	1.384650	-2.293436	4765.252064
HLA A*0212	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.419694	2.126210	-2.293484	26284.139929
HLA B*1517	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.085886	1.792274	-2.293612	12186.696344
HLA A*0219	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.380460	2.086649	-2.293811	24013.735376
HLA A*0206	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.492958	2.199112	-2.293846	31114.137126
HLA A*0202	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.146677	1.852707	-2.293969	14017.693664
HLA B*4001	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.295418	2.001284	-2.294134	19743.209838
HLA A*0203	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.754214	1.459786	-2.294428	5678.241914
HLA A*3101	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.327387	2.032901	-2.294486	21251.383266
HLA A*0211	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.327876	2.032901	-2.294975	21275.309992
HLA B*4601	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.350055	2.055046	-2.295009	22390.048541
HLA A*0216	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.332709	2.037348	-2.295361	21513.386882
HLA B*4403	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.472675	2.177014	-2.295661	29694.407040
HLA B*3901	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.009448	1.713159	-2.296289	10219.928205
HLA A*2603	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.596857	2.300286	-2.296570	39523.617457
HLA B*5701	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.383716	2.086649	-2.297067	24194.469653
HLA B*4601	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.384007	2.086649	-2.297358	24210.705384
HLA A*3101	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.383566	2.086183	-2.297383	24186.094182
HLA A*0216	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.338862	2.041338	-2.297524	21820.368899
HLA A*0301	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.304097	2.006546	-2.297551	20141.729492
HLA B*4001	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.334908	2.037348	-2.297560	21622.599552
HLA A*3101	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-3.212902	0.915076	-2.297826	1632.683278
HLA B*0702	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.384264	2.086183	-2.298081	24224.986112
HLA B*4402	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.062438	1.764296	-2.298142	11546.174840
HLA B*3901	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.370712	2.072193	-2.298519	23480.736085
HLA A*0101	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.385180	2.086649	-2.298531	24276.151320
HLA B*0802	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.363358	2.064809	-2.298548	23086.485220

HLA A*2501	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.299903	2.001284	-2.298619	19948.163919
HLA A*8001	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.370829	2.072193	-2.298637	23487.088353
HLA A*0250	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.422407	2.123741	-2.298667	26448.888500
HLA B*5701	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.353732	2.055046	-2.298686	22580.418104
HLA A*0206	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.502687	2.203513	-2.299174	31819.033129
HLA A*2301	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.063561	1.764296	-2.299265	11576.071044
HLA A*0219	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.944513	1.645215	-2.299298	8800.610056
HLA A*0219	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.423204	2.123741	-2.299463	26497.439009
HLA A*2902	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.371677	2.072193	-2.299485	23533.002752
HLA B*7301	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.599944	2.300286	-2.299657	39805.575796
HLA A*6901	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.064581	1.764802	-2.299779	11603.282339
HLA A*0216	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.423718	2.123741	-2.299978	26528.850870
HLA A*0206	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-3.404747	1.104589	-2.300158	2539.491672
HLA A*0201	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.200785	1.900474	-2.300311	15877.612715
HLA B*4001	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.333259	2.032901	-2.300358	21540.638226
HLA A*0202	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.426594	2.126210	-2.300384	26705.099967
HLA A*2403	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.174001	1.873578	-2.300423	14927.981062
HLA A*0201	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.388006	2.086649	-2.301357	24434.658088
HLA A*6802	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.511728	1.210192	-2.301536	3248.839397
HLA B*1501	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.388467	2.086649	-2.301818	24460.580832
HLA A*0203	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-3.077567	0.775701	-2.301866	1195.547703
HLA A*2601	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.391373	2.089268	-2.302105	24624.820779
HLA A*8001	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.290282	1.987904	-2.302378	19511.101454
HLA B*0801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.308093	2.005692	-2.302401	20327.933578
HLA A*0206	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.194371	1.891829	-2.302542	15644.839440
HLA B*4501	1:139-147	9	LTDAQRAAY	1.167960	1.175930	-4.646433	2.343890	-2.302543	44303.003521
HLA A*0206	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.762446	1.459786	-2.302660	5786.906782
HLA A*0250	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.465279	1.162401	-2.302878	2919.301326
HLA B*4801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.361711	2.058588	-2.303122	22999.099400
HLA A*0212	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.375368	2.072193	-2.303176	23733.860562
HLA B*0803	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.448181	2.144780	-2.303401	28066.048815
HLA B*0702	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.608546	1.305053	-2.303493	4060.184987
HLA A*0250	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.336405	2.032901	-2.303504	21697.241717
HLA A*8001	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.390316	2.086649	-2.303667	24564.945793
HLA A*3201	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.390478	2.086649	-2.303829	24574.117165
HLA A*0219	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.430711	2.126210	-2.304501	26959.417587
HLA B*5701	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.359068	2.054462	-2.304606	22859.549090
HLA B*3501	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.391817	2.086649	-2.305168	24650.011773
HLA A*2601	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.391834	2.086649	-2.305184	24650.945267
HLA A*3101	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.391906	2.086649	-2.305257	24655.079739
HLA A*0201	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.243118	1.937546	-2.305572	17503.231032
HLA B*5401	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.561260	2.255532	-2.305728	36413.266522
HLA A*0206	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-3.365651	1.059725	-2.305926	2320.872927
HLA A*0206	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.312181	2.005692	-2.306489	20520.188073
HLA A*6802	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.315020	2.008310	-2.306709	20654.729645
HLA A*0101	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.361817	2.055046	-2.306771	23004.699097
HLA B*0803	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.379104	2.072193	-2.306911	23938.893227
HLA A*0101	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.396330	2.089268	-2.307062	24907.520230
HLA B*1509	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.365782	2.058588	-2.307194	23215.737669
HLA B*5301	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.452307	2.144780	-2.307527	28333.940130
HLA B*5801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.348984	2.041338	-2.307646	22334.882392
HLA B*4801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.313384	2.005692	-2.307692	20577.104977
HLA A*2902	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.362207	2.054462	-2.307744	23025.367553
HLA A*0211	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-2.943684	0.635887	-2.307797	878.382867
HLA A*6802	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.394202	2.086183	-2.308019	24785.738210
HLA A*0211	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.208675	1.900474	-2.308201	16168.687791
HLA B*4801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.362996	2.054462	-2.308534	23067.259350
HLA B*1517	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.395200	2.086649	-2.308551	24842.791214
HLA A*3001	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-3.960579	1.651959	-2.308619	9132.266082
HLA A*0216	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-2.944534	0.635887	-2.308647	880.104760
HLA B*0801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.398299	2.089268	-2.309031	25020.694495
HLA B*4001	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.367902	2.058588	-2.309313	23329.300822
HLA A*0203	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.395985	2.086649	-2.309336	24887.720306
HLA B*4601	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.398631	2.089268	-2.309362	25039.787421
HLA A*3002	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.435790	2.126210	-2.309580	27276.591040

HLA A*0201	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.201640	1.891829	-2.309811	15908.909709
HLA A*2602	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.342903	2.032901	-2.310002	22024.355210
HLA A*2402	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.342938	2.032901	-2.310037	22026.142523
HLA A*0216	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.396469	2.086183	-2.310286	24915.471567
HLA A*1101	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.375462	2.064809	-2.310653	23738.997020
HLA A*2402	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.434813	2.123741	-2.311072	27215.273716
HLA A*0250	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.514707	2.203513	-2.311194	32711.988440
HLA A*3101	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.828439	1.517234	-2.311204	6736.569913
HLA B*5701	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.400663	2.089268	-2.311395	25157.237052
HLA B*0801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.318008	2.006546	-2.311462	20797.352827
HLA B*1503	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-3.625312	1.313812	-2.311500	4219.993150
HLA A*2902	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.435388	2.123741	-2.311648	27251.369377
HLA B*2705	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.164749	1.852707	-2.312042	14613.316938
HLA B*0702	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.401358	2.089268	-2.312090	25197.554292
HLA A*2601	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.384818	2.072193	-2.312625	24255.934724
HLA A*0212	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.399270	2.086183	-2.313087	25076.660336
HLA B*5801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.350518	2.037348	-2.313170	22413.923414
HLA B*3501	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.077475	1.764296	-2.313178	11952.942591
HLA A*3001	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.224524	1.911098	-2.313427	16769.665539
HLA A*2501	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.168231	1.854767	-2.313464	14730.949486
HLA B*1501	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.886880	1.573351	-2.313529	7706.903325
HLA A*0203	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.354902	2.041338	-2.313564	22641.334589
HLA B*2705	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.386319	2.072193	-2.314127	24339.930630
HLA B*5101	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.432393	2.118146	-2.314247	27064.046878
HLA A*2403	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.317291	2.003005	-2.314286	20763.065154
HLA A*6802	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.103653	1.789240	-2.314413	12695.587280
HLA A*2902	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.176703	1.861442	-2.315261	15021.143091
HLA A*3001	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.217067	1.900474	-2.316593	16484.171929
HLA A*0219	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.402839	2.086183	-2.316656	25283.579871
HLA B*5101	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.371755	2.055046	-2.316709	23537.204388
HLA B*5701	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.349639	2.032901	-2.316738	22368.619203
HLA B*0803	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.403452	2.086649	-2.316803	25319.305022
HLA B*1509	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.389089	2.072193	-2.316897	24495.673174
HLA A*3101	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.375594	2.058588	-2.317005	23746.189929
HLA B*1801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.304985	1.987904	-2.317081	20182.960224
HLA B*0802	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.350151	2.032901	-2.317250	22395.015327
HLA A*0212	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.646076	1.328755	-2.317321	4426.663345
HLA A*0202	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.093080	1.775750	-2.317330	12390.251247
HLA A*3101	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-3.979083	1.661630	-2.317453	9529.784956
HLA A*8001	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.179132	1.861442	-2.317690	15105.404193
HLA A*0202	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-2.484186	0.166266	-2.317920	304.919835
HLA A*2501	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.404220	2.086183	-2.318037	25364.135369
HLA B*5401	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.552780	2.234720	-2.318060	35709.218731
HLA B*4002	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.553304	2.235159	-2.318146	35752.324518
HLA A*0203	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.407460	2.089268	-2.318192	25554.065414
HLA B*3501	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.374010	2.055046	-2.318965	23659.762685
HLA B*5801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.327404	2.008310	-2.319093	21252.188055
HLA A*0216	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.352268	2.032901	-2.319367	22504.442050
HLA B*4001	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.322587	2.003005	-2.319582	21017.797622
HLA A*2501	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.443362	2.123741	-2.319622	27756.358136
HLA B*0802	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.445848	2.126210	-2.319638	27915.681691
HLA B*4801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.172352	1.852642	-2.319709	14871.395955
HLA B*4001	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.405999	2.086183	-2.319816	25468.221746
HLA B*1503	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.620599	1.300706	-2.319893	4174.444381
HLA B*1801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.443701	2.123741	-2.319960	27777.989431
HLA B*0802	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.322998	2.003005	-2.319993	21037.705237
HLA A*3201	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.323381	2.003005	-2.320376	21056.264718
HLA A*0216	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.407108	2.086649	-2.320458	25533.337126
HLA B*4402	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.328928	2.008310	-2.320618	21326.936015
HLA A*0206	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.620641	1.299885	-2.320756	4174.850900
HLA B*5301	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.311864	1.990887	-2.320977	20505.206932
HLA A*3101	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.221635	1.900474	-2.321161	16658.447881
HLA A*2601	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.376242	2.055046	-2.321197	23781.672547
HLA B*5301	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.354477	2.032901	-2.321576	22619.175273
HLA A*3001	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.191787	1.870150	-2.321637	15552.015374

HLA B*0702	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.393981	2.072193	-2.321788	24773.137133
HLA B*3901	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.214158	1.892220	-2.321939	16374.139012
HLA B*5101	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.445898	2.123741	-2.322157	27918.853306
HLA A*6801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.355158	2.032901	-2.322257	22654.689621
HLA A*0250	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.359883	2.037348	-2.322535	22902.502060
HLA B*1509	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.387442	2.064809	-2.322633	24402.953365
HLA B*1517	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.460025	1.137355	-2.322670	2884.200688
HLA A*0202	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.329264	2.006546	-2.322719	21343.441218
HLA A*3301	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.557919	2.235159	-2.322760	36134.218988
HLA A*0101	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.360484	2.037348	-2.323136	22934.242434
HLA B*5801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.356103	2.032901	-2.323202	22704.012097
HLA A*3201	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.381820	2.058588	-2.323232	24089.072147
HLA A*8001	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.096745	1.773509	-2.323236	12495.260354
HLA A*3101	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.178075	1.854767	-2.323308	15068.675565
HLA B*1509	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.331621	2.008310	-2.323311	21459.568040
HLA B*4601	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.314279	1.990887	-2.323392	20619.561583
HLA B*5701	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.382140	2.058588	-2.323551	24106.802081
HLA A*6801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.159491	1.835915	-2.323576	14437.455415
HLA B*0803	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.040987	1.717294	-2.323693	10989.737817
HLA A*0212	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.365075	2.041338	-2.323737	23177.964467
HLA A*2601	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.330395	2.006546	-2.323849	21399.052519
HLA B*4801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.172267	1.848352	-2.323915	14868.499943
HLA B*3501	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.286638	1.962632	-2.324006	19348.073830
HLA B*4801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.361457	2.037348	-2.324109	22985.665686
HLA A*0203	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.325437	2.001284	-2.324153	21156.174050
HLA A*6802	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.216602	1.892220	-2.324382	16466.524229
HLA B*5701	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.389223	2.064809	-2.324414	24503.227914
HLA A*0219	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.396617	2.072193	-2.324425	24923.964781
HLA A*0212	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.361793	2.037348	-2.324445	23003.454602
HLA B*4402	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.383373	2.058588	-2.324785	24175.367346
HLA B*4001	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.380175	2.055046	-2.325130	23998.021211
HLA B*5401	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.560524	2.235159	-2.325366	36351.660283
HLA A*3301	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.560280	2.234720	-2.325560	36331.213556
HLA A*0301	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.367260	2.041338	-2.325922	23294.871214
HLA A*2501	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.332537	2.006546	-2.325992	21504.892452
HLA A*0201	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.488525	1.162401	-2.326124	3079.815704
HLA A*2602	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.391484	2.064809	-2.326674	24631.082800
HLA B*5401	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.290350	0.963515	-2.326835	1951.418277
HLA B*0801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.098728	1.771882	-2.326846	12552.443492
HLA B*0802	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.382029	2.055046	-2.326983	24100.673350
HLA A*0212	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.413634	2.086649	-2.326985	25919.967268
HLA A*3201	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.926647	1.599646	-2.327002	8445.926436
HLA A*6901	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.041495	1.714405	-2.327090	11002.587228
HLA A*3201	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.416423	2.089268	-2.327155	26086.948899
HLA B*4403	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.200874	1.873578	-2.327296	15880.877103
HLA A*0212	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.360299	2.032901	-2.327398	22924.442863
HLA B*5301	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.041875	1.714405	-2.327471	11012.234144
HLA B*2705	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.386098	2.058588	-2.327510	24327.556202
HLA A*8001	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.416787	2.089268	-2.327519	26108.832836
HLA B*4801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.329114	2.001284	-2.327830	21336.052695
HLA A*3301	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-3.976856	1.648791	-2.328065	9481.035854
HLA B*1517	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.787910	1.459786	-2.328124	6136.351165
HLA B*0802	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.414358	2.086183	-2.328175	25963.192308
HLA A*2403	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.386980	2.058588	-2.328391	24376.959816
HLA B*5801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.748641	1.419915	-2.328726	5605.842770
HLA A*6901	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.341282	2.012396	-2.328886	21942.295432
HLA A*0211	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.334675	2.005692	-2.328983	21611.022042
HLA A*0211	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.656513	1.327486	-2.329026	4534.327732
HLA A*3101	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.165346	1.835915	-2.329431	14633.411073
HLA A*3201	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-3.974657	1.645215	-2.329442	9433.148492
HLA B*4501	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.474284	2.144780	-2.329504	29804.651948
HLA A*0250	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.105593	1.776041	-2.329553	12752.445323
HLA A*3001	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.120367	1.790732	-2.329635	13193.712972
HLA B*1517	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.367072	2.037348	-2.329724	23284.791582
HLA A*0301	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.362871	2.032901	-2.329970	23060.646358

HLA A*0101	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.384440	2.054462	-2.329978	24234.817193
HLA A*1101	1:235-243	9	IGVAERIPK	0.603044	0.187675	-3.120840	0.790719	-2.330121	1320.808102
HLA A*2402	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.331576	2.001284	-2.330293	21457.362369
HLA B*4801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.222551	1.892220	-2.330331	16693.631923
HLA B*4601	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.371729	2.041338	-2.330391	23535.803759
HLA B*4402	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.371818	2.041338	-2.330480	23540.642648
HLA B*3501	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.419762	2.089268	-2.330494	26288.263887
HLA B*4002	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.454403	2.123741	-2.330662	28470.999422
HLA A*0301	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.368014	2.037348	-2.330666	23335.359637
HLA B*2705	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.318579	1.987904	-2.330675	20824.711070
HLA A*0219	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.419987	2.089268	-2.330719	26301.920226
HLA A*0212	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.334039	2.003005	-2.331034	21579.361770
HLA B*4403	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-3.236932	0.905846	-2.331087	1725.569585
HLA A*0206	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.023446	1.692204	-2.331242	10554.704443
HLA A*8001	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.337868	2.006546	-2.331323	21770.492625
HLA A*0203	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.600741	1.269415	-2.331326	3987.868526
HLA A*0219	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.319418	1.987904	-2.331514	20864.969331
HLA B*5801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.184226	1.852707	-2.331519	15283.613067
HLA B*4403	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.566264	2.234720	-2.331544	36835.285726
HLA B*4403	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.477035	2.144780	-2.332255	29994.063153
HLA A*0219	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.365289	2.032901	-2.332388	23189.377786
HLA B*0702	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.124652	1.792234	-2.332419	13324.548209
HLA A*0219	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.374095	2.041338	-2.332757	23664.371015
HLA A*2603	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.398079	2.064809	-2.333269	25007.973966
HLA A*6901	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.340032	2.006546	-2.333486	21879.234956
HLA A*0202	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.496273	1.162617	-2.333656	3135.258332
HLA A*0206	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.395847	1.062125	-2.333722	2487.980337
HLA A*2902	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.324833	1.990887	-2.333946	21126.780182
HLA B*0802	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.110518	1.775750	-2.334768	12897.869863
HLA A*0250	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.569558	2.234720	-2.334838	37115.731210
HLA A*6801	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.635165	2.300286	-2.334879	43168.309342
HLA B*5301	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.407256	2.072193	-2.335063	25542.040958
HLA A*2902	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.164133	1.828963	-2.335171	14592.618827
HLA A*6802	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.400235	2.064809	-2.335426	25132.479431
HLA B*4601	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.347830	2.012396	-2.335435	22275.633960
HLA A*1101	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.407650	2.072193	-2.335458	25565.265685
HLA B*3501	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.305805	1.970233	-2.335572	20221.102685
HLA A*3101	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.338693	2.003005	-2.335688	21811.871258
HLA B*3501	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.390248	2.054462	-2.335786	24561.092180
HLA A*0101	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.369037	2.032901	-2.336136	23390.339447
HLA B*4402	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.408341	2.072193	-2.336148	25605.959783
HLA B*4001	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.237028	1.900474	-2.336555	17259.505956
HLA B*0801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.183620	1.846931	-2.336689	15262.295823
HLA A*3301	1:377-385	9	GDAWELLKF	1.384021	0.916265	-4.637186	2.300286	-2.336899	43369.618034
HLA A*2602	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.349583	2.012396	-2.337187	22365.715110
HLA B*1517	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.485536	1.148177	-2.337359	3058.695078
HLA B*0802	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.396244	2.058588	-2.337655	24902.535093
HLA B*3501	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.645452	1.307776	-2.337676	4420.297823
HLA B*3801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.230137	1.892220	-2.337917	16987.807091
HLA A*2602	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.572655	2.234720	-2.337935	37381.320788
HLA A*0301	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.341195	2.003005	-2.338190	21937.903772
HLA B*4601	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.341841	2.003005	-2.338836	21970.565510
HLA A*6901	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.912377	1.573351	-2.339025	8172.906350
HLA B*4002	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.483816	2.144780	-2.339036	30466.033498
HLA B*0801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.397862	2.058588	-2.339274	24995.530349
HLA A*2602	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.465553	2.126210	-2.339343	29211.467037
HLA B*7301	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.595369	2.255532	-2.339838	39388.501898
HLA A*2902	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.343234	2.003005	-2.340229	22041.161674
HLA B*1501	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.348704	2.008310	-2.340394	22320.508340
HLA A*2601	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.381782	2.041338	-2.340445	24086.987130
HLA B*5801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.352863	2.012396	-2.340467	22535.265012
HLA A*6802	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.053628	1.713159	-2.340469	11314.296637
HLA B*4601	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.328383	1.987904	-2.340479	21300.185490
HLA B*4402	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.378033	2.037348	-2.340685	23879.910927
HLA B*3801	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.467052	2.126210	-2.340842	29312.464883

HLA A*8001	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.395353	2.054462	-2.340891	24851.528538
HLA A*6901	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.378338	2.037348	-2.340990	23896.711231
HLA A*3001	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-3.989839	1.648791	-2.341048	9768.751072
HLA A*3001	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.195926	1.854767	-2.341160	15700.969483
HLA B*3801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.413371	2.072193	-2.341179	25904.266920
HLA A*0211	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.395377	1.054023	-2.341354	2485.289853
HLA A*6801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.202810	1.861442	-2.341368	15951.828085
HLA B*0802	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.382713	2.041338	-2.341375	24138.644384
HLA A*3101	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.064034	0.722436	-2.341597	1158.867747
HLA A*6801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-3.733477	1.391860	-2.341618	5413.489971
HLA B*4001	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.347680	2.005692	-2.341988	22267.922738
HLA A*6802	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.428866	2.086649	-2.342217	26845.170093
HLA B*2705	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.345302	2.003005	-2.342297	22146.343256
HLA B*1501	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.330308	1.987904	-2.342404	21394.769587
HLA A*0201	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.401051	2.058588	-2.342462	25179.703225
HLA A*0219	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.401325	2.058588	-2.342737	25195.645940
HLA B*0801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.280520	1.937546	-2.342974	19077.421579
HLA A*0212	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.356157	2.012396	-2.343761	22706.837275
HLA A*2501	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.398981	2.055046	-2.343935	25059.979466
HLA A*3002	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.350685	2.006546	-2.344139	22422.534303
HLA B*1509	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.024273	1.679828	-2.344445	10574.822715
HLA B*0802	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.434098	2.089268	-2.344830	27170.552091
HLA A*1101	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.002122	1.657009	-2.345113	10048.983905
HLA A*6802	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.166321	0.821048	-2.345273	1466.631657
HLA B*4801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.137589	1.792234	-2.345355	13727.414799
HLA A*0211	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.432193	2.086649	-2.345544	27051.604592
HLA A*6901	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.189343	1.843794	-2.345549	15464.760997
HLA A*0216	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.404222	2.058588	-2.345634	25364.272586
HLA B*0702	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.387109	2.041338	-2.345771	24384.214111
HLA A*2902	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.919275	1.573351	-2.345923	8303.756597
HLA B*5101	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.378982	2.032901	-2.346081	23932.159823
HLA A*0219	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.352012	2.005692	-2.346320	22491.175589
HLA A*0301	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-3.674519	1.328104	-2.346415	4726.279051
HLA B*5801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.347788	2.001284	-2.346504	22273.464909
HLA B*3801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.400987	2.054462	-2.346525	25176.025570
HLA A*0203	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.384045	2.037348	-2.346697	24212.801110
HLA B*0702	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.384052	2.037348	-2.346704	24213.194079
HLA A*0216	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.359180	2.012396	-2.346785	22865.485907
HLA B*3801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.348150	2.001284	-2.346866	22292.029175
HLA B*0803	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.309538	1.962632	-2.346906	20395.678911
HLA B*3801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.359408	2.012396	-2.347013	22877.487931
HLA A*3101	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.388417	2.041338	-2.347080	24457.802080
HLA B*1509	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.090886	1.743756	-2.347130	12327.803237
HLA B*0803	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.433333	2.086183	-2.347150	27122.675687
HLA A*0211	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.524201	2.177014	-2.347187	33434.991180
HLA A*3001	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-2.543679	0.196045	-2.347634	349.686878
HLA B*5101	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.434312	2.086649	-2.347663	27183.931444
HLA A*3101	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.360181	2.012396	-2.347786	22918.242767
HLA A*6901	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.677071	1.328755	-2.348316	4754.128330
HLA B*0801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.095735	1.747156	-2.348579	12466.227008
HLA A*8001	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.403818	2.055046	-2.348772	25340.682084
HLA B*5701	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.201561	1.852707	-2.348853	15905.983754
HLA A*6801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-3.677151	1.328104	-2.349047	4755.002866
HLA B*5801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.950640	1.601532	-2.349108	8925.657858
HLA A*3101	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.386496	2.037348	-2.349147	24349.808358
HLA B*5101	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.475529	2.126210	-2.349319	29890.231706
HLA A*3002	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.548436	2.199112	-2.349324	35353.804072
HLA A*6802	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.438626	2.089268	-2.349358	27455.282753
HLA B*3501	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.130000	1.780575	-2.349425	13489.626351
HLA A*0211	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.096661	1.747156	-2.349505	12492.827064
HLA B*4601	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.356074	2.006546	-2.349529	22702.538231
HLA A*0201	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.386972	2.037348	-2.349624	24376.564189
HLA B*4501	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.468084	2.118146	-2.349938	29382.163000
HLA A*0101	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.358250	2.008310	-2.349940	22816.553242
HLA B*3501	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.391404	2.041338	-2.350066	24626.552669

HLA A*6802	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.312917	1.962632	-2.350285	20554.964246
HLA B*5801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.356077	2.005692	-2.350385	22702.661049
HLA B*0803	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.387896	2.037348	-2.350548	24428.446004
HLA B*0801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.179682	1.828963	-2.350719	15124.538445
HLA B*4402	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.405766	2.055046	-2.350720	25454.585152
HLA A*0211	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.203459	1.852707	-2.350752	15975.664019
HLA A*2601	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.353903	2.003005	-2.350898	22589.337366
HLA A*2403	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.392397	2.041338	-2.351060	24682.972186
HLA A*2301	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.354068	2.003005	-2.351063	22597.893393
HLA A*3002	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.187036	1.835915	-2.351121	15382.822126
HLA A*2902	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.437895	2.086649	-2.351246	27409.128749
HLA B*1503	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-3.224212	0.872828	-2.351384	1675.762106
HLA A*6901	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.223155	0.871584	-2.351571	1671.687508
HLA B*1503	1:225-233	9	QLALHQALI	1.319205	0.310263	-3.981108	1.629468	-2.351641	9574.329217
HLA B*1801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.423890	2.072193	-2.351697	26539.329764
HLA A*2902	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.869259	1.517234	-2.352024	7400.460991
HLA B*1503	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.125578	1.773509	-2.352069	13352.979724
HLA B*0802	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.360402	2.008310	-2.352092	22929.900335
HLA B*1502	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.340526	1.987904	-2.352622	21904.105571
HLA A*0201	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.652603	1.299885	-2.352719	4493.692636
HLA A*0211	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.551930	2.199112	-2.352818	35639.354949
HLA A*3301	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.552111	2.199112	-2.352999	35654.204023
HLA B*5701	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.390443	2.037348	-2.353095	24572.123097
HLA A*3001	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.245353	1.892220	-2.353133	17593.513779
HLA A*8001	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.344421	1.990887	-2.353534	22101.460326
HLA B*3501	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.245827	1.892220	-2.353607	17612.750438
HLA B*1509	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.323847	1.970233	-2.353614	21078.831389
HLA B*4403	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.557167	2.203513	-2.353653	36071.718825
HLA B*0803	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.361967	2.008310	-2.353657	23012.665460
HLA B*0801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.362225	2.008310	-2.353915	23026.364092
HLA A*2601	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.391401	2.037348	-2.354053	24626.419442
HLA B*4403	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.345013	1.990887	-2.354126	22131.611619
HLA A*2403	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.355471	2.001284	-2.354187	22670.995882
HLA B*1801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.440865	2.086649	-2.354216	27597.197393
HLA B*1509	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.480463	2.126210	-2.354253	30231.743917
HLA B*4402	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.010124	1.655822	-2.354302	10235.863755
HLA A*0301	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.366800	2.012396	-2.354404	23270.183861
HLA A*3201	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.440630	2.086183	-2.354447	27582.271652
HLA B*1801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.345452	1.990887	-2.354565	22154.012377
HLA B*4601	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.392226	2.037348	-2.354878	24673.226264
HLA B*5701	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.396312	2.041338	-2.354974	24906.442278
HLA A*0212	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.360722	2.005692	-2.355030	22946.777100
HLA A*6802	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.367730	2.012396	-2.355335	23320.089389
HLA A*0216	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.361100	2.005692	-2.355408	22966.772270
HLA B*1503	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.068598	1.713159	-2.355440	11711.121300
HLA B*5401	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.441866	2.086183	-2.355683	27660.871590
HLA B*0802	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.362449	2.006546	-2.355903	23038.201291
HLA A*2301	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.443149	2.086649	-2.356499	27742.697047
HLA B*1509	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.001817	1.645215	-2.356602	10041.919084
HLA A*2402	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.347821	1.990887	-2.356934	22275.151931
HLA A*6802	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.294692	1.937546	-2.357146	19710.233558
HLA B*5801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.345577	1.987904	-2.357673	22160.365377
HLA B*2705	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-3.806053	1.448126	-2.357927	6398.128058
HLA A*0301	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.366330	2.008310	-2.358020	23245.019654
HLA A*3002	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.412521	2.054462	-2.358059	25853.586167
HLA B*4402	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.345983	1.987904	-2.358079	22181.115211
HLA B*7301	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.122787	1.764418	-2.358369	13267.436001
HLA B*4001	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.371099	2.012396	-2.358704	23501.705092
HLA B*1501	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.400050	2.041338	-2.358712	25121.740576
HLA B*5301	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.523433	2.164532	-2.358901	33375.895838
HLA A*6801	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.593831	2.234720	-2.359111	39249.176626
HLA A*2603	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.558248	2.199112	-2.359136	36161.596851
HLA A*0212	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.417762	2.058588	-2.359174	26167.515730
HLA B*0803	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.360473	2.001284	-2.359189	22933.622084
HLA A*0203	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.593208	1.234017	-2.359192	3919.298876

HLA B*1517	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.448592	2.089268	-2.359324	28092.632384
HLA B*0803	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.448628	2.089268	-2.359359	28094.912147
HLA B*1502	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.485644	2.126210	-2.359434	30594.532025
HLA A*3301	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.360851	2.001284	-2.359567	22953.605790
HLA A*1101	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.445804	2.086183	-2.359621	27912.812444
HLA B*0801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.203426	1.843794	-2.359632	15974.454093
HLA B*5101	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.401032	2.041338	-2.359694	25178.613494
HLA A*0301	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.350816	1.990887	-2.359929	22429.328324
HLA A*0211	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.274299	0.914083	-2.360215	1880.609764
HLA A*6901	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.365923	2.005692	-2.360231	23223.274566
HLA A*6801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.082844	0.722436	-2.360407	1210.162951
HLA B*4601	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.208773	1.848352	-2.360422	16172.361982
HLA B*4001	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.213472	1.852707	-2.360765	16348.293406
HLA A*0301	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.366471	2.005692	-2.360779	23252.566058
HLA B*1517	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.071239	1.710232	-2.361008	11782.550245
HLA B*0802	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.415538	2.054462	-2.361075	26033.798050
HLA B*1801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.402444	2.041338	-2.361106	25260.611041
HLA B*0702	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.298749	1.937546	-2.361203	19895.246809
HLA A*0203	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.419863	2.058588	-2.361274	26294.379912
HLA B*1801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.415791	2.054462	-2.361329	26049.013211
HLA B*1517	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.362712	2.001284	-2.361428	23052.164542
HLA A*0211	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-3.429426	1.067986	-2.361439	2687.978455
HLA B*1502	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.448336	2.086649	-2.361687	28076.071662
HLA B*0702	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-2.749020	0.387024	-2.361996	561.073330
HLA A*3001	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.214671	1.852642	-2.362028	16393.461340
HLA A*0101	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.363313	2.001284	-2.362029	23084.112331
HLA B*5401	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.565651	2.203513	-2.362137	36783.311701
HLA A*0202	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.561405	2.199112	-2.362294	36425.482058
HLA B*1501	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.299884	1.937546	-2.362338	19947.300599
HLA A*0250	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.451950	2.089268	-2.362681	28310.650619
HLA B*4402	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.364269	2.001284	-2.362986	23134.995501
HLA A*3002	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.368917	2.005692	-2.363225	23383.886841
HLA B*7301	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.368982	2.005692	-2.363290	23387.429228
HLA B*1501	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.400717	2.037348	-2.363369	25160.367498
HLA A*2601	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.112961	1.749555	-2.363406	12970.641476
HLA A*0216	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.301162	1.937546	-2.363616	20006.091567
HLA B*0802	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.376400	2.012396	-2.364004	23790.294075
HLA A*3201	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-3.692310	1.328104	-2.364205	4923.904944
HLA B*0801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.326884	1.962632	-2.364252	21226.794430
HLA B*3901	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.217255	1.852642	-2.364613	16491.307676
HLA B*0802	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.401986	2.037348	-2.364638	25233.976956
HLA A*8001	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.397557	2.032901	-2.364656	24977.957533
HLA B*1517	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.406024	2.041338	-2.364687	25469.737374
HLA B*7301	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.599888	2.235159	-2.364729	39800.407882
HLA A*3002	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.355642	1.990887	-2.364755	22679.950923
HLA A*2601	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.377297	2.012396	-2.364902	23839.509402
HLA A*2603	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.966448	1.601532	-2.364916	9256.516303
HLA B*0803	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.419720	2.054462	-2.365257	26285.704113
HLA A*0201	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.703014	1.337377	-2.365637	5046.774662
HLA A*3002	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.257476	1.891829	-2.365646	18091.556303
HLA B*4402	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.398809	2.032901	-2.365908	25050.084685
HLA A*8001	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.403379	2.037348	-2.366031	25315.059165
HLA B*0803	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.421385	2.055046	-2.366340	26386.719463
HLA B*4001	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.357317	1.990887	-2.366430	22767.602123
HLA A*0101	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.369441	2.003005	-2.366436	23412.114309
HLA A*2403	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.219144	1.852642	-2.366502	16563.193681
HLA B*4402	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.202543	1.835915	-2.366628	15941.993189
HLA A*3301	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.484779	2.118146	-2.366633	30533.683820
HLA A*0203	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.372493	2.005692	-2.366800	23577.221138
HLA A*0212	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.484094	1.117129	-2.366965	3048.551952
HLA B*3501	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.372723	2.005692	-2.367031	23589.724367
HLA A*0301	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.368498	2.001284	-2.367215	23361.379925
HLA B*1517	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.941059	1.573351	-2.367708	8730.900430
HLA B*4801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.337965	1.970233	-2.367732	21775.321975
HLA B*4403	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.623279	2.255532	-2.367747	42002.872837

HLA A*2403	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.238069	1.870150	-2.367920	17300.919364
HLA A*2403	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.405472	2.037348	-2.368124	25437.377661
HLA B*2705	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.260429	1.892220	-2.368209	18215.002314
HLA B*2705	1:279-287	9	GLLNYLALL	1.290918	0.282433	-3.942365	1.573351	-2.369014	8757.201627
HLA B*4002	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.546089	2.177014	-2.369075	35163.250556
HLA B*2705	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.360022	1.990887	-2.369135	22909.813327
HLA A*6801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-3.461360	1.091927	-2.369433	2893.076939
HLA A*0201	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.376116	2.006546	-2.369570	23774.726126
HLA B*1502	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.205541	1.835915	-2.369626	16052.421771
HLA A*0101	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.376285	2.006546	-2.369739	23783.988471
HLA A*0212	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.371031	2.001284	-2.369748	23498.018274
HLA A*0211	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-3.754571	1.384650	-2.369921	5682.913071
HLA A*6802	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.218453	1.848352	-2.370101	16536.870737
HLA A*0101	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.376639	2.005692	-2.370947	23803.425389
HLA A*3301	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.377633	2.006546	-2.371088	23857.959119
HLA A*0216	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.219497	1.848352	-2.371145	16576.639892
HLA B*4403	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.489309	2.118146	-2.371163	30853.824949
HLA B*5701	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.380352	2.008310	-2.372041	24007.760184
HLA B*0803	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.309679	1.937546	-2.372133	20402.300287
HLA A*6801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-3.067793	0.695627	-2.372166	1168.942239
HLA A*3101	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.373484	2.001284	-2.372200	23631.108791
HLA A*0201	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.378268	2.005692	-2.372576	23892.833189
HLA A*3201	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.422838	1.050133	-2.372705	2647.511331
HLA B*1503	1:210-218	9	THVLRGEDL	1.116170	0.447749	-3.937051	1.563919	-2.373132	8650.691290
HLA B*1502	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.517954	2.144780	-2.373174	32957.475078
HLA B*3501	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.909858	1.536595	-2.373263	8125.645562
HLA B*3501	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.226282	1.852707	-2.373575	16837.663105
HLA A*0101	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.166055	1.792274	-2.373781	14657.338483
HLA A*8001	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.382097	2.008310	-2.373787	24104.454723
HLA B*3501	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.285153	1.911098	-2.374055	19282.034759
HLA B*4403	1:55-63	9	EESYLALLD	1.112493	-0.915046	-2.571530	0.197447	-2.374083	372.846552
HLA A*0250	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-2.849488	0.475212	-2.374276	707.112156
HLA A*1101	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.428826	2.054462	-2.374364	26842.701307
HLA A*0202	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.608903	1.234017	-2.374886	4063.525063
HLA B*1503	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.018512	1.643417	-2.375095	10435.473463
HLA A*0301	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.363701	1.987904	-2.375797	23104.727141
HLA A*2402	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.462802	2.086649	-2.376153	29026.997893
HLA A*0202	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.367091	1.990887	-2.376204	23285.799349
HLA B*4001	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.382812	2.006546	-2.376266	24144.129677
HLA B*5101	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.431157	2.054462	-2.376695	26987.142851
HLA A*6901	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.277176	1.900474	-2.376703	18931.122243
HLA B*7301	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.611454	2.234720	-2.376734	40874.649112
HLA A*2402	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.431310	2.054462	-2.376847	26996.634354
HLA A*0101	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.813961	1.437023	-2.376939	6515.703221
HLA A*3002	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.277418	1.900474	-2.376945	18941.673955
HLA B*4601	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.385267	2.008310	-2.376956	24281.011064
HLA B*5301	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.442028	2.064809	-2.377219	27671.198833
HLA A*2403	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.385565	2.008310	-2.377255	24297.699208
HLA A*6802	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.418608	2.041338	-2.377270	26218.528198
HLA B*1509	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.431845	2.054462	-2.377383	27029.954025
HLA B*4002	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.463580	2.086183	-2.377397	29079.022329
HLA A*0206	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.142391	1.764802	-2.377589	13880.052354
HLA A*0212	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.384186	2.006546	-2.377640	24220.661700
HLA A*3101	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.021332	1.643417	-2.377914	10503.439543
HLA A*6802	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-3.977626	1.599646	-2.377981	9497.874353
HLA A*2602	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.380995	2.003005	-2.377990	24043.373506
HLA A*2601	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.386319	2.008310	-2.378009	24339.930630
HLA B*0801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.214003	1.835915	-2.378088	16368.293625
HLA B*0803	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.436796	2.058588	-2.378207	27339.821321
HLA B*3901	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.369412	1.990887	-2.378526	23410.594475
HLA B*4801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.341252	1.962632	-2.378620	21940.752316
HLA A*3101	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.387149	2.008310	-2.378838	24386.456784
HLA B*0802	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.384766	2.005692	-2.379074	24253.048014
HLA B*4501	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-2.882264	0.502859	-2.379405	762.541737
HLA A*3101	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.385321	2.005692	-2.379629	24284.032476

HLA B*0702	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-3.981221	1.601532	-2.379689	9576.815750
HLA A*0201	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.392134	2.012396	-2.379739	24668.021116
HLA A*2501	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.382767	2.003005	-2.379762	24141.648081
HLA B*5401	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.544917	2.164532	-2.380384	35068.454152
HLA B*5301	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.439319	2.058588	-2.380731	27499.134096
HLA A*2601	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.386587	2.005692	-2.380895	24354.946361
HLA B*4001	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.351202	1.970233	-2.380969	22449.236944
HLA A*0202	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.382443	2.001284	-2.381159	24123.631504
HLA B*1801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.414189	2.032901	-2.381288	25953.081301
HLA A*0219	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.145788	1.764296	-2.381492	13989.057637
HLA B*5801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.292648	1.911098	-2.381550	19617.683273
HLA A*2603	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.414659	2.032901	-2.381758	25981.177157
HLA B*4002	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.637409	2.255532	-2.381877	43391.913121
HLA B*2705	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.092037	1.710050	-2.381987	12360.525692
HLA A*8001	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.394505	2.012396	-2.382109	24803.041611
HLA A*0101	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.394719	2.012396	-2.382323	24815.255153
HLA B*1509	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.282817	1.900474	-2.382344	19178.625259
HLA B*5401	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.559584	2.177014	-2.382570	36273.081952
HLA B*4402	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-3.564507	1.181912	-2.382595	3668.656702
HLA A*0219	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.721481	1.338560	-2.382921	5266.000137
HLA A*2501	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.395698	2.012396	-2.383303	24871.299669
HLA B*1509	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.147786	1.764418	-2.383367	14053.533129
HLA B*4601	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.353864	1.970233	-2.383631	22587.259963
HLA A*1101	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.473286	2.089268	-2.384017	29736.203725
HLA A*2603	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.548742	2.164532	-2.384209	35378.676638
HLA B*4402	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.027760	1.643417	-2.384343	10660.062009
HLA B*1509	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.321913	1.937546	-2.384367	20985.189908
HLA A*8001	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.295526	1.911098	-2.384428	19748.123644
HLA B*4001	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.173841	1.789240	-2.384601	14922.490479
HLA B*4402	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.390523	2.005692	-2.384830	24576.643217
HLA A*0211	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.447033	1.062125	-2.384908	2799.192875
HLA B*4403	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.584376	2.199112	-2.385264	38403.978938
HLA A*0219	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.422645	2.037348	-2.385297	26463.344089
HLA A*0219	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.397808	2.012396	-2.385413	24992.420413
HLA A*2402	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.258991	1.873578	-2.385413	18154.794858
HLA A*1101	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.472104	2.086649	-2.385455	29655.396329
HLA A*0201	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.386768	2.001284	-2.385484	24365.093806
HLA A*6802	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.392332	2.006546	-2.385786	24679.233569
HLA A*3002	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.418848	2.032901	-2.385947	26232.999803
HLA A*2301	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.376886	1.990887	-2.385999	23816.950489
HLA B*1501	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.846093	1.459786	-2.386306	7016.052848
HLA A*0202	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.398755	2.012396	-2.386360	25046.967961
HLA B*5801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.356648	1.970233	-2.386415	22732.525663
HLA A*3002	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.398819	2.012396	-2.386423	25050.626764
HLA A*3101	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.028798	1.642298	-2.386501	10685.582540
HLA A*2403	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.230405	1.843794	-2.386611	16998.287168
HLA A*2602	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.551246	2.164532	-2.386714	35583.292846
HLA A*2403	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.392440	2.005692	-2.386748	24685.375881
HLA B*1509	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.241575	1.854767	-2.386808	17441.129776
HLA A*2601	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.349580	1.962632	-2.386948	22365.594114
HLA A*0101	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.377903	1.990887	-2.387017	23872.806662
HLA A*0203	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.923842	1.536595	-2.387247	8391.546575
HLA A*2603	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.279176	1.891829	-2.387346	19018.478572
HLA B*1801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.163677	1.776041	-2.387637	14577.311638
HLA B*4601	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.389012	2.001284	-2.387728	24491.300441
HLA A*3001	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.199911	1.811844	-2.388067	15845.691488
HLA A*0219	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.394963	2.006546	-2.388417	24829.220850
HLA B*0803	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.394110	2.005692	-2.388418	24780.509326
HLA A*1101	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.391476	2.003005	-2.388471	24630.683049
HLA B*5301	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.506984	2.118146	-2.388838	32135.435279
HLA B*0803	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.376743	1.987904	-2.388839	23809.092115
HLA A*0202	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.218045	1.828963	-2.389082	16521.311563
HLA A*2501	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.478384	2.089268	-2.389116	30087.347770
HLA B*1517	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.397684	2.008310	-2.389373	24985.255510
HLA A*2601	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.380392	1.990887	-2.389505	24009.968234

HLA B*5801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.352477	1.962632	-2.389845	22515.280100
HLA B*5301	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.226047	1.835915	-2.390132	16828.556579
HLA A*3301	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.423293	2.032901	-2.390392	26502.886801
HLA B*4501	1:457-465	9	GTTVSPPLF	1.234422	1.000737	-4.625600	2.235159	-2.390442	42227.978006
HLA B*1502	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.035659	1.645215	-2.390444	10855.721661
HLA B*1501	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.396187	2.005692	-2.390495	24899.302024
HLA B*4002	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.625295	2.234720	-2.390575	42198.290119
HLA A*0250	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.392134	2.001284	-2.390851	24668.021116
HLA B*4002	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-2.798848	0.407915	-2.390933	629.285180
HLA A*3101	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.243835	1.852707	-2.391128	17532.135486
HLA B*0801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-3.775801	1.384650	-2.391151	5967.617232
HLA B*4601	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.397085	2.005692	-2.391393	24950.811571
HLA B*1503	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.239777	1.848352	-2.391425	17369.097681
HLA A*2501	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.478497	2.086649	-2.391847	30095.161707
HLA B*3501	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.053783	1.661630	-2.392152	11318.337159
HLA A*0250	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.292904	1.900474	-2.392430	19629.254799
HLA A*6901	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.383467	1.990887	-2.392580	24180.599354
HLA A*3001	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.266263	1.873578	-2.392685	18461.330703
HLA B*1801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.401133	2.008310	-2.392822	25184.471356
HLA B*0702	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.394204	2.001284	-2.392920	24785.872298
HLA B*5701	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.293418	1.900474	-2.392945	19652.524649
HLA A*2501	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.383881	1.990887	-2.392994	24203.633646
HLA A*8001	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.396326	2.003005	-2.393321	24907.250737
HLA B*5401	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.246116	1.852642	-2.393474	17624.474151
HLA A*2902	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.430844	2.037348	-2.393496	26967.732174
HLA B*4501	1:336-344	9	DVGDFTVRL	1.966030	0.289502	-4.649194	2.255532	-2.393662	44585.517834
HLA B*3901	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.452460	2.058588	-2.393871	28343.905308
HLA A*2902	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-2.917793	0.523921	-2.393872	827.546739
HLA B*4601	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.356622	1.962632	-2.393990	22731.172918
HLA A*3201	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.593887	2.199112	-2.394775	39254.272965
HLA A*3002	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.103014	1.708081	-2.394933	12676.919590
HLA B*2705	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.428070	2.032901	-2.395169	26795.982446
HLA B*1801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.357804	1.962632	-2.395172	22793.112636
HLA A*0206	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.432534	2.037348	-2.395186	27072.833113
HLA B*1501	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.268885	1.873578	-2.395307	18573.126952
HLA A*0101	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.306573	1.911098	-2.395475	20256.906158
HLA B*5401	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.267227	0.871584	-2.395642	1850.234339
HLA A*0101	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.383601	1.987904	-2.395697	24188.056923
HLA A*2601	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.185025	1.789240	-2.395785	15311.751039
HLA B*4403	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.560505	2.164532	-2.395973	36350.087049
HLA A*0301	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.366431	1.970233	-2.396198	23250.427662
HLA B*5401	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.541009	2.144780	-2.396230	34754.370664
HLA B*1503	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.109898	1.713576	-2.396322	12879.462135
HLA B*7301	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.595541	2.199112	-2.396429	39404.060352
HLA A*8001	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.402148	2.005692	-2.396456	25243.398113
HLA B*5101	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.404859	2.008310	-2.396549	25401.485910
HLA B*3901	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.367256	1.970233	-2.397023	23294.619170
HLA A*0101	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.367493	1.970233	-2.397260	23307.350800
HLA A*6901	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.249993	1.852642	-2.397350	17782.500041
HLA A*0250	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.726156	1.328755	-2.397401	5322.998469
HLA B*3501	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.398896	2.001284	-2.397612	25055.099360
HLA B*0702	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.403388	2.005692	-2.397696	25315.606977
HLA B*4601	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.250484	1.852642	-2.397841	17802.617495
HLA B*1501	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.086572	1.688566	-2.398006	12205.962730
HLA B*3901	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.484194	2.086183	-2.398011	30492.580733
HLA B*7301	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-3.558065	1.159900	-2.398165	3614.637803
HLA B*0801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.389089	1.990887	-2.398202	24495.673174
HLA A*2902	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.431157	2.032901	-2.398256	26987.142851
HLA A*2601	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.368679	1.970233	-2.398447	23371.113403
HLA A*2601	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.386357	1.987904	-2.398453	24342.037542
HLA A*2902	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.251114	1.852642	-2.398471	17828.447345
HLA B*5401	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.405515	2.006546	-2.398969	25439.854822
HLA A*3101	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.369243	1.970233	-2.399011	23401.477542
HLA A*0203	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.389994	1.990887	-2.399107	24546.746110
HLA B*4402	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.402366	2.003005	-2.399361	25256.101759

HLA A*0203	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.191787	1.792234	-2.399553	15552.015374
HLA B*1503	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.109635	1.710050	-2.399585	12871.660735
HLA A*8001	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.400893	2.001284	-2.399609	25170.578179
HLA B*7301	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.486252	2.086183	-2.400070	30637.429945
HLA B*5101	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.458855	2.058588	-2.400267	28764.377954
HLA B*5401	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.524063	2.123741	-2.400322	33424.320986
HLA B*5401	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.518577	2.118146	-2.400431	33004.757478
HLA A*1101	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.437782	2.037348	-2.400434	27402.012217
HLA B*4002	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.043985	1.643417	-2.400568	11065.862624
HLA B*1501	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.113817	1.713159	-2.400658	12996.208424
HLA B*3501	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.409008	2.008310	-2.400698	25645.331236
HLA A*2902	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.402030	2.001284	-2.400747	25236.570837
HLA A*0250	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.599923	2.199112	-2.400811	39803.637750
HLA B*5701	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.413277	2.012396	-2.400882	25898.661958
HLA B*1503	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.635015	1.234017	-2.400998	4315.340995
HLA A*3301	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.565714	2.164532	-2.401182	36788.684922
HLA A*0212	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.338745	1.937546	-2.401199	21814.467408
HLA B*5101	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.490514	2.089268	-2.401246	30939.571671
HLA A*0203	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.451450	1.050133	-2.401317	2827.807590
HLA B*4402	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.364086	1.962632	-2.401454	23125.235255
HLA B*5301	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.256311	1.854767	-2.401544	18043.076212
HLA B*4001	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.193882	1.792234	-2.401649	15627.244877
HLA A*0219	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.402940	2.001284	-2.401656	25289.462153
HLA A*0101	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.263150	1.861442	-2.401708	18329.471137
HLA A*6901	1:463-471	9	PLFESLELL	1.291656	0.202256	-3.895813	1.493912	-2.401901	7867.063457
HLA A*0211	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.460944	2.058588	-2.402355	28903.050305
HLA A*0216	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.403753	2.001284	-2.402469	25336.843847
HLA B*5701	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.403760	2.001284	-2.402476	25337.255059
HLA A*3301	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.547586	2.144780	-2.402806	35284.635645
HLA B*1801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.249758	1.846931	-2.402827	17772.882507
HLA B*4001	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.257868	1.854767	-2.403102	18107.908532
HLA A*2402	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.444518	2.041338	-2.403181	27830.334683
HLA A*6802	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.441262	2.037348	-2.403914	27622.440255
HLA B*2705	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.295784	1.891829	-2.403955	19759.879009
HLA B*4001	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-3.585963	1.181912	-2.404051	3854.451374
HLA A*2403	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.416628	2.012396	-2.404232	26099.229881
HLA A*2301	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.530810	2.126210	-2.404600	33947.696769
HLA A*0206	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.458630	1.054023	-2.404607	2874.947259
HLA B*4001	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.342241	1.937546	-2.404695	21990.780719
HLA B*1509	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.093606	1.688566	-2.405040	12405.275043
HLA B*0802	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.342760	1.937546	-2.405214	22017.088301
HLA B*1502	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.408348	2.003005	-2.405343	25606.375363
HLA A*0203	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.277010	0.871584	-2.405426	1892.387159
HLA B*0702	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.179038	1.773509	-2.405529	15102.135804
HLA B*7301	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.609100	2.203513	-2.405586	40653.678986
HLA B*5801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.373236	0.967578	-2.405657	2361.758571
HLA B*4002	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.604984	2.199112	-2.405872	40270.178606
HLA B*0803	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.376120	1.970233	-2.405887	23774.983365
HLA A*2902	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.007531	1.601532	-2.405999	10174.912077
HLA A*0216	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.412793	2.006546	-2.406248	25869.815603
HLA B*5701	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.411962	2.005692	-2.406269	25820.319710
HLA A*1101	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.439427	2.032901	-2.406526	27505.978242
HLA B*5701	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.376778	1.970233	-2.406545	23811.024261
HLA A*0101	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.369271	1.962632	-2.406639	23402.996785
HLA A*0201	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.298998	1.892220	-2.406779	19906.658975
HLA B*5101	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.419196	2.012396	-2.406800	26254.012021
HLA B*0702	1:462-470	9	PPLFESLEL	1.313352	0.107023	-3.827184	1.420375	-2.406809	6717.136849
HLA B*4601	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.943441	1.536595	-2.406846	8778.926505
HLA A*2501	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.199211	1.792274	-2.406937	15820.166485
HLA A*0201	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.398057	1.990887	-2.407170	25006.756382
HLA B*2705	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.262236	1.854767	-2.407469	18290.938298
HLA A*0250	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-3.475645	1.067986	-2.407658	2989.818690
HLA B*5801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.345380	1.937546	-2.407834	22150.297315
HLA B*1502	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.497142	2.089268	-2.407874	31415.371095
HLA B*1502	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.414647	2.006546	-2.408101	25980.474390

HLA B*3801	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.466761	2.058588	-2.408173	29292.807906
HLA A*0219	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.308779	1.900474	-2.408305	20360.070740
HLA B*0803	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.441372	2.032901	-2.408471	27629.464562
HLA A*2902	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.263270	1.854767	-2.408503	18334.529015
HLA B*1517	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.319780	1.911098	-2.408682	20882.359659
HLA A*2603	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.463754	2.055046	-2.408708	29090.665917
HLA A*1101	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.450402	2.041338	-2.409064	28209.899540
HLA B*0702	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.396998	1.987904	-2.409094	24945.817769
HLA B*1509	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.245052	1.835915	-2.409137	17581.335090
HLA A*3201	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.119465	1.710050	-2.409415	13166.332836
HLA A*3001	1:314-322	9	SSPARFDQK	0.878945	0.297758	-3.586338	1.176703	-2.409635	3857.789163
HLA B*5701	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.397794	1.987904	-2.409890	24991.609188
HLA B*5101	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.411203	2.001284	-2.409919	25775.240830
HLA B*1517	1:365-373	9	AAELVQTRI	1.206674	0.321116	-3.938080	1.527790	-2.410290	8671.213680
HLA B*4801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.416910	2.006546	-2.410364	26116.178655
HLA A*0211	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.496616	2.086183	-2.410433	31377.324529
HLA A*2602	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.497241	2.086649	-2.410592	31422.509960
HLA A*0212	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.401521	1.990887	-2.410634	25206.961850
HLA A*2902	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.416393	2.005692	-2.410701	26085.114306
HLA A*0206	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.469357	2.058588	-2.410769	29468.442631
HLA A*2301	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.373454	1.962632	-2.410822	23629.446907
HLA B*0802	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.381103	1.970233	-2.410871	24049.357562
HLA B*5801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.056212	1.645215	-2.410997	11381.827371
HLA B*1517	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.398938	1.987904	-2.411034	25057.539294
HLA A*0301	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.201913	1.790732	-2.411181	15918.896433
HLA A*0250	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.588528	2.177014	-2.411514	38772.853377
HLA A*2902	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.203783	1.792234	-2.411549	15987.595339
HLA B*1503	1:366-374	9	AELVQTRIV	1.123749	0.213984	-3.749350	1.337733	-2.411617	5615.009006
HLA A*6901	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-3.840947	1.429220	-2.411728	6933.419531
HLA B*1801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.501016	2.089268	-2.411748	31696.878489
HLA A*6901	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.349900	1.937546	-2.412354	22382.055541
HLA A*6901	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.162155	1.749555	-2.412600	14526.298763
HLA A*3001	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.256513	1.843794	-2.412719	18051.472714
HLA A*0250	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.241725	1.828963	-2.412762	17447.169514
HLA A*2902	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.283175	1.870150	-2.413025	19194.402389
HLA B*4601	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.324157	1.911098	-2.413059	21093.889272
HLA A*2501	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.454429	2.041338	-2.413091	28472.693747
HLA A*2602	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.265983	1.852642	-2.413341	18449.449551
HLA A*0250	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.752297	1.338560	-2.413737	5653.230734
HLA B*1503	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.189879	1.775750	-2.414129	15483.847849
HLA A*6801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.206447	1.792234	-2.414214	16085.977738
HLA A*2902	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.422527	2.008310	-2.414217	26456.186870
HLA B*4501	1:21-29	9	VGLVRTALF	1.226065	1.008655	-4.649112	2.234720	-2.414392	44577.076539
HLA B*4801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.352202	1.937546	-2.414656	22501.033405
HLA A*6801	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.613820	2.199112	-2.414708	41097.931967
HLA B*5401	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.447709	2.032901	-2.414808	28035.546725
HLA A*0206	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.207124	1.792234	-2.414890	16111.059999
HLA A*2603	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.501611	2.086649	-2.414962	31740.291771
HLA B*3801	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.448045	2.032901	-2.415144	28057.243812
HLA B*0801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.204643	1.789240	-2.415403	16019.282449
HLA A*3001	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.263805	1.848352	-2.415454	18357.157780
HLA A*0203	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.715377	1.299885	-2.415492	5192.504769
HLA A*2601	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.307764	1.892220	-2.415544	20312.543346
HLA A*3002	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.932977	1.517234	-2.415742	8569.920774
HLA A*2603	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.259647	1.843794	-2.415853	18182.217652
HLA B*1801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.208214	1.792274	-2.415940	16151.552599
HLA A*0301	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.129554	1.713576	-2.415977	13475.767772
HLA A*2301	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.716928	1.300706	-2.416222	5211.077885
HLA A*0219	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.354021	1.937546	-2.416475	22595.448483
HLA B*0702	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.424919	2.008310	-2.416609	26602.290104
HLA B*5401	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-3.260056	0.843357	-2.416699	1819.935970
HLA B*3501	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.429334	2.012396	-2.416938	26874.086305
HLA B*1503	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.278666	1.861442	-2.417224	18996.165006
HLA B*4402	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.182135	1.764802	-2.417333	15210.202377
HLA B*5101	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.482272	2.064809	-2.417463	30357.940373

HLA A*0301	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.355790	1.937546	-2.418244	22687.682090
HLA B*1502	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.388728	1.970233	-2.418495	24475.273765
HLA A*3001	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.027779	1.609246	-2.418532	10660.523377
HLA B*1509	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.409488	1.990887	-2.418601	25673.649492
HLA A*2902	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.133078	1.714405	-2.418673	13585.566283
HLA A*0206	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-3.848015	1.429220	-2.418795	7047.169711
HLA A*6802	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.424501	2.005692	-2.418809	26576.685486
HLA A*0203	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.267217	1.848352	-2.418865	18501.924010
HLA A*6901	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.280449	1.861442	-2.419007	19074.325628
HLA A*3002	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.474202	2.055046	-2.419156	29799.009087
HLA B*4001	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.311406	1.892220	-2.419186	20483.586813
HLA A*0250	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.460993	2.041338	-2.419655	28906.334100
HLA A*0301	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.603565	1.183813	-2.419752	4013.884882
HLA A*6802	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.070370	1.650564	-2.419806	11758.989186
HLA A*2601	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.357498	1.937546	-2.419952	22777.088204
HLA B*4001	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.331196	1.911098	-2.420098	21438.565331
HLA A*2403	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.382938	1.962632	-2.420306	24151.184029
HLA B*1503	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.290526	1.870150	-2.420377	19522.082044
HLA A*2602	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.312647	1.892220	-2.420427	20542.180214
HLA B*4001	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.196401	1.775750	-2.420651	15718.136844
HLA B*5701	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-3.880466	1.459786	-2.420679	7593.916495
HLA A*1101	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-3.748791	1.328104	-2.420687	5607.784033
HLA B*5301	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.429237	2.008310	-2.420927	26868.126147
HLA A*1101	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.475987	2.055046	-2.420942	29921.780398
HLA B*1503	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.938310	1.517234	-2.421076	8675.812109
HLA A*0206	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.109935	1.688566	-2.421369	12880.577007
HLA B*3501	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.459045	2.037348	-2.421697	28776.985296
HLA B*0802	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.322214	1.900474	-2.421740	20999.726467
HLA B*1517	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.384823	1.962632	-2.422191	24256.197169
HLA B*4801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.194334	1.771882	-2.422451	15643.485309
HLA A*0201	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.137034	1.714405	-2.422630	13709.899728
HLA A*2902	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.435520	2.012396	-2.423124	27259.626534
HLA B*2705	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.293343	1.870150	-2.423194	19649.122768
HLA A*3002	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.334304	1.911098	-2.423206	21592.557644
HLA B*1503	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.215625	1.792234	-2.423391	16429.507756
HLA A*0203	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.115720	1.692204	-2.423516	13053.282901
HLA B*0802	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.411452	1.987904	-2.423548	25790.025835
HLA A*0203	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.393936	1.970233	-2.423704	24770.590885
HLA A*3101	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.276521	1.852642	-2.423878	18902.569935
HLA B*2705	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.430809	2.006546	-2.424263	26965.543876
HLA A*6901	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.188878	1.764296	-2.424582	15448.204663
HLA B*1517	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.316815	1.892220	-2.424595	20740.275516
HLA A*3201	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.174419	1.749555	-2.424864	14942.363038
HLA A*2403	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.336301	1.911098	-2.425203	21692.077626
HLA B*1501	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.278029	1.852707	-2.425322	18968.335514
HLA A*6802	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.416649	1.990887	-2.425762	26100.500658
HLA A*2403	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-3.323182	0.897326	-2.425856	2104.660603
HLA A*3001	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.218204	1.792274	-2.425930	16527.390416
HLA A*2403	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.202261	1.776041	-2.426220	15931.647218
HLA A*8001	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.389026	1.962632	-2.426394	24492.095425
HLA A*3001	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.287918	1.861442	-2.426476	19405.203669
HLA A*0101	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.281389	1.854767	-2.426622	19115.646315
HLA B*4501	1:127-135	9	NPKLGYDNF	1.158701	1.040411	-4.625751	2.199112	-2.426639	42242.601253
HLA A*0202	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.464226	2.037348	-2.426878	29122.315954
HLA A*6801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.433544	2.006546	-2.426998	27135.884663
HLA A*0206	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.279911	1.852707	-2.427204	19050.709753
HLA B*1509	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.280437	1.852642	-2.427795	19073.809685
HLA B*0802	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.418707	1.990887	-2.427820	26224.486127
HLA A*0301	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.138016	1.710050	-2.427967	13740.937465
HLA B*1509	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.203882	1.775750	-2.428132	15991.228379
HLA A*6801	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.573059	2.144780	-2.428279	37416.120329
HLA B*0801	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.302032	1.873578	-2.428453	20046.177045
HLA B*4801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.246295	1.817618	-2.428677	17631.721971
HLA B*4001	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.275677	1.846931	-2.428746	18865.893932
HLA A*3001	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.275854	1.846931	-2.428922	18873.550164

HLA B*1801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.366635	1.937546	-2.429089	23261.373292
HLA B*7301	1:190-198	9	ASGDPLYTL	1.661474	0.483306	-4.574177	2.144780	-2.429397	37512.595015
HLA B*5701	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.367242	1.937546	-2.429696	23293.863055
HLA B*4001	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.321835	1.891829	-2.430006	20981.443833
HLA B*1801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.203731	1.773509	-2.430223	15985.692648
HLA A*0201	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.400990	1.970233	-2.430757	25176.161770
HLA A*0219	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.322754	1.891829	-2.430925	21025.872154
HLA A*2501	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.323292	1.892220	-2.431072	21051.936505
HLA B*4403	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.485639	2.054462	-2.431177	30594.201000
HLA B*3801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.517731	2.086183	-2.431548	32940.541283
HLA A*1101	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.158119	1.726550	-2.431568	14391.914055
HLA A*1101	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.444044	2.012396	-2.431648	27799.938371
HLA B*5101	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.469268	2.037348	-2.431920	29462.385256
HLA B*5401	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.558179	2.126210	-2.431969	36155.924019
HLA B*4601	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.324363	1.892220	-2.432144	21103.933836
HLA A*0203	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.759937	1.327486	-2.432451	5753.567819
HLA B*1517	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.438389	2.005692	-2.432696	27440.285317
HLA A*0301	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.344329	1.911098	-2.433232	22096.797726
HLA A*0206	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.347748	0.914377	-2.433372	2227.143942
HLA A*2403	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.148063	1.714405	-2.433658	14062.507304
HLA A*2601	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.334299	1.900474	-2.433826	21592.324018
HLA B*4403	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.520863	2.086649	-2.434213	33178.946700
HLA A*1101	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.440832	2.006546	-2.434286	27595.107303
HLA A*0201	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.079768	1.645215	-2.434553	12016.221658
HLA A*3101	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.326466	1.891829	-2.434637	21206.363709
HLA A*0216	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.091835	1.657009	-2.434826	12354.776290
HLA A*0202	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.521619	2.086649	-2.434970	33236.794274
HLA A*2602	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.558858	2.123741	-2.435118	36212.496500
HLA B*4402	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.405536	1.970233	-2.435303	25441.093494
HLA B*0702	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.397975	1.962632	-2.435343	25002.021898
HLA A*2403	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.335827	1.900474	-2.435353	21668.385524
HLA A*2501	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.472837	2.037348	-2.435489	29705.493507
HLA A*0250	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.441208	2.005692	-2.435516	27619.003479
HLA B*4001	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.398318	1.962632	-2.435686	25021.777392
HLA B*0803	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.438830	2.003005	-2.435825	27468.207908
HLA A*6801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-3.868455	1.432365	-2.436090	7386.781450
HLA B*3801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.373658	1.937546	-2.436112	23640.570969
HLA B*0803	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.065638	1.629468	-2.436170	11631.564363
HLA A*6801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.439244	2.003005	-2.436239	27494.373956
HLA B*7301	1:205-213	9	ALMKITHVL	1.662500	0.455646	-4.554789	2.118146	-2.436643	35874.772710
HLA B*0801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.348049	1.911098	-2.436951	22286.844090
HLA B*4002	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.474336	2.037348	-2.436988	29808.199437
HLA A*6802	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.094753	1.657009	-2.437744	12438.068559
HLA B*3801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.290465	1.852642	-2.437823	19519.336317
HLA B*4501	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.602474	2.164532	-2.437942	40038.177982
HLA A*3301	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-3.164117	0.726109	-2.438008	1459.208121
HLA A*0212	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.152433	1.714405	-2.438028	14204.724111
HLA B*3501	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.329873	1.891829	-2.438043	21373.367783
HLA A*3201	1:463-471	9	PLFESLELL	1.291656	0.202256	-3.932389	1.493912	-2.438478	8558.338028
HLA B*4801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.151643	1.713159	-2.438484	14178.927314
HLA B*5301	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.708117	1.269415	-2.438702	5106.425444
HLA B*1503	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-2.634750	0.196045	-2.438705	431.270819
HLA A*3301	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.293595	1.854767	-2.438828	19660.500115
HLA A*2602	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.525016	2.086183	-2.438834	33497.815349
HLA B*1801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.494156	2.055046	-2.439110	31200.100918
HLA B*1501	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.231448	1.792234	-2.439214	17039.165972
HLA A*0216	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.430158	1.990887	-2.439271	26925.165211
HLA A*0212	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.215338	1.776041	-2.439297	16418.667752
HLA A*3001	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.212852	1.773509	-2.439343	16324.961264
HLA A*3001	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.257300	1.817618	-2.439682	18084.217293
HLA B*2705	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.275623	1.835915	-2.439708	18863.546643
HLA B*3901	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.013075	1.573351	-2.439724	10305.651443
HLA A*1101	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.445625	2.005692	-2.439933	27901.338406
HLA A*1101	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.276190	1.835915	-2.440275	18888.156659
HLA A*0203	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-3.888811	1.448126	-2.440685	7741.251692

HLA B*0801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.293338	1.852642	-2.440696	19648.910170
HLA B*7301	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.605334	2.164532	-2.440801	40302.652416
HLA B*4002	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.513086	2.072193	-2.440893	32590.107981
HLA A*2603	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.258524	1.817618	-2.440906	18135.260505
HLA B*7301	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-3.671911	1.230828	-2.441083	4697.982898
HLA A*0211	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.355469	0.914377	-2.441092	2267.089651
HLA A*3001	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.042900	1.601532	-2.441368	11038.239487
HLA B*4801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.352896	1.911098	-2.441798	22536.971863
HLA B*4002	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.645378	2.203513	-2.441865	44195.520336
HLA B*4002	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.528550	2.086649	-2.441901	33771.481256
HLA B*5701	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.294830	1.852642	-2.442188	19716.525743
HLA A*3001	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.071733	1.629468	-2.442265	11795.943733
HLA A*6901	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.290731	1.848352	-2.442379	19531.272477
HLA B*5101	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.412756	1.970233	-2.442523	25867.576455
HLA B*1503	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.979384	1.536595	-2.442789	9536.386292
HLA B*0802	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.405627	1.962632	-2.442995	25446.461766
HLA B*5701	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.334997	1.891829	-2.443168	21627.045092
HLA A*0250	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.529915	2.086649	-2.443266	33877.796933
HLA A*2902	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.344026	1.900474	-2.443552	22081.382287
HLA A*3301	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.620636	2.177014	-2.443622	41748.014427
HLA A*2601	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.313913	1.870150	-2.443763	20602.167195
HLA A*3001	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.233065	1.789240	-2.443825	17102.703983
HLA A*2501	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.452476	2.008310	-2.444166	28344.978690
HLA A*0211	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.414403	1.970233	-2.444170	25965.861147
HLA B*5701	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.407068	1.962632	-2.444436	25530.988981
HLA A*0101	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.752475	1.307776	-2.444700	5655.555547
HLA A*6801	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.621801	2.177014	-2.444787	41860.187514
HLA A*0206	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.262527	1.817618	-2.444909	18303.212456
HLA B*1509	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.297624	1.852707	-2.444917	19843.758263
HLA B*5701	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.356096	1.911098	-2.444998	22703.643622
HLA B*1517	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.038939	1.593495	-2.445444	10938.016662
HLA B*2705	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.383335	1.937546	-2.445790	24173.274860
HLA B*5801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.338242	1.892220	-2.446022	21789.227058
HLA B*5801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.210442	1.764296	-2.446145	16234.599821
HLA B*1517	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.003311	1.556999	-2.446312	10076.529718
HLA B*1801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.458761	2.012396	-2.446365	28758.154144
HLA B*4403	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.452960	2.006546	-2.446414	28376.584996
HLA B*0801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-3.876335	1.429823	-2.446513	7522.036260
HLA B*4501	1:311-319	9	DVNSSPARF	1.154757	1.048756	-4.650340	2.203513	-2.446827	44703.380268
HLA A*3001	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.157221	1.710050	-2.447171	14362.202758
HLA B*0802	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.283163	1.835915	-2.447248	19193.883198
HLA B*4402	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.339823	1.892220	-2.447603	21868.703075
HLA B*5801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.339602	1.891829	-2.447773	21857.585020
HLA B*1517	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.309411	1.861442	-2.447969	20389.721510
HLA A*6801	1:243-251	9	KFAHLPTVL	1.684551	0.479981	-4.612535	2.164532	-2.448002	40976.494350
HLA B*7301	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.460474	2.012396	-2.448078	28871.794757
HLA A*3101	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.195410	1.747156	-2.448254	15682.293688
HLA A*3301	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.158386	1.710050	-2.448337	14400.792680
HLA A*3201	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.348880	1.900474	-2.448406	22329.566538
HLA A*3101	1:467-475	9	SLELLGRDR	0.924235	0.540201	-3.913086	1.464436	-2.448650	8186.270048
HLA B*4601	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.322303	1.873578	-2.448725	21004.043946
HLA B*1501	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-2.644782	0.196045	-2.448737	441.349231
HLA B*1501	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.319079	1.870150	-2.448930	20848.721348
HLA B*4002	1:465-473	9	FESLELLGR	0.858673	0.563144	-3.870875	1.421817	-2.449059	7428.056859
HLA B*2705	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.419480	1.970233	-2.449247	26271.203434
HLA B*4601	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.196504	1.747156	-2.449349	15721.878758
HLA B*4002	1:437-445	9	IEGLALKPR	0.838298	0.545124	-3.832785	1.383422	-2.449364	6804.330008
HLA B*1509	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.293273	1.843794	-2.449479	19645.934040
HLA A*6802	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.302220	1.852707	-2.449512	20054.854731
HLA B*5101	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.437573	1.987904	-2.449669	27388.821868
HLA A*2402	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.508291	2.058588	-2.449702	32232.240920
HLA A*0216	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.267353	1.817618	-2.449735	18507.730336
HLA A*0211	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.226404	1.776041	-2.450363	16842.400445
HLA B*1801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.420669	1.970233	-2.450436	26343.216849
HLA A*2301	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.487803	2.037348	-2.450455	30747.017236

HLA B*2705	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.350931	1.900474	-2.450458	22435.274781
HLA A*0301	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.342461	1.891829	-2.450632	22001.966525
HLA A*3101	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.870725	1.419915	-2.450810	7425.485466
HLA A*3001	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.692803	1.241782	-2.451021	4929.502057
HLA A*0219	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.299558	1.848352	-2.451206	19932.306374
HLA A*2603	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.224717	1.773509	-2.451208	16777.106396
HLA B*5101	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.287178	1.835915	-2.451263	19372.163129
HLA A*2301	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.484197	2.032901	-2.451296	30492.745695
HLA B*4801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.306256	1.854767	-2.451489	20242.117230
HLA B*5301	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.577819	2.126210	-2.451609	37828.472953
HLA A*8001	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.306608	1.854767	-2.451842	20258.550039
HLA B*4501	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.263857	1.811844	-2.452013	18359.342734
HLA A*2403	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.422259	1.970233	-2.452027	26439.875646
HLA A*2601	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.228274	1.776041	-2.452234	16915.084786
HLA A*0211	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.453745	2.001284	-2.452461	28427.905083
HLA A*2603	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.097915	1.645215	-2.452700	12528.969533
HLA B*4402	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.353347	1.900474	-2.452873	22560.393149
HLA B*0802	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.217805	1.764802	-2.453003	16512.197474
HLA B*5801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.196782	1.743756	-2.453026	15731.918289
HLA A*0216	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.345654	1.892220	-2.453435	22164.321939
HLA B*5101	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.345948	1.892220	-2.453728	22179.315324
HLA A*0206	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.687808	1.234017	-2.453791	4873.130560
HLA A*8001	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.391585	1.937546	-2.454039	24636.813278
HLA B*3801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.445200	1.990887	-2.454313	27874.031068
HLA B*1503	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.134393	1.679828	-2.454566	13626.786679
HLA B*4601	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.309461	1.854767	-2.454694	20392.038070
HLA A*0219	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.425123	1.970233	-2.454891	26614.813694
HLA A*3002	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.298688	1.843794	-2.454894	19892.448598
HLA B*4501	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.578794	2.123741	-2.455053	37913.497218
HLA A*2603	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.689110	1.234017	-2.455093	4887.757623
HLA B*0702	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.309928	1.854767	-2.455162	20414.003306
HLA A*1101	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.463498	2.008310	-2.455187	29073.516850
HLA B*2705	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.161027	1.705831	-2.455196	14488.626577
HLA A*0101	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.307936	1.852642	-2.455293	20320.566798
HLA A*0250	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.425687	1.970233	-2.455455	26649.392103
HLA A*1101	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.443464	1.987904	-2.455559	27762.815717
HLA A*0101	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.227579	1.771882	-2.455696	16888.019876
HLA B*7301	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-3.339036	0.883265	-2.455771	2182.912845
HLA A*3001	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.182539	1.726550	-2.455989	15224.362071
HLA A*3301	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.444074	1.987904	-2.456170	27801.893570
HLA B*1501	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.085693	1.629468	-2.456226	12181.291391
HLA A*2602	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.511418	2.055046	-2.456372	32465.168783
HLA A*3001	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.029945	1.573351	-2.456594	10713.830026
HLA B*3801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.426963	1.970233	-2.456730	26727.791648
HLA B*4501	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.515471	2.058588	-2.456882	32769.553706
HLA A*2403	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.309653	1.852707	-2.456946	20401.086207
HLA B*2705	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.368188	1.911098	-2.457091	23344.703393
HLA A*0101	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.394730	1.937546	-2.457185	24815.926401
HLA A*2403	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.349188	1.891829	-2.457359	22345.397010
HLA B*1801	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.460450	2.003005	-2.457445	28870.232867
HLA A*0101	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.201260	1.743756	-2.457504	15894.973216
HLA B*3501	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.146287	1.688566	-2.457720	14005.110842
HLA B*0801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-3.245738	0.787998	-2.457741	1760.914814
HLA B*2705	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.115208	1.657009	-2.458199	13037.897510
HLA A*2603	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.499548	2.041338	-2.458210	31589.886596
HLA B*4002	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.164171	1.705831	-2.458340	14593.881993
HLA B*3901	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.395959	1.937546	-2.458413	24886.239312
HLA B*1517	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.103667	1.645215	-2.458452	12695.999377
HLA A*3002	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.545008	2.086183	-2.458826	35075.853874
HLA B*1517	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.621242	1.162401	-2.458842	4180.636789
HLA B*3501	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.169269	1.710232	-2.459038	14766.215853
HLA B*4501	1:332-340	9	IRMLDVGDF	0.959983	1.217031	-4.636504	2.177014	-2.459490	43301.630180
HLA A*0301	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.360473	1.900474	-2.459999	22933.622084
HLA B*5101	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.308356	1.848352	-2.460004	20340.254159
HLA A*0219	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.450897	1.990887	-2.460010	28242.119148

HLA A*0250	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.224379	1.764296	-2.460082	16764.041716
HLA B*3501	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.250869	1.790732	-2.460137	17818.419374
HLA A*0212	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.207556	1.747156	-2.460401	16127.105249
HLA B*0801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.210211	1.749555	-2.460656	16225.995018
HLA B*1502	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.584679	2.123741	-2.460939	38430.789496
HLA B*5101	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.398682	1.937546	-2.461136	25042.767772
HLA A*2501	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.423819	1.962632	-2.461187	26535.022868
HLA A*6801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.462541	2.001284	-2.461258	29009.572480
HLA B*3501	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.226174	1.764802	-2.461372	16833.473491
HLA B*3801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.449281	1.987904	-2.461377	28137.197256
HLA A*0101	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.361981	1.900474	-2.461507	23013.412448
HLA B*0802	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.353680	1.891829	-2.461851	22577.730797
HLA A*2501	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.432085	1.970233	-2.461852	27044.873505
HLA A*2601	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.373082	1.911098	-2.461985	23609.257972
HLA A*2603	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.226366	1.764296	-2.462070	16840.942660
HLA A*2501	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.468030	2.005692	-2.462338	29378.507279
HLA A*6901	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.179809	1.717294	-2.462515	15128.957483
HLA A*2603	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-3.979774	1.517234	-2.462539	9544.954210
HLA A*6802	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.323992	1.861442	-2.462550	21085.902692
HLA B*5801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-3.999265	1.536595	-2.462670	9983.094378
HLA B*5101	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.453658	1.990887	-2.462771	28422.215355
HLA B*4403	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.227546	1.764296	-2.463249	16886.740852
HLA A*2301	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.505471	2.041338	-2.464133	32023.671236
HLA B*4403	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.300117	1.835915	-2.464202	19957.986816
HLA A*3201	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.319197	1.854767	-2.464430	20854.361574
HLA B*0702	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.375841	1.911098	-2.464743	23759.682507
HLA B*5101	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.470508	2.005692	-2.464816	29546.662554
HLA A*0211	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.282481	1.817618	-2.464863	19163.794140
HLA B*4601	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.577796	1.112802	-2.464994	3782.646537
HLA B*4002	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.506632	2.041338	-2.465294	32109.368486
HLA A*8001	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.357150	1.891829	-2.465321	22758.858718
HLA A*6801	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.551643	2.086183	-2.465461	35615.840504
HLA A*2403	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.357733	1.892220	-2.465513	22789.413690
HLA B*1801	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.466881	2.001284	-2.465597	29300.891034
HLA B*5401	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.538141	2.072193	-2.465948	34525.558090
HLA A*0211	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.794902	1.328755	-2.466147	6235.944947
HLA A*0216	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.242291	1.776041	-2.466251	17469.931678
HLA B*1509	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.213914	1.747156	-2.466758	16364.929046
HLA A*0301	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.359274	1.892220	-2.467055	22870.434432
HLA A*0250	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.175152	1.708081	-2.467072	14967.605332
HLA A*0250	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.214422	1.747156	-2.467266	16384.063233
HLA A*0101	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.359502	1.892220	-2.467282	22882.439054
HLA A*3301	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.591227	2.123741	-2.467487	39014.614595
HLA B*0803	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.458568	1.990887	-2.467681	28745.399542
HLA B*4801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.296647	1.828963	-2.467684	19799.149824
HLA B*0801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.737222	1.269415	-2.467807	5460.374321
HLA A*0301	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.303862	1.835915	-2.467947	20130.835986
HLA A*0216	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.439272	1.970233	-2.469039	27496.158912
HLA B*5301	1:365-373	9	AAELVQTRI	1.206674	0.321116	-3.997113	1.527790	-2.469323	9933.745942
HLA A*2403	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.317780	1.848352	-2.469428	20786.442087
HLA A*0203	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.298479	1.828963	-2.469516	19882.873084
HLA B*1503	1:1-9	9	VTATETVRV	1.280980	0.156043	-3.906686	1.437023	-2.469663	8066.517305
HLA B*5301	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.511072	2.041338	-2.469734	32439.361001
HLA A*3001	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.242404	1.771882	-2.470522	17474.468766
HLA A*0201	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.246579	1.776041	-2.470539	17643.267414
HLA A*6901	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.344127	1.873578	-2.470549	22086.519572
HLA A*2501	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.220187	1.749555	-2.470632	16603.026139
HLA A*0202	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-2.945996	0.475212	-2.470783	883.071257
HLA B*1503	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.025880	1.554677	-2.471203	10614.025898
HLA A*1101	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.472639	2.001284	-2.471356	29691.997486
HLA B*5301	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.560715	2.089268	-2.471446	36367.593108
HLA B*0702	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.289088	1.817618	-2.471470	19457.554197
HLA A*0202	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.163687	1.692204	-2.471483	14577.627088
HLA A*3101	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.363823	1.892220	-2.471603	23111.227744
HLA A*0212	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.609030	1.137355	-2.471675	4064.712330

HLA B*1801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.252265	1.780575	-2.471690	17875.770503
HLA A*3001	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-3.920059	1.448126	-2.471934	8318.774243
HLA A*3002	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.513365	2.041338	-2.472028	32611.095492
HLA B*1503	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.236481	1.764418	-2.472063	17237.763983
HLA B*3901	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.324784	1.852707	-2.472077	21124.380154
HLA A*0250	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.530700	2.058588	-2.472111	33939.066162
HLA B*1801	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.346033	1.873578	-2.472455	22183.635299
HLA B*5801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.219614	1.747156	-2.472458	16581.124388
HLA B*5401	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.559138	2.086649	-2.472489	36235.816771
HLA A*2603	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.410155	1.937546	-2.472609	25713.125024
HLA B*5401	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.531579	2.058588	-2.472990	34007.804541
HLA B*5801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.343394	1.870150	-2.473245	22049.271502
HLA A*3301	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.004636	1.530697	-2.473939	10107.321950
HLA B*1509	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.436610	1.962632	-2.473978	27328.139291
HLA A*2602	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.263279	1.789240	-2.474039	18334.925771
HLA B*4501	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.636824	1.162617	-2.474207	4333.354535
HLA A*3201	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.411774	1.937546	-2.474228	25809.147322
HLA B*5401	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-3.376586	0.902312	-2.474274	2380.048821
HLA A*0211	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.131381	1.657009	-2.474373	13532.605375
HLA A*0212	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.444617	1.970233	-2.474384	27836.658880
HLA B*1509	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.266977	1.792274	-2.474703	18491.717304
HLA B*1502	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.516370	2.041338	-2.475033	32837.522204
HLA B*3901	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.481706	2.006546	-2.475160	30318.385988
HLA B*4801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.251301	1.776041	-2.475261	17836.165009
HLA A*0301	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.328130	1.852707	-2.475423	21287.744108
HLA A*0250	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.267776	1.792234	-2.475542	18525.761572
HLA A*0203	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.322479	1.846931	-2.475548	21012.567891
HLA A*3301	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.564901	2.089268	-2.475633	36719.887474
HLA B*1502	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.190137	1.714405	-2.475733	15493.064840
HLA B*4002	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.484053	2.008310	-2.475743	30482.684651
HLA A*0250	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.368045	1.892220	-2.475825	23337.000837
HLA B*3501	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.251783	1.775750	-2.476033	17855.956775
HLA B*3901	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.012831	1.536595	-2.476236	10299.854821
HLA A*3002	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.477555	2.001284	-2.476271	30029.945065
HLA B*1509	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.368146	1.891829	-2.476317	23342.430244
HLA B*1502	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.548530	2.072193	-2.476338	35361.455306
HLA B*0702	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.329170	1.852707	-2.476463	21338.823092
HLA B*3501	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.331252	1.854767	-2.476485	21441.349038
HLA A*0202	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.538747	1.062125	-2.476622	3457.381633
HLA A*0203	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.294558	1.817618	-2.476940	19704.156575
HLA B*4801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.269223	1.792274	-2.476949	18587.601502
HLA B*1502	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.369173	1.892220	-2.476953	23397.679869
HLA A*2902	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.248877	1.771882	-2.476994	17736.863059
HLA B*0702	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.220779	1.743756	-2.477023	16625.676348
HLA B*4801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.266282	1.789240	-2.477042	18462.129710
HLA B*3801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.320877	1.843794	-2.477083	20935.183933
HLA B*1509	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.483734	2.006546	-2.477188	30460.265419
HLA A*6901	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.329901	1.852707	-2.477194	21374.755358
HLA A*6901	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.034475	1.556999	-2.477476	10826.162938
HLA B*5401	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.566903	2.089268	-2.477635	36889.528373
HLA B*1502	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.785424	1.307776	-2.477649	6101.329084
HLA A*2603	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.486205	2.008310	-2.477895	30634.115222
HLA A*2902	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.313911	1.835915	-2.477996	20602.055740
HLA A*6801	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.601793	2.123741	-2.478052	39975.412620
HLA A*8001	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.351798	1.873578	-2.478220	22480.105910
HLA B*5101	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.333268	1.854767	-2.478501	21541.104361
HLA A*6802	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.370378	1.891829	-2.478549	23462.705010
HLA A*3101	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.322371	1.843794	-2.478577	21007.339461
HLA B*5801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.327103	1.848352	-2.478751	21237.476736
HLA A*2301	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.537417	2.058588	-2.478829	34468.077923
HLA A*3002	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.565484	2.086649	-2.478835	36769.185866
HLA B*0802	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.325794	1.846931	-2.478863	21173.577993
HLA A*0201	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.136137	1.657009	-2.479128	13681.596411
HLA B*4001	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.340993	1.861442	-2.479551	21927.699526
HLA A*8001	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.450054	1.970233	-2.479821	28187.321940

HLA A*6801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.122364	1.642298	-2.480066	13254.522725
HLA B*0801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.328701	1.848352	-2.480349	21315.747444
HLA A*0301	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.324154	1.843794	-2.480360	21093.775157
HLA A*2402	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.309522	1.828963	-2.480559	20394.906557
HLA A*8001	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.324432	1.843794	-2.480638	21107.245024
HLA B*7301	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.606920	2.126210	-2.480710	40450.093651
HLA A*2402	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.518391	2.037348	-2.481043	32990.654878
HLA B*5801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.342532	1.861442	-2.481090	22005.537661
HLA B*4403	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.546040	2.064809	-2.481230	35159.255968
HLA B*3801	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.487817	2.006546	-2.481271	30748.015280
HLA B*5301	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.487009	2.005692	-2.481317	30690.846379
HLA B*1503	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.328360	1.846931	-2.481429	21299.033205
HLA B*3801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.317442	1.835915	-2.481527	20770.255255
HLA A*0301	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.257647	1.776041	-2.481607	18098.702466
HLA B*3501	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.231176	1.749555	-2.481620	17028.476447
HLA B*4801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.255345	1.773509	-2.481836	18003.002641
HLA A*0203	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.196255	1.714405	-2.481851	15712.865658
HLA B*0801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-3.712858	1.230828	-2.482030	5162.478502
HLA B*1517	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.352261	1.870150	-2.482112	22504.076813
HLA A*0201	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.330879	1.848352	-2.482527	21422.913712
HLA B*3901	1:233-241	9	IRIGVAERI	1.016372	0.381644	-3.881025	1.398016	-2.483009	7603.700367
HLA A*0301	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.356796	1.873578	-2.483218	22740.274751
HLA A*0203	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.335991	1.852707	-2.483284	21676.592727
HLA A*6801	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.555482	2.072193	-2.483290	35932.071590
HLA A*3001	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.196810	1.713159	-2.483651	15732.939617
HLA A*2603	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.607808	2.123741	-2.484067	40532.896223
HLA A*3301	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.556582	2.072193	-2.484389	36023.160681
HLA B*1509	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.333338	1.848352	-2.484987	21544.600695
HLA A*8001	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.249396	1.764296	-2.485100	17758.081677
HLA A*8001	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.385744	1.900474	-2.485270	24307.691300
HLA A*3002	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.522878	2.037348	-2.485530	33333.310893
HLA B*4402	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.423251	1.937546	-2.485705	26500.306128
HLA A*2301	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.329513	1.843794	-2.485720	21355.684087
HLA A*6802	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.333080	1.846931	-2.486149	21531.783579
HLA B*5401	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-2.851645	0.365377	-2.486268	710.632606
HLA A*0206	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.755830	1.269415	-2.486415	5699.415732
HLA B*1501	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.277167	1.790732	-2.486435	18930.712586
HLA A*0212	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.335126	1.848352	-2.486775	21633.481045
HLA A*1101	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.477745	1.990887	-2.486858	30043.107101
HLA B*4601	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.330855	1.843794	-2.487061	21421.754788
HLA B*5801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.330980	1.843794	-2.487186	21427.897802
HLA B*3901	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.398372	1.911098	-2.487274	25024.890981
HLA A*0202	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.279512	1.792234	-2.487278	19033.197228
HLA B*4601	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.279585	1.792274	-2.487310	19036.389488
HLA B*3501	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.231246	1.743756	-2.487490	17031.240336
HLA A*2902	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.334802	1.846931	-2.487871	21617.336279
HLA A*0203	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.252702	1.764802	-2.487900	17893.766860
HLA B*1502	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.089716	1.601532	-2.488184	12294.635296
HLA B*1503	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.097690	1.609455	-2.488235	12522.464310
HLA A*3001	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.268892	1.780575	-2.488317	18573.428391
HLA B*5101	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.389111	1.900474	-2.488637	24496.865873
HLA A*2902	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.458965	1.970233	-2.488733	28771.692652
HLA A*0202	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.279587	1.790732	-2.488855	19036.492473
HLA A*0211	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.495540	2.006546	-2.488994	31299.676250
HLA B*0803	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.381226	1.892220	-2.489006	24056.123940
HLA A*0101	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.380930	1.891829	-2.489100	24039.731766
HLA A*0212	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.381867	1.892220	-2.489647	24091.678672
HLA A*0202	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.459959	1.970233	-2.489727	28837.608700
HLA A*6802	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-3.185817	0.695627	-2.490190	1533.970761
HLA B*1501	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-3.442898	0.952354	-2.490544	2772.667108
HLA A*0211	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.481650	1.990887	-2.490763	30314.449785
HLA A*3001	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.653261	1.162401	-2.490861	4500.504700
HLA B*5301	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.577586	2.086649	-2.490937	37808.218241
HLA A*0250	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.497812	2.006546	-2.491266	31463.845252
HLA A*0203	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.361448	1.870150	-2.491298	22985.168292

HLA A*0202	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.309308	1.817618	-2.491690	20384.868618
HLA A*0206	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.280961	1.789240	-2.491722	19096.834316
HLA A*0202	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-3.814676	1.322784	-2.491892	6526.427804
HLA B*0702	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.335913	1.843794	-2.492120	21672.723230
HLA A*0216	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.345114	1.852707	-2.492407	22136.760589
HLA A*3301	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.546998	2.054462	-2.492536	35236.946409
HLA B*4002	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.328515	1.835915	-2.492600	21306.639440
HLA A*0203	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.655080	1.162401	-2.492679	4519.388966
HLA B*7301	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.616451	2.123741	-2.492711	41347.703382
HLA A*6901	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.384562	1.891829	-2.492732	24241.635751
HLA A*1101	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.463091	1.970233	-2.492858	29046.319360
HLA A*2403	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.049878	1.556999	-2.492879	11217.027453
HLA A*6801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-3.793944	1.300814	-2.493129	6222.195931
HLA B*4002	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.285449	1.792274	-2.493175	19295.182762
HLA B*5701	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.385401	1.892220	-2.493181	24288.499600
HLA A*0211	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.093071	1.599646	-2.493425	12389.983131
HLA A*6901	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.144280	1.650564	-2.493716	13940.555834
HLA B*1509	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.340927	1.846931	-2.493996	21924.378238
HLA B*4601	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.284854	1.790732	-2.494123	19268.791473
HLA B*5401	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.549228	2.055046	-2.494182	35418.317536
HLA B*4601	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.386054	1.891829	-2.494224	24325.055752
HLA A*6802	1:463-471	9	PLFESLELL	1.291656	0.202256	-3.988162	1.493912	-2.494250	9731.090482
HLA A*0101	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.364544	1.870150	-2.494395	23149.643594
HLA A*0301	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.355973	1.861442	-2.494531	22697.257662
HLA B*3801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.341578	1.846931	-2.494647	21957.257409
HLA B*5301	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.549775	2.055046	-2.494730	35462.990623
HLA A*1101	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.012258	1.517234	-2.495023	10286.267849
HLA B*3501	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.432804	1.937546	-2.495258	27089.681371
HLA A*2601	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.331193	1.835915	-2.495278	21438.449351
HLA B*4601	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.365571	1.870150	-2.495421	23204.436909
HLA B*1509	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.032116	1.536595	-2.495520	10767.519729
HLA A*0202	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.269806	0.774156	-2.495651	1861.257545
HLA B*4801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.210108	1.714405	-2.495703	16222.133121
HLA A*3201	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.286558	1.790732	-2.495826	19344.515346
HLA B*5101	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.407000	1.911098	-2.495902	25526.983821
HLA A*6802	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.052956	1.556999	-2.495957	11296.804373
HLA B*1503	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.138261	1.642298	-2.495963	13748.670683
HLA B*4002	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.585281	2.089268	-2.496012	38484.050384
HLA A*2501	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.348674	1.852642	-2.496031	22318.938626
HLA A*2501	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.407148	1.911098	-2.496050	25535.685487
HLA B*5401	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.560870	2.064809	-2.496060	36380.580573
HLA B*1502	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.344588	1.848352	-2.496236	22109.951174
HLA B*1501	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.314146	1.817618	-2.496527	20613.204239
HLA B*0803	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.260953	1.764296	-2.496657	18236.990249
HLA A*3201	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.538211	2.041338	-2.496873	34531.161928
HLA B*1502	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.397484	1.900474	-2.497010	24973.768917
HLA B*1502	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.534438	2.037348	-2.497090	34232.445004
HLA B*3501	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.340906	1.843794	-2.497112	21923.310788
HLA B*4001	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.349794	1.852642	-2.497152	22376.607405
HLA B*1502	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.917132	1.419915	-2.497217	8262.888267
HLA A*3201	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.147804	1.650564	-2.497240	14054.141367
HLA A*0219	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.389536	1.892220	-2.497316	24520.864705
HLA B*1509	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.286896	1.789240	-2.497656	19359.591060
HLA A*2902	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.341529	1.843794	-2.497735	21954.763038
HLA B*4002	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.510313	2.012396	-2.497918	32382.726146
HLA B*4801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.143509	1.645215	-2.498294	13915.841037
HLA B*3801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.399204	1.900474	-2.498730	25072.862089
HLA A*2301	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.327874	1.828963	-2.498911	21275.194896
HLA A*3201	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.806899	1.307776	-2.499123	6410.600939
HLA B*4403	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.500645	2.001284	-2.499362	31669.796762
HLA A*2402	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.355393	1.854767	-2.500626	22666.948873
HLA A*6901	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.370933	1.870150	-2.500783	23492.679771
HLA B*3801	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.463617	1.962632	-2.500985	29081.539466
HLA A*2902	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.393248	1.892220	-2.501028	24731.358185
HLA A*0206	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.471453	1.970233	-2.501220	29610.989833

HLA B*5801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.348204	1.846931	-2.501273	22294.803088
HLA A*0301	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.353927	1.852642	-2.501285	22590.559458
HLA A*0250	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.587661	2.086183	-2.501478	38695.530307
HLA B*0801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-3.345098	0.843615	-2.501483	2213.594503
HLA A*0101	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.375086	1.873578	-2.501508	23718.457856
HLA B*1801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.401990	1.900474	-2.501517	25234.249984
HLA B*4403	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.313617	1.811844	-2.501773	20588.128595
HLA A*3101	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.294269	1.792234	-2.502035	19691.049468
HLA B*4402	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.277975	1.775750	-2.502225	18965.975479
HLA B*5401	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.556695	2.054462	-2.502232	36032.516199
HLA B*1801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.413407	1.911098	-2.502309	25906.369093
HLA A*2403	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.363774	1.861442	-2.502331	23108.602280
HLA A*3101	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.266956	1.764418	-2.502538	18490.816982
HLA A*0211	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.349498	1.846931	-2.502567	22361.359676
HLA B*1801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.539959	2.037348	-2.502611	34670.428471
HLA A*3002	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.357672	1.854767	-2.502905	22786.208422
HLA B*1517	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.279084	1.776041	-2.503044	19014.466368
HLA B*1501	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.276554	1.773509	-2.503045	18904.001640
HLA A*2402	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.395414	1.892220	-2.503194	24855.024329
HLA A*2601	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.320818	1.817618	-2.503200	20932.352699
HLA A*0206	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.160473	1.657009	-2.503464	14470.140261
HLA B*4402	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.414605	1.911098	-2.503507	25977.944586
HLA B*3501	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.641194	1.137355	-2.503839	4377.178573
HLA A*3101	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.275802	1.771882	-2.503920	18871.304014
HLA A*2601	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.296212	1.792274	-2.503938	19779.344164
HLA B*1801	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.339884	1.835915	-2.503969	21871.779280
HLA A*3301	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.568952	2.064809	-2.504143	37063.963013
HLA A*3001	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.254123	1.749555	-2.504568	17952.428801
HLA B*2705	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.366088	1.861442	-2.504646	23232.070706
HLA B*5301	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.296959	1.792274	-2.504685	19813.400741
HLA B*1501	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.152945	1.648036	-2.504909	14221.486418
HLA A*2601	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.378864	1.873578	-2.505286	23925.687182
HLA B*5301	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.506618	2.001284	-2.505334	32108.326254
HLA B*5701	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.366823	1.861442	-2.505381	23271.442787
HLA B*5101	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.358196	1.852642	-2.505554	22813.714413
HLA B*3801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.397632	1.891829	-2.505803	24982.282003
HLA B*5401	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.508810	2.003005	-2.505805	32270.800366
HLA B*5401	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.547160	2.041338	-2.505823	35250.102195
HLA A*0301	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.154627	1.648791	-2.505837	14276.679896
HLA B*3901	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.813872	1.307776	-2.506096	6514.363888
HLA B*0803	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.417354	1.911098	-2.506256	26142.895296
HLA A*8001	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.278205	1.771882	-2.506323	18976.033320
HLA A*3001	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.643680	1.137355	-2.506325	4402.303903
HLA A*2301	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.515008	2.008310	-2.506697	32734.648218
HLA B*1502	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.024198	1.517234	-2.506963	10572.992198
HLA B*4601	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.324812	1.817618	-2.507194	21125.751565
HLA A*3201	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.515764	2.008310	-2.507454	32791.721157
HLA A*2403	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.354660	1.846931	-2.507729	22628.721931
HLA B*1517	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.336694	1.828963	-2.507731	21711.684222
HLA B*5801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.283891	1.776041	-2.507851	19226.099607
HLA A*0101	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.475476	0.967578	-2.507897	2988.654346
HLA B*0802	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.400470	1.892220	-2.508250	25146.079502
HLA B*4801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.369741	1.861442	-2.508299	23428.332012
HLA A*2301	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.514406	2.005692	-2.508714	32689.344347
HLA A*0301	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.363600	1.854767	-2.508833	23099.353023
HLA A*3002	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.809967	1.300706	-2.509261	6456.054237
HLA B*1503	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.235908	1.726550	-2.509357	17215.024922
HLA A*2301	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.521795	2.012396	-2.509400	33250.282563
HLA B*4801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.379576	1.870150	-2.509427	23964.938243
HLA A*0201	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.362181	1.852707	-2.509474	23023.997382
HLA A*0301	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.321429	1.811844	-2.509585	20961.816259
HLA A*2601	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.357973	1.848352	-2.509621	22801.992557
HLA A*3001	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.274857	1.764802	-2.510056	18830.307761
HLA A*2602	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.286165	1.776041	-2.510125	19327.046407
HLA B*5401	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.501141	1.990887	-2.510254	31705.968051

HLA A*1101	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.421508	1.911098	-2.510410	26394.143467
HLA A*0301	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.284604	0.774156	-2.510448	1925.766058
HLA A*0216	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.425060	0.914377	-2.510684	2661.095376
HLA A*8001	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.363442	1.852707	-2.510735	23090.981890
HLA A*0203	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.301759	1.790732	-2.511027	20033.601071
HLA A*0219	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.365839	1.854767	-2.511072	23218.752134
HLA B*0802	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.340190	1.828963	-2.511227	21887.166797
HLA A*2501	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.411830	1.900474	-2.511356	25812.498531
HLA A*6801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.028892	1.517234	-2.511658	10687.895103
HLA B*5101	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.329321	1.817618	-2.511703	21346.212573
HLA A*3101	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.695538	1.183813	-2.511725	4960.641620
HLA A*2402	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.839355	1.327486	-2.511868	6908.034990
HLA B*4403	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.601206	2.089268	-2.511937	39921.383527
HLA B*4001	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.283891	1.771882	-2.512009	19226.099607
HLA A*0203	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.301252	1.789240	-2.512012	20010.204758
HLA B*0802	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.255827	1.743756	-2.512071	18022.979537
HLA A*3201	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.385833	1.873578	-2.512255	24312.688886
HLA B*0802	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.423385	1.911098	-2.512287	26508.479120
HLA B*4002	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.566816	2.054462	-2.512354	36882.145087
HLA B*1801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.365324	1.852642	-2.512682	23191.259642
HLA B*5801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.284577	1.771882	-2.512695	19256.494839
HLA A*2601	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.404547	1.891829	-2.512717	25383.215727
HLA B*1502	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.365392	1.852642	-2.512750	23194.898330
HLA B*7301	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.475722	1.962632	-2.513090	29903.494280
HLA A*6802	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.192952	1.679828	-2.513124	15593.802214
HLA A*6901	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.303874	1.790732	-2.513142	20131.380522
HLA A*3001	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.289011	1.775750	-2.513261	19454.080821
HLA A*2501	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.360247	1.846931	-2.513316	22921.714614
HLA B*0801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.366126	1.852707	-2.513418	23234.081719
HLA A*3001	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.278043	1.764418	-2.513625	18968.951224
HLA A*3101	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.360621	1.846931	-2.513690	22941.439722
HLA A*0216	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.676108	1.162401	-2.513707	4743.595100
HLA B*2705	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.304670	1.790732	-2.513938	20168.334391
HLA B*4001	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.331694	1.817618	-2.514076	21463.167252
HLA A*0201	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.361161	1.846931	-2.514230	22970.002937
HLA B*1502	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.367493	1.852707	-2.514786	23307.350800
HLA A*6801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.290923	1.776041	-2.514883	19539.938684
HLA B*1501	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.290639	1.775750	-2.514889	19527.152093
HLA A*0202	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.573496	2.058588	-2.514907	37453.788852
HLA A*2602	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.604415	2.089268	-2.515147	40217.491660
HLA B*4402	1:465-473	9	FESLELLGR	0.858673	0.563144	-3.936990	1.421817	-2.515173	8649.474595
HLA A*0219	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.815968	1.300706	-2.515262	6545.875711
HLA A*0201	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.388913	1.873578	-2.515335	24485.736274
HLA A*0212	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.307809	1.792234	-2.515575	20314.631336
HLA B*4001	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.262734	1.747156	-2.515578	18311.928145
HLA A*2603	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.519042	2.003005	-2.516037	33040.129731
HLA A*2602	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.553605	2.037348	-2.516257	35777.090354
HLA B*5301	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.408529	1.892220	-2.516309	25617.044214
HLA A*2501	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.360177	1.843794	-2.516383	22917.994798
HLA B*1503	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.297112	1.780575	-2.516537	19820.369206
HLA B*1509	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.427647	1.911098	-2.516549	26769.901754
HLA B*1502	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.549721	2.032901	-2.516820	35458.578328
HLA A*2902	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.817528	1.300706	-2.516822	6569.431869
HLA A*0101	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.365221	1.848352	-2.516869	23185.739965
HLA A*0206	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.260960	1.743756	-2.517204	18237.286232
HLA B*3501	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.165247	1.648036	-2.517210	14630.086515
HLA B*4402	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.378709	1.861442	-2.517267	23917.145976
HLA B*1801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.523186	2.005692	-2.517494	33356.942432
HLA A*0206	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.391218	1.873578	-2.517640	24616.029991
HLA B*1501	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.306937	1.789240	-2.517697	20273.899362
HLA A*3101	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.391338	1.873578	-2.517760	24622.822597
HLA B*1503	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.718582	1.200757	-2.517824	5230.962439
HLA B*4403	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.644262	2.126210	-2.518052	44082.097020
HLA B*0702	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.391726	1.873578	-2.518147	24644.811522
HLA B*5701	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.347233	1.828963	-2.518271	22245.045768

HLA A*0203	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.294093	1.775750	-2.518343	19683.061609
HLA A*0211	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.347431	1.828963	-2.518468	22255.156897
HLA B*4002	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.644699	2.126210	-2.518489	44126.476486
HLA A*2403	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.845985	1.327486	-2.518498	7014.307086
HLA B*5301	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.572979	2.054462	-2.518517	37409.238782
HLA B*5801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.336139	1.817618	-2.518521	21683.981868
HLA A*0250	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.292700	0.774156	-2.518544	1962.003841
HLA A*0216	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.486297	0.967578	-2.518719	3064.061073
HLA A*0301	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.367084	1.848352	-2.518732	23285.421431
HLA A*3002	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.232003	1.713159	-2.518844	17060.934345
HLA A*0211	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.539433	1.020365	-2.519068	3462.847532
HLA A*0301	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.366227	1.846931	-2.519295	23239.487182
HLA B*4403	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.120865	1.601532	-2.519333	13208.853476
HLA B*4001	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.292854	1.773509	-2.519346	19627.024891
HLA A*0211	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.391035	0.871584	-2.519451	2460.567019
HLA B*4001	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.367848	1.848352	-2.519496	23326.398197
HLA A*0219	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.586724	1.067176	-2.519547	3861.213397
HLA A*0212	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.295568	1.775750	-2.519818	19750.046771
HLA A*3301	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.606128	2.086183	-2.519945	40376.414948
HLA B*0803	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.267114	1.747156	-2.519958	18497.520426
HLA B*0801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.293630	1.773509	-2.520121	19662.095597
HLA A*0219	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.367223	1.846931	-2.520292	23292.854939
HLA B*1501	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.332183	1.811844	-2.520338	21487.332423
HLA B*4001	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.394434	1.873578	-2.520856	24799.016487
HLA B*4001	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.364791	1.843794	-2.520997	23162.797216
HLA A*2902	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.338935	1.817618	-2.521317	21824.028625
HLA A*6901	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.301926	1.780575	-2.521351	20041.297498
HLA A*3101	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.369779	1.848352	-2.521427	23430.360014
HLA A*2601	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.374147	1.852642	-2.521504	23667.187658
HLA A*2902	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.374219	1.852707	-2.521512	23671.157134
HLA A*6802	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.339290	1.817618	-2.521672	21841.863810
HLA B*4403	1:90-98	9	RAEIYRDVL	1.662274	0.461467	-4.645498	2.123741	-2.521757	44207.715755
HLA B*2705	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.395449	1.873578	-2.521871	24857.041354
HLA B*1517	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.763734	1.241782	-2.521952	5804.088213
HLA A*2902	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.413804	1.891829	-2.521974	25930.065373
HLA A*2402	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.527862	2.005692	-2.522170	33717.992568
HLA B*5801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.313373	1.790732	-2.522641	20576.548386
HLA A*0201	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.392926	1.870150	-2.522777	24713.035211
HLA A*6801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-3.678133	1.155314	-2.522819	4765.767681
HLA A*0211	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.313800	1.790732	-2.523068	20596.818029
HLA B*0702	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.211635	1.688566	-2.523069	16279.277497
HLA A*3001	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-3.780632	1.257536	-2.523095	6034.363954
HLA A*0202	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.491067	0.967578	-2.523489	3097.896271
HLA A*2402	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.486243	1.962632	-2.523611	30636.766972
HLA B*3901	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-3.953441	1.429823	-2.523618	8983.401730
HLA B*4402	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.215855	1.692204	-2.523651	16438.220483
HLA A*0216	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.397444	1.873578	-2.523866	24971.472232
HLA B*4801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.299644	1.775750	-2.523894	19936.296541
HLA B*5101	1:462-470	9	PPLFESLEL	1.313352	0.107023	-3.944287	1.420375	-2.523912	8796.040652
HLA A*2902	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.174537	1.650564	-2.523972	14946.405411
HLA B*4501	1:181-189	9	SVPDFALTR	1.418756	0.707454	-4.650401	2.126210	-2.524191	44709.668559
HLA B*0803	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.379019	1.854767	-2.524253	23934.231438
HLA B*4001	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.237456	1.713159	-2.524297	17276.508032
HLA A*1101	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.377053	1.852707	-2.524346	23826.100387
HLA A*0219	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.342064	1.817618	-2.524446	21981.859952
HLA A*2301	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.377180	1.852642	-2.524537	23833.061818
HLA B*3901	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.242153	1.717294	-2.524858	17464.356454
HLA B*4601	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.377636	1.852707	-2.524929	23858.088188
HLA B*4601	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.371969	1.846931	-2.525038	23548.794604
HLA B*1509	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.342971	1.817618	-2.525353	22027.810812
HLA A*3002	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.098912	1.573351	-2.525560	12557.741381
HLA B*7301	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.597754	2.072193	-2.525562	39605.380537
HLA B*0803	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.426051	1.900474	-2.525578	26671.747865
HLA A*0301	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.297511	1.771882	-2.525629	19838.606010
HLA B*5801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.239223	1.713159	-2.526064	17346.936116

HLA A*2403	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.318365	1.792234	-2.526131	20814.461589
HLA A*3002	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.374638	1.848352	-2.526286	23693.962496
HLA B*4403	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.584935	2.058588	-2.526347	38453.457967
HLA A*2602	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.176938	1.650564	-2.526374	15029.271561
HLA A*0301	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.188154	1.661630	-2.526524	15422.485589
HLA B*4402	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.418427	1.891829	-2.526598	26207.608844
HLA A*0212	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.865175	1.338560	-2.526616	7331.205086
HLA A*0101	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.370493	1.843794	-2.526699	23468.925436
HLA B*4402	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.381592	1.854767	-2.526826	24076.434500
HLA A*0212	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.768762	1.241782	-2.526980	5871.673555
HLA B*4601	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.300535	1.773509	-2.527026	19977.214821
HLA A*3001	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-3.002336	0.475212	-2.527124	1005.394256
HLA B*0702	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.388699	1.861442	-2.527257	24473.684915
HLA A*0219	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.401192	1.873578	-2.527613	25187.877716
HLA A*0216	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.320104	1.792234	-2.527870	20897.955512
HLA A*8001	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.420147	1.892220	-2.527927	26311.597758
HLA B*5401	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.565733	2.037348	-2.528385	36790.277138
HLA B*4601	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.304224	1.775750	-2.528474	20147.614436
HLA A*2602	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.534358	2.005692	-2.528666	34226.148996
HLA A*3002	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.537283	2.008310	-2.528973	34457.450859
HLA A*2603	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.618307	2.089268	-2.529039	41524.793866
HLA A*2402	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.537607	2.008310	-2.529297	34483.185180
HLA A*3101	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.321657	1.792274	-2.529383	20972.819053
HLA B*4801	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.403069	1.873578	-2.529491	25296.987998
HLA A*0101	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.376501	1.846931	-2.529570	23795.828942
HLA B*1517	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.138919	1.609246	-2.529672	13769.512524
HLA B*5101	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.247002	1.717294	-2.529707	17660.456444
HLA A*0212	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.347363	1.817618	-2.529744	22251.665631
HLA B*1503	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.235590	1.705831	-2.529759	17202.456777
HLA A*2601	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.376935	1.846931	-2.530004	23819.656431
HLA A*0216	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.277397	1.747156	-2.530241	18940.751727
HLA B*7301	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-3.398319	0.867880	-2.530438	2502.180308
HLA B*5701	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.323001	1.792274	-2.530727	21037.819049
HLA A*2902	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.274573	1.743756	-2.530817	18817.985539
HLA B*4402	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.321570	1.790732	-2.530838	20968.621430
HLA A*0212	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.377920	1.846931	-2.530989	23873.710724
HLA A*0216	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.245780	1.714405	-2.531376	17610.844881
HLA A*6802	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.375340	1.843794	-2.531546	23732.319842
HLA B*1501	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.296574	1.764802	-2.531772	19795.829655
HLA B*3901	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.117209	1.585411	-2.531798	13098.130828
HLA B*7301	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.586279	2.054462	-2.531817	38572.634822
HLA A*2403	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.360968	1.828963	-2.532006	22959.815453
HLA A*2301	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.502269	1.970233	-2.532036	31788.407413
HLA A*3101	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.393840	1.861442	-2.532398	24765.097242
HLA B*0803	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.379790	1.846931	-2.532859	23976.739085
HLA B*1502	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.538681	2.005692	-2.532989	34568.544099
HLA B*4001	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.403189	1.870150	-2.533039	25303.968510
HLA A*0201	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.645851	1.112802	-2.533049	4424.364957
HLA A*3201	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.403278	1.870150	-2.533128	25309.170928
HLA A*0201	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.280560	1.747156	-2.533404	19079.176174
HLA A*6801	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.598431	2.064809	-2.533622	39667.135720
HLA B*5701	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.403783	1.870150	-2.533634	25338.625814
HLA A*0250	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-2.914367	0.380458	-2.533909	821.045041
HLA B*5101	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.244507	1.710232	-2.534275	17559.282698
HLA B*1517	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.299142	1.764802	-2.534340	19913.229321
HLA B*0803	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.310330	1.775750	-2.534580	20432.896855
HLA A*0201	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.396159	1.861442	-2.534717	24897.685646
HLA B*4001	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.327018	1.792274	-2.534744	21233.341012
HLA A*2301	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.028676	1.493912	-2.534764	10682.576957
HLA B*1502	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.248017	1.713159	-2.534858	17701.778471
HLA B*1517	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.381804	1.846931	-2.534873	24088.159930
HLA B*5801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.245155	1.710050	-2.535105	17585.520563
HLA A*8001	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.387781	1.852642	-2.535138	24421.971259
HLA B*7301	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.624449	2.089268	-2.535181	42116.186390
HLA B*5401	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.523287	1.987904	-2.535383	33364.703002

HLA A*2603	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.300206	1.764802	-2.535404	19962.090116
HLA A*0202	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.652820	1.117129	-2.535691	4495.929747
HLA A*2403	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.353542	1.817618	-2.535923	22570.525509
HLA A*2603	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.541773	2.005692	-2.536081	34815.530034
HLA B*5701	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.383037	1.846931	-2.536106	24156.672172
HLA A*2501	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.526793	0.990658	-2.536135	3363.513235
HLA A*3201	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-3.922977	1.386690	-2.536287	8374.856973
HLA A*1101	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.474164	1.937546	-2.536618	29796.429850
HLA A*0219	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.329084	1.792234	-2.536850	21334.552214
HLA B*0803	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.372970	1.835915	-2.537055	23603.128042
HLA A*0203	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.182332	1.645215	-2.537117	15217.115930
HLA B*5801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.366081	1.828963	-2.537118	23231.693660
HLA A*0101	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.389881	1.852707	-2.537174	24540.372769
HLA A*3201	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.284439	1.747156	-2.537283	19250.349466
HLA B*0802	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.354991	1.817618	-2.537373	22645.989578
HLA B*0801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.407535	1.870150	-2.537386	25558.489626
HLA B*0802	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.390229	1.852642	-2.537586	24560.029220
HLA B*5101	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.500222	1.962632	-2.537590	31638.972356
HLA A*3301	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.055014	1.517234	-2.537779	11350.467696
HLA A*0101	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.330094	1.792234	-2.537860	21384.239536
HLA B*1502	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.311469	1.773509	-2.537960	20486.579008
HLA B*1503	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.131687	1.593495	-2.538192	13542.126009
HLA A*6802	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-2.933102	0.394899	-2.538203	857.238713
HLA B*1501	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.843292	1.305053	-2.538239	6970.954780
HLA A*6901	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.806589	1.268289	-2.538300	6406.024729
HLA A*2402	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.382191	1.843794	-2.538397	24109.671385
HLA B*4402	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.391051	1.852642	-2.538409	24606.576737
HLA B*0802	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.327737	1.789240	-2.538497	21268.520349
HLA B*5401	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.546862	2.008310	-2.538552	35225.891721
HLA B*4801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.382563	1.843794	-2.538769	24130.288237
HLA B*4001	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.230997	1.692204	-2.538793	17021.476601
HLA A*2601	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.367958	1.828963	-2.538995	23332.330033
HLA B*3901	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.286344	1.747156	-2.539188	19334.994386
HLA A*2403	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.311169	1.771882	-2.539286	20472.397663
HLA B*1503	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.231528	1.692204	-2.539324	17042.300380
HLA A*0101	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.368315	1.828963	-2.539353	23351.524172
HLA B*2705	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.315555	1.776041	-2.539515	20680.222038
HLA B*4403	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.580969	2.041338	-2.539632	38103.903584
HLA A*0216	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.409831	1.870150	-2.539681	25693.935676
HLA B*0801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.096849	1.556999	-2.539850	12498.235019
HLA B*4001	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.304731	1.764802	-2.539930	20171.171410
HLA B*5101	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-3.924758	1.384650	-2.540108	8409.270227
HLA A*1101	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.440703	1.900474	-2.540229	27586.897768
HLA A*3201	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.577643	2.037348	-2.540295	37813.127478
HLA B*4001	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-3.386924	0.846543	-2.540381	2437.382001
HLA A*2601	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.393093	1.852707	-2.540386	24722.529364
HLA A*2402	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.552999	2.012396	-2.540603	35727.189263
HLA A*2403	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.287951	1.747156	-2.540795	19406.673444
HLA A*3201	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.452399	1.911098	-2.541301	28339.918816
HLA B*3901	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.433325	1.891829	-2.541496	27122.235499
HLA B*0702	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.330914	1.789240	-2.541674	21424.652216
HLA B*5801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.353676	1.811844	-2.541831	22577.486512
HLA B*5301	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.512200	1.970233	-2.541967	32523.707273
HLA A*2902	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.252622	1.710232	-2.542390	17890.475851
HLA B*4801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.389341	1.846931	-2.542410	24509.856798
HLA B*5801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.331720	1.789240	-2.542480	21464.444537
HLA B*4002	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.198304	1.655822	-2.542482	15787.165010
HLA B*2705	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.386686	1.843794	-2.542892	24360.480807
HLA B*5701	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.307283	1.764296	-2.542986	20290.028668
HLA B*0802	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.386855	1.843794	-2.543061	24369.971355
HLA B*1509	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.316706	1.773509	-2.543197	20735.114839
HLA B*3801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.307494	1.764296	-2.543198	20299.910086
HLA B*3901	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.387029	1.843794	-2.543235	24379.729383
HLA A*3301	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.546291	2.003005	-2.543286	35179.614081
HLA B*4403	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.551855	2.008310	-2.543544	35633.185724

HLA B*4501	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.630222	2.086649	-2.543573	42679.735931
HLA B*5301	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.580969	2.037348	-2.543621	38103.903584
HLA B*2705	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.317146	1.773509	-2.543637	20756.102117
HLA B*4403	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.616099	2.072193	-2.543906	41314.164018
HLA B*0801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.405416	1.861442	-2.543974	25434.075154
HLA B*1502	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.552285	2.008310	-2.543974	35668.480392
HLA B*4501	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.545560	2.001284	-2.544277	35120.475005
HLA A*0101	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.362505	1.817618	-2.544887	23041.192704
HLA A*0301	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.362517	1.817618	-2.544899	23041.815964
HLA B*4501	1:281-289	9	LNYLALLGW	1.664731	0.421452	-4.631166	2.086183	-2.544984	42772.655776
HLA A*3201	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.557468	2.012396	-2.545072	36096.705907
HLA A*6901	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.357153	1.811844	-2.545309	22758.981841
HLA A*3301	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.632075	2.086649	-2.545426	42862.299575
HLA A*6901	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.374499	1.828963	-2.545536	23686.400982
HLA A*2603	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.582952	2.037348	-2.545604	38278.281764
HLA A*2301	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.419205	1.873578	-2.545627	26254.580153
HLA B*1502	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.483214	1.937546	-2.545668	30423.869329
HLA B*5401	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.546975	2.001284	-2.545691	35235.040181
HLA A*3301	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.601177	2.055046	-2.546132	39918.791968
HLA B*7301	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.604838	2.058588	-2.546249	40256.673725
HLA A*1101	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.438581	1.892220	-2.546361	27452.460828
HLA B*3801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.318252	1.771882	-2.546370	20809.057302
HLA B*1502	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.338615	1.792234	-2.546382	21807.977612
HLA A*3201	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.290162	1.743756	-2.546406	19505.718999
HLA B*0702	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.663538	1.117129	-2.546409	4608.269473
HLA A*0101	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.382433	1.835915	-2.546518	24123.109485
HLA B*0702	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.259696	1.713159	-2.546537	18184.283409
HLA B*4001	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.322639	1.776041	-2.546598	21020.299258
HLA B*3801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.395005	1.848352	-2.546654	24831.638788
HLA B*7301	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.549728	2.003005	-2.546723	35459.153813
HLA A*0201	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.364584	1.817618	-2.546966	23151.772721
HLA B*1801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.318849	1.771882	-2.546967	20837.670929
HLA B*1501	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.393948	1.846931	-2.547017	24771.260925
HLA B*5401	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.559422	2.012396	-2.547027	36259.544378
HLA B*0802	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.339668	1.792274	-2.547394	21860.896190
HLA B*1503	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.312278	1.764802	-2.547476	20524.740068
HLA A*8001	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.383758	1.835915	-2.547843	24196.825777
HLA B*4501	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.510513	1.962632	-2.547881	32397.620461
HLA B*0802	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.256066	1.708081	-2.547986	18032.927519
HLA B*4501	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.602519	2.054462	-2.548057	40042.293634
HLA B*5701	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.339085	1.790732	-2.548353	21831.586130
HLA B*1517	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.816715	1.268289	-2.548426	6557.146566
HLA A*0301	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.275027	1.726550	-2.548476	18837.643820
HLA B*5301	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.561478	2.012396	-2.549083	36431.591363
HLA B*4402	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.366720	1.817618	-2.549102	23265.904025
HLA A*0301	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.341378	1.792234	-2.549145	21947.162893
HLA B*5701	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.393130	1.843794	-2.549337	24724.669395
HLA B*5401	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.512029	1.962632	-2.549397	32510.865484
HLA B*0802	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.266813	1.717294	-2.549518	18484.715960
HLA A*0250	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.264045	1.714405	-2.549641	18367.290214
HLA A*2601	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.393725	1.843794	-2.549931	24758.533267
HLA A*1101	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.361842	1.811844	-2.549998	23006.068119
HLA B*0702	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-3.539029	0.989026	-2.550003	3459.626848
HLA A*0301	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.342372	1.792274	-2.550098	21997.443919
HLA A*0101	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.264588	1.714405	-2.550183	18390.257878
HLA B*1509	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.263361	1.713159	-2.550202	18338.397746
HLA B*1503	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.600501	1.050133	-2.550368	3985.668592
HLA B*4002	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.583284	2.032901	-2.550383	38307.491361
HLA A*0201	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.342920	1.792234	-2.550686	22025.189271
HLA A*2601	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.315600	1.764802	-2.550798	20682.347824
HLA A*0203	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.412258	1.861442	-2.550815	25837.926028
HLA B*5301	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.538965	1.987904	-2.551061	34591.179958
HLA A*1101	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.331652	1.780575	-2.551077	21461.077313
HLA A*2902	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.878793	1.327486	-2.551307	7564.722198
HLA B*3901	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.000092	1.448126	-2.551966	10002.123107

HLA A*0202	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.207871	1.655822	-2.552049	16138.800431
HLA A*0250	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.399049	1.846931	-2.552118	25063.911354
HLA A*3002	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.422422	1.870150	-2.552272	26449.747027
HLA A*2601	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.364380	1.811844	-2.552536	23140.878664
HLA A*0301	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.019475	1.466619	-2.552857	10458.645601
HLA A*3001	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.245200	1.692204	-2.552996	17587.328235
HLA A*2601	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.343904	1.790732	-2.553172	22075.171354
HLA A*2501	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.445141	1.891829	-2.553312	27870.261438
HLA B*0801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-2.249900	-0.303590	-2.553489	177.786889
HLA A*8001	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.401112	1.846931	-2.554181	25183.245179
HLA A*3001	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-3.941078	1.386690	-2.554388	8731.278304
HLA B*5701	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.402951	1.848352	-2.554599	25290.146229
HLA A*3001	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.271911	1.717294	-2.554617	18702.995267
HLA A*3002	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.091233	1.536595	-2.554638	12337.677612
HLA A*6802	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.424804	1.870150	-2.554654	26595.239182
HLA B*1801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.403083	1.848352	-2.554731	25297.809135
HLA A*2403	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.330911	1.775750	-2.555161	21424.536312
HLA B*4801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.367007	1.811844	-2.555162	23281.264741
HLA B*5801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.347499	1.792234	-2.555265	22258.648711
HLA B*0802	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.416736	1.861442	-2.555294	26105.725611
HLA A*8001	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.344600	1.789240	-2.555360	22110.549244
HLA B*1503	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-3.618216	1.062587	-2.555630	4151.607628
HLA B*0702	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.425833	1.870150	-2.555683	26658.332158
HLA B*1501	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.305368	1.749555	-2.555812	20200.765649
HLA A*1101	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.408637	1.852642	-2.555995	25623.419934
HLA A*6901	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.331894	1.775750	-2.556143	21473.039157
HLA A*3001	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.623432	1.067176	-2.556256	4201.768859
HLA B*7301	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.611456	2.055046	-2.556411	40874.870240
HLA A*6901	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.669487	1.112802	-2.556685	4671.827115
HLA A*8001	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.427355	1.870150	-2.557206	26751.949823
HLA A*2602	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.598685	2.041338	-2.557347	39690.318731
HLA B*4501	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.646706	2.089268	-2.557437	44330.814469
HLA A*0212	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.427597	1.870150	-2.557448	26766.860660
HLA B*4601	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.346789	1.789240	-2.557549	22222.312522
HLA A*6901	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-3.880358	1.322784	-2.557574	7592.026947
HLA B*0802	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.349928	1.792234	-2.557694	22383.508602
HLA B*4801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.005957	1.448126	-2.557831	10138.098587
HLA A*2601	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.272259	1.714405	-2.557854	18717.976070
HLA B*5301	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.826207	1.268289	-2.557918	6702.036837
HLA B*4402	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.428070	1.870150	-2.557920	26795.982446
HLA A*0202	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.085881	1.527790	-2.558091	12186.564487
HLA B*1503	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-3.785594	1.227496	-2.558097	6103.706088
HLA B*4403	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.546044	1.987904	-2.558140	35159.636385
HLA B*0702	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.250397	1.692204	-2.558193	17799.054374
HLA A*6801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.022690	1.464436	-2.558253	10536.334318
HLA B*4801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.075760	1.517234	-2.558525	11905.830890
HLA B*4403	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.596142	2.037348	-2.558794	39458.670088
HLA B*3901	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-3.816424	1.257536	-2.558887	6552.749335
HLA B*0802	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.432879	1.873578	-2.559301	27094.371447
HLA A*2402	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.529715	1.970233	-2.559483	33862.222129
HLA B*1503	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.204718	1.645215	-2.559503	16022.055890
HLA B*4601	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.388817	1.828963	-2.559854	24480.305806
HLA A*2501	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.430008	1.870150	-2.559858	26915.844447
HLA B*1509	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.421512	1.861442	-2.560070	26394.429048
HLA B*0803	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.334022	1.773509	-2.560513	21578.544591
HLA A*0101	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.336677	1.776041	-2.560637	21710.862033
HLA B*5801	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.190128	1.629468	-2.560660	15492.729581
HLA B*5401	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.566732	2.005692	-2.561039	36874.962767
HLA B*1501	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.305030	1.743756	-2.561273	20185.034895
HLA A*3101	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.378918	1.817618	-2.561300	23928.664379
HLA B*7301	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.241175	1.679828	-2.561348	17425.096871
HLA B*1801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.308974	1.747156	-2.561818	20369.214888
HLA B*2705	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.408846	1.846931	-2.561915	25635.760073
HLA B*3501	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.830610	1.268289	-2.562321	6770.328564
HLA A*3002	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.326631	1.764296	-2.562334	21214.395915

HLA A*0301	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.326633	1.764296	-2.562337	21214.510683
HLA A*6802	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.436164	1.873578	-2.562585	27300.063703
HLA A*0206	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.090505	1.527790	-2.562715	12317.003858
HLA A*6901	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.764143	1.200757	-2.563385	5809.554293
HLA B*5701	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.381073	1.817618	-2.563455	24047.666265
HLA A*2402	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.433661	1.870150	-2.563512	27143.225762
HLA A*0301	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.269620	1.705831	-2.563789	18604.603383
HLA A*0212	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.437374	1.873578	-2.563795	27376.230272
HLA B*7301	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.596732	2.032901	-2.563831	39512.286707
HLA A*3002	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.410803	1.846931	-2.563872	25751.546724
HLA B*4801	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.173353	1.609455	-2.563897	14905.708287
HLA A*0216	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.410839	1.846931	-2.563907	25753.636504
HLA B*1501	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.157479	1.593495	-2.563985	14370.752073
HLA B*1801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.393025	1.828963	-2.564062	24718.651030
HLA B*0803	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.272214	1.708081	-2.564134	18716.052188
HLA B*3901	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.272257	1.708081	-2.564176	18717.874809
HLA A*0301	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.344884	1.780575	-2.564309	22125.027472
HLA B*5801	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.274714	1.710232	-2.564483	18824.094723
HLA B*3901	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.355682	1.790732	-2.564950	22682.036851
HLA B*0702	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.340760	1.775750	-2.565010	21915.958655
HLA B*0801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.279493	1.714405	-2.565088	19032.373506
HLA B*7301	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.571642	2.006546	-2.565096	37294.261710
HLA B*1517	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.532756	0.967578	-2.565178	3410.013779
HLA A*3101	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.217199	1.651959	-2.565239	16489.166628
HLA B*0702	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.394371	1.828963	-2.565408	24795.394433
HLA A*2602	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.002507	1.437023	-2.565485	10057.903539
HLA B*1502	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.139036	1.573351	-2.565685	13773.237605
HLA B*3901	1:452-460	9	RVAATGTTV	1.107071	0.312844	-3.985699	1.419915	-2.565784	9676.075546
HLA A*3201	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.571705	2.005692	-2.566013	37299.709569
HLA A*0219	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.903557	1.337377	-2.566180	8008.599134
HLA B*1502	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.567540	2.001284	-2.566256	36943.651036
HLA A*0101	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.313481	1.747156	-2.566325	20581.669598
HLA A*6801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-3.583449	1.016861	-2.566588	3832.204021
HLA B*4001	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.378911	1.811844	-2.567067	23928.276028
HLA B*1509	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.338998	1.771882	-2.567116	21827.216628
HLA B*3801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.331936	1.764802	-2.567134	21475.130260
HLA A*0212	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.534730	0.967578	-2.567151	3425.545191
HLA B*0802	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.437343	1.870150	-2.567194	27374.305009
HLA A*0212	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.152781	1.585411	-2.567369	14216.101871
HLA A*2602	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.530113	1.962632	-2.567481	33893.195542
HLA A*0211	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.153152	1.585411	-2.567741	14228.258456
HLA A*8001	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.416400	1.848352	-2.568048	26085.537662
HLA B*4601	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.311808	1.743756	-2.568052	20502.544763
HLA A*3101	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.341656	1.773509	-2.568147	21961.177708
HLA B*7301	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.633051	2.064809	-2.568241	42958.637999
HLA A*0203	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.442070	1.873578	-2.568492	27673.893530
HLA A*2301	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.416961	1.848352	-2.568609	26119.287124
HLA B*4402	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.421475	1.852707	-2.568768	26392.144491
HLA B*4002	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.333658	1.764802	-2.568856	21560.457858
HLA B*4501	1:299-307	9	GLDEMVAAF	1.156237	0.908572	-4.633781	2.064809	-2.568972	43030.975692
HLA B*3501	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.439162	1.870150	-2.569012	27489.168496
HLA B*4001	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.398245	1.828963	-2.569283	25017.581427
HLA A*0201	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.398370	1.828963	-2.569407	25024.755600
HLA B*3901	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.707060	1.137355	-2.569705	5094.009225
HLA B*1503	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.220446	1.650564	-2.569881	16612.909337
HLA A*6801	1:131-139	9	GYDNFDRHL	1.691359	0.397909	-4.659151	2.089268	-2.569883	45619.543227
HLA A*0101	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.345737	1.775750	-2.569987	22168.519065
HLA A*0212	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.431540	1.861442	-2.570098	27010.950931
HLA A*8001	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.387734	1.817618	-2.570116	24419.328998
HLA B*2705	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.283804	1.713576	-2.570228	19222.251582
HLA A*2501	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.444039	1.873578	-2.570461	27799.637584
HLA A*8001	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.172145	1.601532	-2.570613	14864.317811
HLA B*0801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.259257	1.688566	-2.570691	18165.896594
HLA B*3801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.425511	1.854767	-2.570744	26638.581527
HLA A*2902	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.419097	1.848352	-2.570745	26248.047385

HLA A*3002	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.399733	1.828963	-2.570770	25103.399987
HLA A*2601	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.180274	1.609246	-2.571028	15145.171670
HLA B*5101	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.363358	1.792274	-2.571084	23086.485220
HLA B*4601	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.383035	1.811844	-2.571191	24156.541488
HLA A*0101	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.383093	1.811844	-2.571249	24159.808814
HLA A*2301	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.343192	1.771882	-2.571310	22039.015454
HLA A*1101	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.463216	1.891829	-2.571386	29054.648835
HLA B*4403	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.583836	2.012396	-2.571440	38356.223563
HLA B*0803	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.336329	1.764802	-2.571528	21693.485893
HLA A*0301	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.360940	1.789240	-2.571700	22958.324981
HLA B*2705	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.420460	1.848352	-2.572108	26330.536166
HLA A*6802	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.401175	1.828963	-2.572212	25186.923889
HLA B*5401	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.427008	1.854767	-2.572241	26730.539083
HLA A*6801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-3.539964	0.967687	-2.572277	3467.083920
HLA A*3002	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.880099	1.307776	-2.572324	7587.510369
HLA A*0211	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.280428	1.708081	-2.572347	19073.396941
HLA B*5101	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.434030	1.861442	-2.572588	27166.289724
HLA B*4601	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.344522	1.771882	-2.572640	22106.602281
HLA B*5401	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.542873	1.970233	-2.572640	34903.788653
HLA B*1801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.287305	1.714405	-2.572900	19377.823223
HLA A*6801	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.473671	1.900474	-2.573197	29762.598041
HLA B*4002	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.564124	1.990887	-2.573237	36654.192988
HLA B*3901	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.385095	1.811844	-2.573251	24271.423854
HLA B*1801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.234937	1.661630	-2.573307	17176.604601
HLA A*3301	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.362587	1.789240	-2.573347	23045.555877
HLA A*2501	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.345316	1.771882	-2.573434	22147.062124
HLA A*3301	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.585847	2.012396	-2.573451	38534.257969
HLA A*0212	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.426221	1.852707	-2.573514	26682.138855
HLA B*4801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.128271	1.554677	-2.573593	13436.021786
HLA B*0802	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.426336	1.852707	-2.573629	26689.212815
HLA A*6801	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.628685	2.055046	-2.573639	42528.998961
HLA B*0803	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.345568	1.771882	-2.573685	22159.885842
HLA B*5801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.338622	1.764802	-2.573821	21808.331551
HLA B*4002	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.628951	2.055046	-2.573905	42555.005629
HLA A*0301	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.347464	1.773509	-2.573955	22256.842532
HLA B*0803	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.426735	1.852707	-2.574028	26713.769672
HLA B*0803	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.426728	1.852642	-2.574086	26713.336120
HLA A*0219	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.815954	1.241782	-2.574172	6545.663240
HLA A*3002	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.544677	1.970233	-2.574444	35049.108413
HLA A*2602	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.131677	1.556999	-2.574679	13541.832966
HLA B*0802	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.350910	1.776041	-2.574870	22434.182457
HLA B*4402	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.423439	1.848352	-2.575087	26511.777708
HLA B*0803	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.448675	1.873578	-2.575096	28097.952118
HLA A*0201	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.364486	1.789240	-2.575246	23146.512881
HLA A*2501	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.290148	1.714405	-2.575743	19505.085867
HLA B*5801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.351547	1.775750	-2.575797	22467.096884
HLA A*6802	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.366694	1.790732	-2.575962	23264.519541
HLA B*4402	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.423143	1.846931	-2.576212	26493.712217
HLA A*3101	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.365585	1.789240	-2.576345	23205.190122
HLA A*2301	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.468798	1.892220	-2.576578	29430.524847
HLA A*2501	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.425154	1.848352	-2.576802	26616.685541
HLA A*2601	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.323983	1.747156	-2.576827	21085.446407
HLA A*2403	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.150201	1.573351	-2.576850	14131.907704
HLA B*7301	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-3.502617	0.925719	-2.576898	3181.390209
HLA A*0216	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.162385	1.585411	-2.576974	14534.002200
HLA B*3501	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.405945	1.828963	-2.576982	25465.052997
HLA B*0801	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.845332	1.268289	-2.577043	7003.765853
HLA B*4501	1:460-468	9	VSPPLFESL	1.613644	0.458549	-4.649269	2.072193	-2.577076	44593.236989
HLA B*5101	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.324258	1.747156	-2.577102	21098.796814
HLA A*0202	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-3.563943	0.986777	-2.577167	3663.896507
HLA A*6901	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-3.532385	0.955018	-2.577367	3407.100272
HLA B*4801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.321152	1.743756	-2.577396	20948.439199
HLA A*3301	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.547656	1.970233	-2.577423	35290.362688
HLA A*3201	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.547830	1.970233	-2.577597	35304.493371
HLA B*2705	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.430929	1.852642	-2.578287	26972.984813

HLA A*1101	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.451903	1.873578	-2.578325	28307.587635
HLA A*0201	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.390332	1.811844	-2.578488	24565.876066
HLA A*2602	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.586947	2.008310	-2.578636	38631.943696
HLA A*2301	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.414783	1.835915	-2.578868	25988.627655
HLA B*3901	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.449161	1.870150	-2.579011	28129.435152
HLA A*2602	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.426127	1.846931	-2.579196	26676.365583
HLA B*0702	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.344017	1.764802	-2.579215	22080.904461
HLA B*5801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.359984	1.780575	-2.579409	22907.830380
HLA A*3301	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.620868	2.041338	-2.579531	41770.379777
HLA B*3501	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.692460	1.112802	-2.579658	4925.610057
HLA B*4002	1:77-85	9	EVGGPYGPY	0.951232	1.107356	-4.638306	2.058588	-2.579718	43481.678601
HLA A*2501	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.180067	1.600184	-2.579883	15137.963220
HLA A*2602	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.415881	1.835915	-2.579966	26054.368808
HLA B*5701	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.372537	1.792234	-2.580303	23579.644715
HLA B*4601	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.372807	1.792234	-2.580574	23594.319055
HLA A*3301	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.491842	1.911098	-2.580744	31034.285852
HLA B*4002	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.543385	1.962632	-2.580753	34944.976923
HLA B*3901	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.325031	1.743756	-2.581275	21136.383021
HLA B*5401	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.482044	1.900474	-2.581571	30342.013942
HLA A*2902	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.331137	1.749555	-2.581582	21435.666021
HLA A*2501	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.355283	1.773509	-2.581774	22661.186199
HLA A*3001	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.296254	1.714405	-2.581850	19781.270331
HLA A*0250	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.572995	1.990887	-2.582108	37410.655468
HLA A*2601	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.355708	1.773509	-2.582199	22683.386672
HLA A*0212	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.371447	1.789240	-2.582207	23520.529587
HLA B*3501	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.394211	1.811844	-2.582367	24786.274568
HLA A*0216	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.373219	1.790732	-2.582487	23616.667096
HLA B*3501	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.573153	0.990658	-2.582495	3742.425632
HLA B*4403	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.545469	1.962632	-2.582837	35113.065870
HLA A*2301	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.429778	1.846931	-2.582847	26901.578279
HLA B*0801	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.192355	1.609455	-2.582900	15572.389301
HLA A*0216	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.296177	1.713159	-2.583018	19777.739168
HLA A*6801	1:478-486	9	QRLRAARQL	1.551442	0.535207	-4.669813	2.086649	-2.583164	46753.367311
HLA B*0802	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.330376	1.747156	-2.583220	21398.126407
HLA B*4002	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.783996	1.200757	-2.583239	6081.293484
HLA B*4002	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.584757	2.001284	-2.583473	38437.651017
HLA B*4002	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.475882	1.892220	-2.583662	29914.496976
HLA A*0211	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.298146	1.714405	-2.583741	19867.604842
HLA B*1502	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.412737	1.828963	-2.583774	25866.456953
HLA B*1509	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.413061	1.828963	-2.584099	25885.775147
HLA B*7301	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.592618	2.008310	-2.584308	39139.765221
HLA A*3201	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.373564	1.789240	-2.584324	23635.455808
HLA A*0203	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.292631	1.708081	-2.584551	19616.940380
HLA B*4402	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.428551	1.843794	-2.584757	26825.716406
HLA A*2501	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.402519	1.817618	-2.584901	25264.984447
HLA B*4601	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.360943	1.776041	-2.584902	22958.449183
HLA A*2402	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.433624	1.848352	-2.585272	27140.876394
HLA A*1101	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.433673	1.848352	-2.585321	27143.959981
HLA A*3301	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-3.677282	1.091927	-2.585355	4756.443631
HLA A*3201	1:239-247	9	ERIPKFAHL	1.486988	0.514296	-4.586827	2.001284	-2.585543	38621.286445
HLA A*8001	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.329314	1.743756	-2.585558	21345.866134
HLA A*3101	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.045583	1.459786	-2.585797	11106.645854
HLA B*4001	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.366588	1.780575	-2.586014	23258.856599
HLA A*6901	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.122613	1.536595	-2.586018	13262.125688
HLA A*2402	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-3.924716	1.338560	-2.586156	8408.451388
HLA B*1503	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-3.149005	0.562720	-2.586285	1409.306161
HLA A*0201	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.377293	1.790732	-2.586561	23839.251465
HLA A*0219	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.448170	1.861442	-2.586727	28065.289654
HLA A*1101	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.448205	1.861442	-2.586763	28067.567198
HLA B*3801	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.448381	1.861442	-2.586939	28078.957691
HLA B*3801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.498275	1.911098	-2.587177	31497.395662
HLA B*1801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.431061	1.843794	-2.587267	26981.157619
HLA B*5301	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.304764	1.717294	-2.587470	20172.699201
HLA B*5101	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.124126	1.536595	-2.587531	13308.411099
HLA B*4501	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.575575	1.987904	-2.587671	37633.538255

HLA B*1509	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.302076	1.714405	-2.587672	20048.237656
HLA A*2403	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.238408	1.650564	-2.587843	17314.402447
HLA A*2603	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.498987	1.911098	-2.587889	31549.068419
HLA B*0803	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.377215	1.789240	-2.587975	23834.995910
HLA B*4002	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.558365	1.970233	-2.588132	36171.379686
HLA A*0219	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.364319	1.776041	-2.588278	23137.623963
HLA A*8001	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.417281	1.828963	-2.588318	26138.511328
HLA A*0101	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.379247	1.790732	-2.588515	23946.794443
HLA B*3801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.332333	1.743756	-2.588577	21494.773333
HLA B*3901	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.462454	1.873578	-2.588876	29003.766334
HLA A*0219	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.459128	1.870150	-2.588978	28782.434622
HLA B*5101	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.432776	1.843794	-2.588982	27087.922802
HLA B*1502	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.018888	1.429823	-2.589065	10444.510134
HLA A*3001	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.237207	1.648036	-2.589170	17266.603688
HLA A*6801	1:60-68	9	ALLDALRWL	1.537707	0.516755	-4.644619	2.054462	-2.590157	44118.360775
HLA A*2602	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.490768	1.900474	-2.590294	30957.653955
HLA A*2601	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.190523	1.600184	-2.590338	15506.816725
HLA B*5401	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.464029	1.873578	-2.590450	29109.084887
HLA B*4002	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.445247	1.854767	-2.590480	27877.047140
HLA B*3801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.154402	1.563919	-2.590482	14269.267237
HLA A*3001	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.279223	1.688566	-2.590657	19020.536440
HLA A*6802	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.366461	1.775750	-2.590711	23252.062888
HLA A*3002	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.220277	1.629468	-2.590809	16606.439670
HLA B*0801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.371395	1.780575	-2.590821	23517.730397
HLA B*5701	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.366922	1.776041	-2.590881	23276.731016
HLA B*2705	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.402770	1.811844	-2.590926	25279.613522
HLA B*3501	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.247946	1.657009	-2.590938	17698.905765
HLA B*4801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.381820	1.790732	-2.591088	24089.072147
HLA B*0802	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.439592	1.848352	-2.591240	27516.396515
HLA B*1503	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.801462	1.210192	-2.591270	6330.850158
HLA A*3001	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.248555	1.657009	-2.591546	17723.722168
HLA A*0201	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.367491	1.775750	-2.591740	23307.224710
HLA A*3001	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.191430	1.599646	-2.591784	15539.232160
HLA A*0301	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.221329	1.629468	-2.591861	16646.736353
HLA B*3901	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.453306	1.861442	-2.591863	28399.160556
HLA A*2601	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.367639	1.775750	-2.591889	23315.169703
HLA B*4601	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.356370	1.764296	-2.592074	22718.018601
HLA A*0203	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.892810	1.300706	-2.592104	7812.859447
HLA A*0211	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.305264	1.713159	-2.592106	20195.957729
HLA B*5101	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.483997	1.891829	-2.592167	30478.727117
HLA A*6901	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.272047	1.679828	-2.592220	18708.864693
HLA B*1503	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.309656	1.717294	-2.592361	20401.196575
HLA A*0301	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.368271	1.775750	-2.592521	23349.124041
HLA A*0216	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.421580	1.828963	-2.592618	26398.570310
HLA A*8001	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.368696	1.776041	-2.592655	23371.998466
HLA A*0211	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.368508	1.775750	-2.592758	23361.885461
HLA B*4501	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.605200	2.012396	-2.592804	40290.226457
HLA A*3101	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.336787	1.743756	-2.593031	21716.383042
HLA B*4601	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.307457	1.714405	-2.593052	20298.153038
HLA B*5801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.357484	1.764418	-2.593066	22776.348887
HLA B*4403	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.358067	1.764802	-2.593265	22806.927341
HLA B*0801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.384137	1.790732	-2.593405	24217.910203
HLA B*4402	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.422558	1.828963	-2.593595	26458.047561
HLA B*3501	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.320210	1.726550	-2.593659	20903.043635
HLA B*4402	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.382990	1.789240	-2.593750	24154.058615
HLA A*3001	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-3.594200	1.000328	-2.593872	3928.256751
HLA A*6802	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.121683	1.527790	-2.593893	13233.744434
HLA A*3101	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.223481	1.629468	-2.594014	16729.433295
HLA A*0301	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.167408	1.573351	-2.594057	14703.083395
HLA A*0216	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.455528	1.861442	-2.594086	28544.873048
HLA A*6901	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.320670	1.726550	-2.594120	20925.219687
HLA A*2301	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.446931	1.852707	-2.594224	27985.389141
HLA A*2301	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.494701	1.900474	-2.594227	31239.284570
HLA B*1801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.358736	1.764418	-2.594318	22842.118604
HLA A*6901	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-3.643182	1.048747	-2.594435	4397.257810

HLA A*0101	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.024513	1.429823	-2.594690	10580.659604
HLA A*0216	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.466280	0.871584	-2.594696	2926.036944
HLA A*3001	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.923725	1.328755	-2.594969	8389.277015
HLA B*5101	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.368771	1.773509	-2.595262	23376.044893
HLA A*2603	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.195457	1.600184	-2.595272	15683.990569
HLA A*2501	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.339045	1.743756	-2.595289	21829.578412
HLA B*2705	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.246013	1.650564	-2.595449	17620.279406
HLA A*2403	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.386204	1.790732	-2.595472	24333.479345
HLA B*1517	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.322120	1.726550	-2.595569	20995.182711
HLA A*2602	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.506728	1.911098	-2.595630	32116.491309
HLA A*8001	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.387879	1.792234	-2.595646	24427.520936
HLA B*5101	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.448419	1.852707	-2.595711	28081.388261
HLA A*3301	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.413510	1.817618	-2.595892	25912.536453
HLA B*1801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.386867	1.790732	-2.596135	24370.630558
HLA A*6901	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-3.664172	1.067986	-2.596186	4615.005553
HLA A*2902	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.258021	1.661630	-2.596391	18114.277167
HLA A*6802	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.340366	1.743756	-2.596610	21896.049135
HLA A*0301	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.361615	1.764802	-2.596813	22993.998640
HLA B*4002	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.508140	1.911098	-2.597042	32221.082989
HLA A*1101	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.370639	1.773509	-2.597130	23476.798542
HLA B*0803	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.445602	1.848352	-2.597250	27899.829016
HLA A*3101	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.362284	1.764802	-2.597482	23029.478555
HLA A*2301	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.489445	1.891829	-2.597616	30863.507583
HLA A*0203	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.409471	1.811844	-2.597627	25672.677270
HLA A*0219	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.373416	1.775750	-2.597666	23627.401673
HLA B*0803	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.441704	1.843794	-2.597910	27650.548202
HLA B*4501	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.635299	2.037348	-2.597951	43181.622933
HLA A*0216	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.363017	1.764802	-2.598216	23068.382499
HLA B*4402	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.390647	1.792274	-2.598373	24583.690943
HLA A*0301	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.345633	1.747156	-2.598477	22163.242807
HLA A*6802	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.348180	1.749555	-2.598625	22293.596997
HLA B*2705	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-3.546205	0.947523	-2.598681	3517.260914
HLA A*3002	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.035734	1.437023	-2.598711	10857.601128
HLA A*0301	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.363172	1.764418	-2.598754	23076.620598
HLA A*0101	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.372479	1.773509	-2.598970	23576.455849
HLA B*1801	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.453794	1.854767	-2.599028	28431.134894
HLA B*0801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.019532	1.420375	-2.599156	10460.003612
HLA A*3201	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.451912	1.852707	-2.599205	28308.200205
HLA A*0212	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.428255	1.828963	-2.599293	26807.436994
HLA A*2402	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.446332	1.846931	-2.599401	27946.809305
HLA B*5401	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-2.921115	0.321711	-2.599403	833.901400
HLA B*1501	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.256510	1.657009	-2.599501	18051.375058
HLA A*0203	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.288069	1.688566	-2.599502	19411.923552
HLA B*5401	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.537098	1.937546	-2.599552	34442.727537
HLA A*3101	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.312726	1.713159	-2.599567	20545.959013
HLA A*2902	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.388843	1.789240	-2.599603	24481.762643
HLA A*0211	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.349188	1.749555	-2.599633	22345.397010
HLA A*6901	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.059581	1.459786	-2.599795	11470.468480
HLA B*7301	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.537443	1.937546	-2.599897	34470.129138
HLA A*0219	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.452676	1.852707	-2.599969	28358.015858
HLA A*0301	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.209380	1.609246	-2.600133	16194.950339
HLA B*5301	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.511260	1.911098	-2.600162	32453.403507
HLA B*1801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.350034	1.749555	-2.600478	22388.958418
HLA B*4001	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.317792	1.717294	-2.600497	20787.004356
HLA A*2403	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.389750	1.789240	-2.600510	24532.939296
HLA A*0101	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.381261	1.780575	-2.600686	24058.076134
HLA B*1509	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.470976	1.870150	-2.600826	29578.488672
HLA A*3301	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.638983	2.037348	-2.601635	43549.477950
HLA A*2402	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.437900	1.835915	-2.601985	27409.425312
HLA B*0803	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.394254	1.792234	-2.602020	24788.688323
HLA A*2601	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.382816	1.780575	-2.602242	24144.390913
HLA B*0801	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.312557	1.710232	-2.602326	20537.957673
HLA A*3101	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.247852	1.645215	-2.602637	17695.076214
HLA B*7301	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.572878	1.970233	-2.602645	37400.537461
HLA B*0802	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.374539	1.771882	-2.602657	23688.579476

HLA A*3101	1:314-322	9	SSPARFDQK	0.878945	0.297758	-3.779588	1.176703	-2.602885	6019.886862
HLA A*2902	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.378933	1.776041	-2.602892	23929.441100
HLA B*0802	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.352611	1.749555	-2.603056	22522.224066
HLA A*3002	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.248437	1.645215	-2.603222	17718.928648
HLA A*2602	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.495122	1.891829	-2.603292	31269.550413
HLA A*2601	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.375251	1.771882	-2.603369	23727.441553
HLA A*0219	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.317886	1.714405	-2.603481	20791.503059
HLA B*5701	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.313596	1.710050	-2.603546	20587.126204
HLA A*1101	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.458533	1.854767	-2.603766	28743.066995
HLA B*4601	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.251861	1.648036	-2.603824	17859.144818
HLA B*2705	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.379724	1.775750	-2.603974	23973.107438
HLA B*7301	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.591986	1.987904	-2.604082	39082.848104
HLA B*1517	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.253148	1.648791	-2.604357	17912.168942
HLA A*6901	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.296602	1.692204	-2.604398	19797.114816
HLA A*0101	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.368740	1.764296	-2.604444	23374.400948
HLA B*3801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.457448	1.852707	-2.604741	28671.317173
HLA A*6801	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.457387	1.852642	-2.604744	28667.284632
HLA A*6901	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.314855	1.710050	-2.604805	20646.909340
HLA B*1502	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.312889	1.708081	-2.604808	20553.629888
HLA A*1101	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-3.905915	1.300814	-2.605101	8052.216417
HLA A*0216	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.394409	1.789240	-2.605169	24797.540771
HLA A*2501	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.441168	1.835915	-2.605253	27616.463528
HLA B*4601	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.122491	1.517234	-2.605257	13258.395388
HLA A*0211	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.874681	1.269415	-2.605266	7493.442603
HLA A*6901	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.293900	1.688566	-2.605334	19674.331925
HLA A*0203	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.349465	1.743756	-2.605709	22359.666126
HLA A*2403	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.313899	1.708081	-2.605818	20601.498473
HLA B*4402	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.207373	1.601532	-2.605841	16120.301508
HLA A*0211	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.395210	1.789240	-2.605970	24843.328807
HLA B*5701	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.377892	1.771882	-2.606009	23872.160925
HLA A*2403	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.349818	1.743756	-2.606062	22377.817987
HLA A*6901	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.319237	1.713159	-2.606078	20856.279599
HLA B*5801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.319770	1.713576	-2.606194	20881.907779
HLA A*1101	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.453306	1.846931	-2.606374	28399.160556
HLA B*1517	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.418232	1.811844	-2.606388	26195.843725
HLA A*1101	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.319704	1.713159	-2.606545	20878.744892
HLA A*3001	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.286436	1.679828	-2.606608	19339.074223
HLA A*0211	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.371447	1.764802	-2.606645	23520.529587
HLA A*0219	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.395952	1.789240	-2.606712	24885.835420
HLA B*1501	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.298954	1.692204	-2.606750	19904.612917
HLA A*2402	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.507576	1.900474	-2.607102	32179.275140
HLA B*7301	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.598017	1.990887	-2.607130	39629.385009
HLA B*1501	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.317181	1.710050	-2.607131	20757.786509
HLA B*1801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.499059	1.891829	-2.607230	31554.359849
HLA A*6901	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.351171	1.743756	-2.607415	22447.658177
HLA A*2501	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.419581	1.811844	-2.607737	26277.315490
HLA A*0212	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.419696	1.811844	-2.607852	26284.282124
HLA A*0101	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.372805	1.764802	-2.608003	23594.191413
HLA B*5801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.357822	1.749555	-2.608267	22794.099124
HLA B*4501	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.663333	2.055046	-2.608287	46060.963241
HLA B*0801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.420237	1.811844	-2.608392	26317.007341
HLA A*6802	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.297074	1.688566	-2.608508	19818.653664
HLA B*1503	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-3.258289	0.649772	-2.608518	1812.547080
HLA A*0202	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.397985	1.789240	-2.608745	25002.562937
HLA A*2501	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.461470	1.852707	-2.608763	28938.096690
HLA B*4601	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.373679	1.764802	-2.608877	23641.722033
HLA A*8001	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.356112	1.747156	-2.608956	22704.503407
HLA A*0206	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-3.615933	1.006851	-2.609081	4129.834061
HLA B*0802	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.322681	1.713576	-2.609105	21022.346273
HLA B*5701	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.389698	1.780575	-2.609123	24530.019619
HLA B*0803	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.385281	1.776041	-2.609240	24281.799222
HLA B*4403	1:218-226	9	LLPSTPRQL	1.694547	0.360499	-4.664433	2.055046	-2.609387	46177.729437
HLA B*4002	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.615119	2.005692	-2.609427	41221.067462
HLA B*0802	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.400301	1.790732	-2.609569	25136.286710
HLA A*0212	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.400327	1.790732	-2.609595	25137.782584

HLA B*2705	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.947154	1.337377	-2.609777	8854.287093
HLA B*0803	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.400543	1.790732	-2.609811	25150.297019
HLA B*5301	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.547386	1.937546	-2.609840	35268.414067
HLA A*0101	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.374410	1.764418	-2.609992	23681.532132
HLA B*2705	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.357237	1.747156	-2.610082	22763.414721
HLA A*0301	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.353859	1.743756	-2.610103	22587.015575
HLA A*0201	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.375192	1.764802	-2.610391	23724.232699
HLA B*4002	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.613435	2.003005	-2.610430	41061.485156
HLA B*4801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.391007	1.780575	-2.610432	24604.047609
HLA B*2705	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.382328	1.771882	-2.610445	24117.237550
HLA B*4002	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.357623	1.747156	-2.610467	22783.619881
HLA A*2602	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.844542	1.234017	-2.610525	6991.046512
HLA A*2902	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.318675	1.708081	-2.610595	20829.330616
HLA B*4801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.375458	1.764802	-2.610656	23738.740171
HLA B*4001	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.266550	1.655822	-2.610728	18473.519322
HLA B*4501	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.652241	2.041338	-2.610903	44899.457860
HLA A*0301	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.948281	1.337377	-2.610905	8877.309313
HLA A*0206	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.472416	1.861442	-2.610974	29676.741517
HLA B*1801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.386914	1.775750	-2.611164	24373.267549
HLA A*0101	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.360884	1.749555	-2.611328	22955.344326
HLA A*3201	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.429153	1.817618	-2.611535	26862.893927
HLA B*4002	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.618188	2.006546	-2.611642	41513.338575
HLA A*2902	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.376118	1.764296	-2.611821	23774.854745
HLA A*0219	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.440959	1.828963	-2.611996	27603.169950
HLA B*4403	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.617821	2.005692	-2.612129	41478.318476
HLA B*4001	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.356096	1.743756	-2.612340	22703.643622
HLA A*0250	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.403146	1.790732	-2.612414	25301.504580
HLA B*3901	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.304658	1.692204	-2.612454	20167.788856
HLA A*2601	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.339020	1.726550	-2.612469	21828.279399
HLA A*0212	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.325653	1.713159	-2.612494	21166.706306
HLA A*2602	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.456496	1.843794	-2.612702	28608.566939
HLA A*2603	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.575465	1.962632	-2.612833	37623.970587
HLA A*6802	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.073114	1.459786	-2.613328	11833.526549
HLA A*6801	1:94-102	9	YRDVLARLL	1.616307	0.425031	-4.654821	2.041338	-2.613483	45166.956949
HLA A*3201	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-3.914209	1.300706	-2.613503	8207.466539
HLA A*0250	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.633925	1.020365	-2.613560	4304.522260
HLA A*0250	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-3.871101	1.257536	-2.613564	7431.915617
HLA B*1509	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.404401	1.790732	-2.613669	25374.703291
HLA A*2602	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.431317	1.817618	-2.613698	26997.072504
HLA B*4402	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.405982	1.792234	-2.613748	25467.257302
HLA B*4402	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.328334	1.714405	-2.613930	21297.765763
HLA A*2902	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.379010	1.764802	-2.614208	23933.713517
HLA B*1517	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.306432	1.692204	-2.614228	20250.331968
HLA A*3001	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.270180	1.655822	-2.614357	18628.573235
HLA B*5101	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.390278	1.775750	-2.614528	24562.819587
HLA A*0219	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.634945	1.020365	-2.614580	4314.640686
HLA A*1101	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.458451	1.843794	-2.614657	28737.625122
HLA A*0202	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.012817	1.398016	-2.614801	10299.520500
HLA A*0250	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.292206	0.677348	-2.614858	1959.776120
HLA A*2402	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.407202	1.792234	-2.614968	25538.863025
HLA A*0211	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.485249	1.870150	-2.615100	30566.738468
HLA A*2902	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.044963	1.429823	-2.615140	11090.794546
HLA A*8001	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.391021	1.775750	-2.615271	24604.846253
HLA B*1801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.380086	1.764802	-2.615285	23993.088306
HLA A*6802	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.427252	1.811844	-2.615408	26745.582677
HLA A*6802	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.307706	1.692204	-2.615501	20309.796316
HLA A*2603	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.407848	1.792274	-2.615574	25576.885967
HLA A*0206	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.444786	1.828963	-2.615824	27847.503705
HLA B*0803	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.486050	1.870150	-2.615901	30623.179182
HLA A*0101	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.308288	1.692204	-2.616084	20337.063293
HLA A*3201	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.075924	1.459786	-2.616138	11910.340390
HLA A*6801	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.607042	1.990887	-2.616155	40461.474439
HLA B*1502	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.391986	1.775750	-2.616236	24659.615119
HLA B*4501	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.649191	2.032901	-2.616290	44585.276632
HLA B*2705	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.434362	1.817618	-2.616743	27187.019923

HLA A*3301	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.625060	2.008310	-2.616750	42175.467486
HLA B*4601	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.366349	1.749555	-2.616793	23246.025700
HLA B*5701	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.428695	1.811844	-2.616851	26834.570440
HLA A*6801	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.587348	1.970233	-2.617116	38667.698297
HLA B*4601	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.330402	1.713159	-2.617243	21399.399822
HLA B*5701	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.343834	1.726550	-2.617283	22071.588918
HLA B*2705	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.327549	1.710232	-2.617318	21259.317513
HLA B*7301	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-3.874987	1.257536	-2.617451	7498.714487
HLA B*4402	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.323294	1.705831	-2.617463	21052.050394
HLA A*2402	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.509376	1.891829	-2.617546	32312.901936
HLA A*2603	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.453606	1.835915	-2.617691	28418.832814
HLA A*3301	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.410228	1.792274	-2.617954	25717.437645
HLA A*0203	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.367514	1.749555	-2.617959	23308.485639
HLA A*2402	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.470788	1.852707	-2.618081	29565.690134
HLA B*4403	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.621183	2.003005	-2.618178	41800.671154
HLA B*4403	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.040132	1.421817	-2.618316	10968.118123
HLA B*1801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.173230	1.554677	-2.618553	14901.515689
HLA B*0702	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.430800	1.811844	-2.618956	26964.960360
HLA A*3201	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.756343	1.137355	-2.618987	5706.141336
HLA B*5101	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.489290	1.870150	-2.619141	30852.489652
HLA A*0201	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.400026	1.780575	-2.619452	25120.381554
HLA B*1503	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-3.888900	1.269415	-2.619485	7742.843270
HLA B*1502	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.437143	1.817618	-2.619525	27361.720086
HLA B*1509	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.337022	1.717294	-2.619728	21728.134543
HLA A*3002	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.396117	1.776041	-2.620076	24895.261278
HLA A*0250	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.491936	0.871584	-2.620352	3104.103413
HLA B*4001	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.411243	1.790732	-2.620511	25777.611439
HLA B*4601	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.401149	1.780575	-2.620575	25185.425090
HLA A*3301	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.626312	2.005692	-2.620620	42297.254720
HLA B*2705	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.265857	1.645215	-2.620641	18444.060627
HLA B*2705	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.269696	1.648791	-2.620905	18607.824425
HLA A*0206	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.411835	1.790732	-2.621103	25812.777818
HLA B*4402	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.334295	1.713159	-2.621136	21592.090395
HLA B*1509	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.370723	1.749555	-2.621168	23481.371235
HLA A*6901	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.385617	1.764418	-2.621199	24300.591233
HLA A*3001	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.264952	1.643417	-2.621535	18405.685180
HLA B*5301	1:27-35	9	ALFNWAYAR	1.194354	0.768278	-4.584188	1.962632	-2.621556	38387.361633
HLA A*2501	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.251240	1.629468	-2.621773	17833.656402
HLA A*2902	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.433748	1.811844	-2.621904	27148.659454
HLA B*5401	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.081887	1.459786	-2.622101	12075.000752
HLA A*6901	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.231408	1.609246	-2.622162	17037.598984
HLA B*5701	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.332439	1.710232	-2.622207	21500.006765
HLA B*2705	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.402977	1.780575	-2.622403	25291.651259
HLA A*0216	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.398403	1.775750	-2.622653	25026.651008
HLA B*0803	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.484265	1.861442	-2.622822	30497.529980
HLA B*0801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.336214	1.713159	-2.623055	21687.736047
HLA A*3001	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.265591	1.642298	-2.623293	18432.788896
HLA B*1801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.493573	1.870150	-2.623424	31158.269292
HLA B*2705	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.372995	1.749555	-2.623440	23604.532677
HLA A*2601	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.387945	1.764418	-2.623527	24431.221421
HLA A*0101	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.281300	1.657009	-2.624291	19111.717005
HLA A*0201	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.368186	1.743756	-2.624430	23344.577102
HLA B*4403	1:424-432	9	TAPLIEAAL	1.633673	0.399228	-4.657389	2.032901	-2.624488	45434.820725
HLA A*6802	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.280470	1.655822	-2.624648	19075.254361
HLA B*1502	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.400719	1.776041	-2.624679	25160.503613
HLA B*5701	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.413982	1.789240	-2.624742	25940.728752
HLA B*3901	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.304743	1.679828	-2.624915	20171.717037
HLA B*1502	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.254426	1.629468	-2.624959	17964.961737
HLA A*0211	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.225206	1.600184	-2.625021	16795.995577
HLA B*2705	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.339475	1.714405	-2.625071	21851.200608
HLA A*0201	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.338442	1.713159	-2.625283	21799.248932
HLA B*0802	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.339816	1.714405	-2.625411	21868.348156
HLA B*4801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.389923	1.764418	-2.625505	24542.762578
HLA B*4501	1:122-130	9	VAAGRNPKL	1.539580	0.463425	-4.628610	2.003005	-2.625605	42521.637129
HLA A*6901	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.339264	1.713576	-2.625688	21840.564066

HLA B*1801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.317973	1.692204	-2.625769	20795.665225
HLA B*4001	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.375505	1.749555	-2.625949	23741.308789
HLA B*1517	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.276669	1.650564	-2.626105	18909.013464
HLA B*4001	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.390694	1.764418	-2.626276	24586.350988
HLA A*1101	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.418641	1.792274	-2.626367	26220.514024
HLA B*2705	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.255923	1.629468	-2.626455	18026.977576
HLA B*4402	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.390920	1.764418	-2.626501	24599.123210
HLA A*3101	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.402364	1.775750	-2.626614	25255.965126
HLA B*3501	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.836850	1.210192	-2.626658	6868.311406
HLA A*0219	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.417481	1.790732	-2.626749	26150.533640
HLA B*1501	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.163358	1.536595	-2.626763	14566.590399
HLA B*3801	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.496942	1.870150	-2.626793	31400.928353
HLA A*2501	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.455765	1.828963	-2.626803	28560.474194
HLA A*8001	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.438671	1.811844	-2.626826	27458.104969
HLA B*1503	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.283114	1.655822	-2.627291	19191.702749
HLA B*1509	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.144806	1.517234	-2.627572	13957.459451
HLA B*0702	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.335671	1.708081	-2.627591	21660.650150
HLA A*2501	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.418369	1.790732	-2.627637	26204.064578
HLA B*4402	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-3.523166	0.895455	-2.627711	3335.535261
HLA B*5801	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.354465	1.726550	-2.627915	22618.563445
HLA A*1101	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.392242	1.764296	-2.627946	24674.160638
HLA B*5701	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.392792	1.764802	-2.627991	24705.415783
HLA A*0202	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.501874	1.873578	-2.628296	31759.529282
HLA A*2403	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.440141	1.811844	-2.628297	27551.251966
HLA A*0203	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.237759	1.609455	-2.628304	17288.569095
HLA B*4801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.377899	1.749555	-2.628343	23872.548365
HLA A*0219	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.375643	1.747156	-2.628487	23748.887831
HLA B*3801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.418021	1.789240	-2.628781	26183.092334
HLA A*2501	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.274059	1.645215	-2.628843	18795.703837
HLA B*1502	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-3.928738	1.299885	-2.628854	8486.689950
HLA B*4601	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.355428	1.726550	-2.628878	22668.788333
HLA B*4002	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.529372	1.900474	-2.628899	33835.486822
HLA A*2402	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-3.951716	1.322784	-2.628933	8947.800642
HLA A*2501	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.393864	1.764802	-2.629062	24766.437043
HLA B*4501	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.637554	2.008310	-2.629244	43406.469779
HLA A*1101	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.291031	1.661630	-2.629401	19544.801899
HLA B*0802	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.403071	1.773509	-2.629562	25297.124852
HLA B*0702	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.343993	1.714405	-2.629589	22079.709941
HLA A*2603	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.476685	1.846931	-2.629754	29969.895475
HLA A*6802	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.230062	1.600184	-2.629878	16984.866476
HLA A*6802	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-3.226360	0.596390	-2.629969	1684.068663
HLA A*0250	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.482709	1.852707	-2.630002	30388.503102
HLA A*0206	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.285881	1.655822	-2.630059	19314.399128
HLA B*5401	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.522430	1.892220	-2.630210	33298.885744
HLA A*3301	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.621331	1.990887	-2.630444	41814.920212
HLA B*2705	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.357202	1.726550	-2.630652	22761.567583
HLA B*1501	1:229-237	9	HQALIRIGV	1.172366	0.156389	-3.959728	1.328755	-2.630973	9114.399137
HLA A*2601	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.395285	1.764296	-2.630989	24847.629968
HLA A*3002	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.378263	1.747156	-2.631107	23892.574675
HLA A*2601	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.375234	1.743756	-2.631478	23726.543030
HLA B*4402	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.407794	1.776041	-2.631753	25573.703698
HLA B*1509	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.505372	1.873578	-2.631794	32016.395793
HLA B*4402	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.375563	1.743756	-2.631807	23744.519952
HLA A*6802	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.396338	1.764296	-2.632041	24907.924474
HLA A*0211	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.505784	1.873578	-2.632205	32046.721047
HLA A*6802	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.205747	1.573351	-2.632396	16060.065671
HLA B*2705	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.424656	1.792234	-2.632422	26586.176457
HLA B*4402	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.406133	1.773509	-2.632624	25476.076431
HLA B*0801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-3.422932	0.790220	-2.632712	2648.084302
HLA A*6802	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.342765	1.710050	-2.632715	22017.326522
HLA B*5401	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.425173	1.792274	-2.632899	26617.837513
HLA A*2902	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.423911	1.790732	-2.633179	26540.621969
HLA B*5301	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.494631	1.861442	-2.633188	31234.214950
HLA A*3001	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.161131	1.527790	-2.633341	14492.075790
HLA B*1503	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.232994	1.599646	-2.633349	17099.928496

HLA A*3301	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.339323	1.705831	-2.633491	21843.518142
HLA B*5301	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.278798	1.645215	-2.633582	19001.920838
HLA A*0201	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.398100	1.764418	-2.633681	25009.191609
HLA A*2402	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.486328	1.852642	-2.633685	30642.734247
HLA B*4501	1:23-31	9	LVRTALFNW	1.553174	0.453372	-4.640322	2.006546	-2.633776	43683.975988
HLA A*0219	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.398621	1.764802	-2.633820	25039.245577
HLA B*5301	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.344064	1.710232	-2.633832	22083.293695
HLA B*0802	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.398511	1.764296	-2.634214	25032.879787
HLA B*1509	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-3.514726	0.880484	-2.634242	3271.343781
HLA A*3101	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.129864	1.495432	-2.634432	13485.394327
HLA B*0802	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.415044	1.780575	-2.634470	26004.238453
HLA A*6801	1:57-65	9	SYLALLDAL	1.498520	0.489384	-4.622374	1.987904	-2.634470	41915.479989
HLA A*1101	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.228067	1.593495	-2.634573	16907.033934
HLA A*2501	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.285284	1.650564	-2.634720	19287.877210
HLA B*0803	1:479-487	9	RLRAARQLV	1.087444	0.249933	-3.972124	1.337377	-2.634747	9378.295788
HLA A*2403	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.282813	1.648036	-2.634776	19178.417751
HLA B*5301	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.483311	1.848352	-2.634959	30430.618257
HLA A*0212	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.292220	1.657009	-2.635211	19598.377211
HLA A*6802	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-3.361615	0.726109	-2.635506	2299.402225
HLA A*0216	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.235210	1.599646	-2.635564	17187.387113
HLA B*1501	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.416308	1.780575	-2.635734	26080.034568
HLA B*1501	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.291609	1.655822	-2.635787	19570.830077
HLA A*0216	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.328007	1.692204	-2.635803	21281.756405
HLA B*3501	1:199-207	9	VNPCDDALM	0.975652	0.107530	-3.719183	1.083182	-2.636002	5238.211983
HLA A*0212	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.344137	1.708081	-2.636056	22086.997519
HLA B*0801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.870123	1.234017	-2.636107	7415.208795
HLA B*4403	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.528700	1.892220	-2.636481	33783.176078
HLA B*1503	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-3.504511	0.867880	-2.636630	3195.292537
HLA A*2902	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.281849	1.645215	-2.636634	19135.926116
HLA A*2601	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.657194	1.020365	-2.636829	4541.447076
HLA B*4501	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.607199	1.970233	-2.636966	40476.142867
HLA A*6801	1:259-267	9	SKRDPQSNL	1.509811	0.502585	-4.649509	2.012396	-2.637113	44617.850715
HLA A*1101	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.413193	1.776041	-2.637152	25893.618529
HLA A*3301	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.489950	1.852642	-2.637308	30899.426621
HLA B*4801	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.266968	1.629468	-2.637500	18491.317155
HLA B*4501	1:372-380	9	RIVVLGDAW	1.407862	0.583025	-4.628406	1.990887	-2.637519	42501.628589
HLA B*3501	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.330049	1.692204	-2.637845	21382.041608
HLA B*0802	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.449805	1.811844	-2.637961	28171.162603
HLA A*8001	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.283203	1.645215	-2.637988	19195.648504
HLA B*3801	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.430748	1.792234	-2.638514	26961.751247
HLA A*2603	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.508699	1.870150	-2.638550	32262.596081
HLA A*3001	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.300375	1.661630	-2.638745	19969.867105
HLA A*0206	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.706007	1.067176	-2.638831	5081.678179
HLA B*1501	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.365449	1.726550	-2.638899	23197.910089
HLA B*5401	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.549999	1.911098	-2.638901	35481.221137
HLA B*4501	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.644622	2.005692	-2.638930	44118.599451
HLA B*2705	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.331198	1.692204	-2.638994	21438.681312
HLA A*0206	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.509280	1.870150	-2.639130	32305.735553
HLA A*2501	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.419863	1.780575	-2.639288	26294.379912
HLA A*3001	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.076441	1.437023	-2.639418	11924.524226
HLA B*1501	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.349698	1.710232	-2.639466	22371.644701
HLA A*6801	1:51-59	9	QRDSEESYL	1.503495	0.502197	-4.645160	2.005692	-2.639468	44173.290293
HLA B*5701	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.353314	1.713576	-2.639738	22558.684524
HLA B*3901	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.404295	1.764418	-2.639877	25368.526698
HLA B*5701	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.416139	1.775750	-2.640389	26069.878059
HLA A*6801	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.578089	1.937546	-2.640543	37852.014778
HLA B*5101	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.431312	1.790732	-2.640580	26996.780403
HLA B*2705	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.429862	1.789240	-2.640623	26906.818033
HLA A*6801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-3.954573	1.313812	-2.640761	9006.857115
HLA A*2403	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.405968	1.764802	-2.641166	25466.430665
HLA A*8001	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.406184	1.764802	-2.641383	25479.108712
HLA A*2501	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.388544	1.747156	-2.641388	24464.948080
HLA A*0211	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.503237	1.861442	-2.641795	31859.338797
HLA B*1502	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.135798	1.493912	-2.641887	13670.942269
HLA A*0202	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.196598	1.554677	-2.641921	15725.281271

HLA A*6801	1:432-440	9	LKDALIEGL	1.577897	0.430413	-4.650545	2.008310	-2.642234	44724.425329
HLA A*2601	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.359671	1.717294	-2.642377	22891.353775
HLA B*5801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.359838	1.717294	-2.642544	22900.148081
HLA A*3002	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.535011	1.892220	-2.642791	34277.662112
HLA A*3001	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.072080	1.429220	-2.642861	11805.392097
HLA B*3901	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.392416	1.749555	-2.642861	24684.040466
HLA A*6901	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.351373	1.708081	-2.643293	22458.104391
HLA A*0212	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.408193	1.764802	-2.643391	25597.234170
HLA A*0216	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.091553	1.448126	-2.643427	12346.758336
HLA B*5101	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.291647	1.648036	-2.643610	19572.524166
HLA A*0219	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.455585	1.811844	-2.643740	28548.579479
HLA B*1517	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.198450	1.554677	-2.643772	15792.461121
HLA B*1801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.496703	1.852707	-2.643996	31383.605828
HLA B*1501	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.294567	1.650564	-2.644003	19704.582969
HLA B*1801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-2.801972	0.157454	-2.644518	633.829311
HLA A*2902	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.425147	1.780575	-2.644572	26616.253565
HLA B*5701	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.388406	1.743756	-2.644650	24457.140519
HLA B*4402	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.230222	1.585411	-2.644811	16991.115890
HLA B*5101	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.473934	1.828963	-2.644971	29780.636889
HLA A*3201	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.181759	1.536595	-2.645164	15197.042392
HLA A*2402	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.218580	1.573351	-2.645229	16541.702425
HLA B*0702	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.409788	1.764418	-2.645370	25691.433774
HLA A*6801	1:472-480	9	GRDRSMQRL	1.664791	0.372557	-4.682954	2.037348	-2.645605	48189.627035
HLA B*4402	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.426181	1.780575	-2.645606	26679.685061
HLA B*0801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.162874	1.517234	-2.645639	14550.365892
HLA B*3901	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.475193	1.828963	-2.646231	29867.117142
HLA A*0250	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.463888	1.817618	-2.646269	29099.637805
HLA B*4801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.354355	1.708081	-2.646274	22612.813072
HLA A*3301	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.546900	1.900474	-2.646426	35228.940944
HLA A*6901	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.356676	1.710232	-2.646444	22734.001476
HLA B*5101	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.411370	1.764802	-2.646568	25785.143056
HLA A*1101	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.438992	1.792234	-2.646759	27478.463219
HLA A*6801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.352651	1.705831	-2.646820	22524.295487
HLA A*2301	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.517160	1.870150	-2.647010	32897.265997
HLA A*6901	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.232524	1.585411	-2.647113	17081.436758
HLA B*1801	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.373869	1.726550	-2.647319	23652.084130
HLA A*2902	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.394759	1.747156	-2.647603	24817.537470
HLA A*0201	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.397315	1.749555	-2.647760	24964.043228
HLA B*1502	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.502565	1.854767	-2.647798	31810.083241
HLA B*0702	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.438541	1.790732	-2.647809	27449.936193
HLA A*0212	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.428429	1.780575	-2.647855	26818.171012
HLA A*2402	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.437350	1.789240	-2.648110	27374.749288
HLA A*0101	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.361354	1.713159	-2.648195	22980.194941
HLA A*1101	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.420138	1.771882	-2.648255	26311.028393
HLA A*0219	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.428880	1.780575	-2.648306	26846.041484
HLA A*0301	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.361504	1.713159	-2.648345	22988.152819
HLA A*6801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-3.757931	1.109528	-2.648403	5727.047385
HLA B*0803	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.466169	1.817618	-2.648551	29252.900463
HLA B*1509	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.356763	1.708081	-2.648682	22738.552503
HLA A*6802	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.429284	1.780575	-2.648710	26871.033376
HLA B*0801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.413357	1.764418	-2.648939	25903.426098
HLA A*3301	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.291384	1.642298	-2.649086	19560.668618
HLA B*0802	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.341341	1.692204	-2.649137	21945.263267
HLA B*0802	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.362637	1.713159	-2.649478	23048.174178
HLA B*0803	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.306714	1.657009	-2.649705	20263.482482
HLA A*2403	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.363027	1.713159	-2.649868	23068.881694
HLA A*2603	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.542264	1.892220	-2.650044	34854.917062
HLA A*2402	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.422086	1.771882	-2.650203	26429.293041
HLA A*0301	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.367516	1.717294	-2.650222	23308.611736
HLA B*4601	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.414896	1.764418	-2.650478	25995.377120
HLA A*6801	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.542866	1.892220	-2.650646	34903.222181
HLA A*2602	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.441462	1.790732	-2.650730	27635.145095
HLA B*1501	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.364312	1.713576	-2.650736	23137.248451
HLA B*5801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.342950	1.692204	-2.650746	22026.738326
HLA A*3201	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.892613	1.241782	-2.650831	7809.309850

HLA A*3201	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.543084	1.892220	-2.650864	34920.787097
HLA A*3001	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.260876	1.609455	-2.651420	18233.734757
HLA B*1509	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.280943	1.629468	-2.651475	19096.007840
HLA A*2603	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.260838	1.609246	-2.651592	18232.156545
HLA A*3002	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.071662	1.419915	-2.651747	11794.029446
HLA A*0216	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.395536	1.743756	-2.651780	24862.017384
HLA B*5701	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.416266	1.764418	-2.651848	26077.495070
HLA B*5801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.340678	1.688566	-2.652112	21911.809346
HLA B*3801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.427924	1.775750	-2.652174	26786.996229
HLA B*0801	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.378961	1.726550	-2.652411	23930.994618
HLA A*0216	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.037139	1.384650	-2.652489	10892.783581
HLA B*5101	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.441807	1.789240	-2.652567	27657.130787
HLA B*3501	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-3.653275	1.000328	-2.652947	4500.650786
HLA A*0206	1:366-374	9	AELVQTRIV	1.123749	0.213984	-3.990915	1.337733	-2.653182	9792.985403
HLA A*0216	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.402745	1.749555	-2.653189	25278.109208
HLA A*0216	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.433913	1.780575	-2.653338	27158.942387
HLA A*0301	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.367899	1.714405	-2.653495	23329.174613
HLA B*4801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.370879	1.717294	-2.653584	23489.756818
HLA B*5701	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.304402	1.650564	-2.653838	20155.899862
HLA A*6802	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.102107	1.448126	-2.653981	12650.475049
HLA A*0202	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.334156	1.679828	-2.654328	21585.199657
HLA B*4402	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.371720	1.717294	-2.654425	23535.294460
HLA A*0101	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.368022	1.713576	-2.654445	23335.738365
HLA B*4402	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.426481	1.771882	-2.654599	26698.166229
HLA A*6802	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.209347	1.554677	-2.654669	16193.723805
HLA B*4403	1:150-158	9	EGRQPVVRL	1.670340	0.299893	-4.624921	1.970233	-2.654689	42162.007922
HLA A*2402	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.369152	1.714405	-2.654747	23396.540687
HLA B*0801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.300126	1.645215	-2.654911	19958.418703
HLA B*1502	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.528517	1.873578	-2.654939	33768.923553
HLA B*4601	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.343582	1.688566	-2.655016	22058.816296
HLA B*1502	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.501966	1.846931	-2.655035	31766.230795
HLA B*5801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.363271	1.708081	-2.655190	23081.864556
HLA B*2705	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.420185	1.764802	-2.655383	26313.875342
HLA A*2402	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.420441	1.764802	-2.655639	26329.396629
HLA B*5701	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.300993	1.645215	-2.655778	19998.300472
HLA A*1101	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.445146	1.789240	-2.655906	27870.562989
HLA A*2603	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.427893	1.771882	-2.656011	26785.112404
HLA A*2402	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.400092	1.743756	-2.656336	25124.187000
HLA A*0203	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.369525	1.713159	-2.656366	23416.674403
HLA A*8001	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.370867	1.714405	-2.656462	23489.121442
HLA A*6802	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.420948	1.764418	-2.656530	26360.181461
HLA B*0802	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.345189	1.688566	-2.656623	22140.593158
HLA A*2601	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.286121	1.629468	-2.656653	19325.059923
HLA A*0203	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.366903	1.710050	-2.656853	23275.723642
HLA B*4601	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.367234	1.710232	-2.657003	23293.485006
HLA A*0216	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.468970	1.811844	-2.657125	29442.149902
HLA B*5801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.362965	1.705831	-2.657134	23065.637120
HLA B*1502	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.374476	1.717294	-2.657181	23685.119608
HLA A*2403	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.437825	1.780575	-2.657250	27404.680700
HLA B*1517	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.433274	1.775750	-2.657524	27119.007668
HLA A*8001	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.349935	1.692204	-2.657731	22383.871881
HLA A*2902	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.370996	1.713159	-2.657837	23496.111527
HLA B*1501	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.720052	1.062125	-2.657927	5248.707598
HLA B*1517	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.407568	1.749555	-2.658013	25560.425460
HLA A*0201	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.366128	1.708081	-2.658047	23234.207414
HLA B*4501	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.494046	1.835915	-2.658131	31192.168839
HLA B*1503	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.087390	1.429220	-2.658170	12228.963826
HLA A*2402	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.448926	1.790732	-2.658194	28114.221555
HLA A*0101	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.308897	1.650564	-2.658332	20365.578771
HLA A*2902	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.434477	1.775750	-2.658727	27194.227737
HLA A*0101	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.366842	1.708081	-2.658762	23272.449976
HLA B*1501	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.423378	1.764418	-2.658960	26508.048900
HLA A*3001	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.259161	1.600184	-2.658976	18161.867746
HLA B*3801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.432503	1.773509	-2.658994	27070.929187
HLA A*2601	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.320649	1.661630	-2.659019	20924.200883

HLA B*2705	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.402893	1.743756	-2.659137	25286.726038
HLA A*8001	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.449901	1.790732	-2.659169	28177.411814
HLA A*2601	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.372941	1.713576	-2.659365	23601.595808
HLA B*1502	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.316443	1.657009	-2.659434	20722.555081
HLA A*0101	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.386169	1.726550	-2.659619	24331.504803
HLA A*0250	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.269113	1.609455	-2.659658	18582.875930
HLA B*1503	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.316824	1.657009	-2.659815	20740.724331
HLA A*0219	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.373096	1.713159	-2.659938	23610.024326
HLA A*2602	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.431859	1.771882	-2.659977	27030.831414
HLA B*5401	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.370373	1.710232	-2.660142	23462.451151
HLA A*2603	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.533764	1.873578	-2.660185	34179.335644
HLA A*2402	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.477806	1.817618	-2.660188	30047.333176
HLA B*1501	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.434524	0.774156	-2.660368	2719.719818
HLA B*1503	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.191129	1.530697	-2.660432	15528.475498
HLA B*5801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.188248	1.527790	-2.660458	15425.823308
HLA B*0702	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.410127	1.749555	-2.660571	25711.455816
HLA A*0201	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.353055	1.692204	-2.660851	22545.264120
HLA B*3901	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-3.541515	0.880484	-2.661031	3479.485363
HLA A*2902	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.309844	1.648791	-2.661053	20410.027943
HLA B*4402	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.408242	1.747156	-2.661086	25600.142377
HLA B*4402	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.387659	1.726550	-2.661108	24415.101977
HLA A*2602	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.534767	1.873578	-2.661189	34258.381948
HLA A*0250	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.715325	1.054023	-2.661302	5191.886806
HLA B*4801	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.371539	1.710232	-2.661307	23525.492605
HLA B*5101	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.353532	1.692204	-2.661328	22570.037098
HLA A*0219	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.046067	1.384650	-2.661417	11119.030413
HLA B*0802	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.425838	1.764418	-2.661419	26658.620597
HLA B*1501	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.306951	1.645215	-2.661736	20274.557450
HLA B*4801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.354098	1.692204	-2.661894	22599.482726
HLA A*6802	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.271249	1.609246	-2.662002	18674.483941
HLA A*2501	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.438029	1.775750	-2.662279	27417.582033
HLA A*2601	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.312856	1.650564	-2.662291	20552.073247
HLA B*3501	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.682686	1.020365	-2.662321	4815.996579
HLA A*3002	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.443088	1.780575	-2.662513	27738.795113
HLA B*4402	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.045982	1.383422	-2.662561	11116.865126
HLA A*0201	1:361-369	9	AFAAAAELV	0.982214	0.345272	-3.990126	1.327486	-2.662639	9775.200640
HLA A*0211	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.351281	1.688566	-2.662715	22453.366552
HLA A*0250	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.264367	1.601532	-2.662835	18380.908266
HLA B*3901	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.389578	1.726550	-2.663028	24523.252614
HLA A*0203	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.257004	1.593495	-2.663509	18071.894459
HLA B*1517	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.293042	1.629468	-2.663575	19635.521132
HLA A*0211	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.273232	1.609455	-2.663776	18759.945593
HLA B*5101	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.444580	1.780575	-2.664005	27834.249493
HLA A*0203	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.319939	1.655822	-2.664117	20890.043117
HLA A*1101	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.481800	1.817618	-2.664182	30324.947462
HLA B*0702	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.445209	1.780575	-2.664635	27874.634256
HLA A*0206	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.476493	1.811844	-2.664648	29956.603451
HLA B*0702	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.309865	1.645215	-2.664650	20411.021711
HLA A*0250	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.429456	1.764802	-2.664654	26881.647431
HLA B*3501	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-2.917788	0.252948	-2.664840	827.537785
HLA A*8001	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.353866	1.688566	-2.665300	22587.382158
HLA A*2902	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.357724	1.692204	-2.665520	22788.920543
HLA B*3501	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.430041	1.764418	-2.665623	26917.883088
HLA B*7301	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.317700	1.651959	-2.665741	20782.619059
HLA A*3101	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.159660	1.493912	-2.665748	14443.080073
HLA B*3801	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.494854	1.828963	-2.665891	31250.271571
HLA B*5401	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.050597	1.384650	-2.665947	11235.611791
HLA A*0250	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.119092	0.452989	-2.666102	1315.502590
HLA A*2301	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.064238	1.398016	-2.666222	11594.121177
HLA A*2602	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.410089	1.743756	-2.666333	25709.230374
HLA B*1517	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.446917	1.780575	-2.666343	27984.480769
HLA A*3002	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.539938	1.873578	-2.666360	34668.740444
HLA B*4002	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.558229	1.891829	-2.666399	36160.031843
HLA B*5301	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.455913	1.789240	-2.666674	28570.209920
HLA B*5701	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.416527	1.749555	-2.666971	26093.159248

HLA A*8001	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.447561	1.780575	-2.666986	28025.993193
HLA A*0202	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.126927	1.459786	-2.667140	13394.508863
HLA B*4601	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.375458	1.708081	-2.667377	23738.740171
HLA B*5401	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.503380	1.835915	-2.667465	31869.854217
HLA A*0201	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.377575	1.710050	-2.667525	23854.732614
HLA A*6801	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.578667	1.911098	-2.667569	37902.423013
HLA B*4001	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.222278	1.554677	-2.667601	16683.159168
HLA A*0101	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.377997	1.710232	-2.667766	23877.973191
HLA B*4001	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.311192	1.643417	-2.667775	20473.505227
HLA B*3901	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.448538	1.780575	-2.667964	28089.137107
HLA B*3801	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.444011	1.776041	-2.667970	27797.832927
HLA B*0803	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.479897	1.811844	-2.668053	30192.353958
HLA B*0802	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.378136	1.710050	-2.668086	23885.595861
HLA B*3801	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.541672	1.873578	-2.668094	34807.432006
HLA B*4002	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.605717	1.937546	-2.668171	40338.207450
HLA B*1801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.480202	1.811844	-2.668358	30213.595274
HLA B*1509	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.223115	1.554677	-2.668437	16715.320568
HLA A*0212	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-3.831080	1.162401	-2.668679	6777.657873
HLA A*0301	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.360900	1.692204	-2.668696	22956.213644
HLA A*1101	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.433530	1.764802	-2.668728	27135.003864
HLA A*0212	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.433328	1.764418	-2.668910	27122.382227
HLA A*0250	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.268558	1.599646	-2.668913	18559.165683
HLA A*1101	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.444723	1.775750	-2.668973	27843.436401
HLA B*5401	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.517625	1.848352	-2.669273	32932.523048
HLA A*0203	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.449880	1.780575	-2.669305	28176.039917
HLA A*2301	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.458695	1.789240	-2.669455	28753.798278
HLA A*6801	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.434275	1.764802	-2.669473	27181.578553
HLA B*5701	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.382722	1.713159	-2.669563	24139.166739
HLA A*3201	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.067753	1.398016	-2.669737	11688.335383
HLA B*4801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.379849	1.710050	-2.669799	23979.982092
HLA A*0206	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.320400	1.650564	-2.669836	20912.205377
HLA B*5401	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.498874	1.828963	-2.669911	31540.876988
HLA A*2601	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.327025	1.657009	-2.670017	21233.685625
HLA B*4402	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.419623	1.749555	-2.670068	26279.874447
HLA A*0212	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.419654	1.749555	-2.670098	26281.722738
HLA A*6802	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.397019	1.726550	-2.670469	24947.032385
HLA A*2301	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.488256	1.817618	-2.670638	30779.137227
HLA A*2301	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.315854	1.645215	-2.670638	20694.435389
HLA B*5801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.350508	1.679828	-2.670681	22413.438392
HLA A*0202	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.414530	1.743756	-2.670774	25973.447766
HLA A*2402	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.362984	1.692204	-2.670780	23066.635402
HLA A*3201	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.198610	1.527790	-2.670820	15798.271801
HLA B*3501	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.300300	1.629468	-2.670832	19966.410292
HLA B*1501	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.280341	1.609455	-2.670886	19069.579480
HLA B*0702	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.130733	1.459786	-2.670947	13512.414521
HLA B*3501	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.379095	1.708081	-2.671014	23938.375206
HLA A*2403	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.271307	1.600184	-2.671123	18677.009784
HLA A*0203	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-2.837426	0.166266	-2.671160	687.742792
HLA A*0201	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.398203	1.726550	-2.671653	25015.145384
HLA A*6901	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.327747	1.655822	-2.671925	21268.980595
HLA A*3201	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.855796	1.183813	-2.671983	7174.575740
HLA B*4001	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.382067	1.710050	-2.672017	24102.759551
HLA B*4001	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.317376	1.645215	-2.672161	20767.109279
HLA A*2402	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.070300	1.398016	-2.672284	11757.080896
HLA A*0301	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.316164	1.643417	-2.672747	20709.218674
HLA B*4601	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.365073	1.692204	-2.672869	23177.839077
HLA A*0201	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.282423	1.609455	-2.672968	19161.202466
HLA A*2603	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.526055	1.852707	-2.673348	33578.010195
HLA B*1502	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.361936	1.688566	-2.673370	23011.047069
HLA A*2902	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.437804	1.764418	-2.673385	27403.346426
HLA A*6802	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.381829	1.708081	-2.673749	24089.593430
HLA A*2602	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.438050	1.764296	-2.673754	27418.917000
HLA A*2603	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.522209	1.848352	-2.673857	33281.956580
HLA B*5101	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.445787	1.771882	-2.673905	27911.755427
HLA B*5401	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.565757	1.891829	-2.673927	36792.267505

HLA A*0201	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.387656	1.713576	-2.674080	24414.969894
HLA A*0101	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.380032	1.705831	-2.674201	23990.103092
HLA A*6802	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.072499	1.398016	-2.674483	11816.765696
HLA B*1501	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.168513	1.493912	-2.674601	14740.515728
HLA B*0801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.322832	1.648036	-2.674795	21029.626161
HLA A*2403	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.385069	1.710232	-2.674838	24269.979534
HLA A*0301	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.276403	1.601532	-2.674871	18897.457586
HLA B*0801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.354733	1.679828	-2.674905	22632.517235
HLA A*2501	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.439213	1.764296	-2.674917	27492.440384
HLA A*8001	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.424827	1.749555	-2.675272	26596.677994
HLA A*8001	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.385509	1.710232	-2.675277	24294.544665
HLA A*2601	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.385466	1.710050	-2.675417	24292.179025
HLA A*0101	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.385624	1.710050	-2.675574	24300.985627
HLA A*2601	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.386063	1.710232	-2.675832	24325.582141
HLA A*0101	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.355696	1.679828	-2.675869	22682.773107
HLA B*5101	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.468143	1.792234	-2.675909	29386.137124
HLA B*1517	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.389557	1.713576	-2.675981	24522.058630
HLA A*2601	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.368242	1.692204	-2.676038	23347.608296
HLA B*4001	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.389627	1.713576	-2.676051	24526.038802
HLA B*5301	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.519852	1.843794	-2.676058	33101.853801
HLA B*3801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.493698	1.817618	-2.676080	31167.204400
HLA B*5101	1:412-420	9	AALAALTSV	1.136579	0.168474	-3.981165	1.305053	-2.676112	9575.572403
HLA B*1509	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.403031	1.726550	-2.676481	25294.798431
HLA A*2602	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.249943	1.573351	-2.676592	17780.479927
HLA A*2601	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.321868	1.645215	-2.676653	20983.032995
HLA A*6901	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.286210	1.609455	-2.676755	19329.033095
HLA A*1101	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.423986	1.747156	-2.676830	26545.216985
HLA A*3101	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.391288	1.714405	-2.676884	24620.025415
HLA A*0219	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.426446	1.749555	-2.676891	26695.999805
HLA A*0301	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.365517	1.688566	-2.676951	23201.549820
HLA B*5801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.332883	1.655822	-2.677061	21522.001099
HLA A*2402	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.322284	1.645215	-2.677069	21003.134929
HLA A*2601	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.385349	1.708081	-2.677268	24285.609014
HLA A*3001	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.232003	1.554677	-2.677325	17060.934345
HLA B*5401	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.538965	1.861442	-2.677523	34591.179958
HLA A*8001	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.357395	1.679828	-2.677567	22771.667103
HLA B*5401	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.530279	1.852707	-2.677572	33906.216492
HLA A*2402	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.234583	1.556999	-2.677584	17162.578878
HLA B*4001	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.387844	1.710232	-2.677613	24425.538763
HLA A*6802	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.394994	1.717294	-2.677699	24830.967115
HLA A*0203	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.442176	1.764418	-2.677758	27680.631422
HLA B*1509	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.369993	1.692204	-2.677789	23441.897618
HLA A*3101	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.395144	1.717294	-2.677850	24839.565901
HLA B*5101	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.490070	1.811844	-2.678226	30907.953083
HLA A*0206	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-3.665192	0.986777	-2.678415	4625.853817
HLA B*4601	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.395849	1.717294	-2.678554	24879.912422
HLA A*0202	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.329154	1.650564	-2.678590	21338.015022
HLA B*1509	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.288045	1.609455	-2.678590	19410.873417
HLA B*1502	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.549016	1.870150	-2.678867	35401.076908
HLA A*6802	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.746310	1.067176	-2.679134	5575.838979
HLA A*2403	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.389195	1.710050	-2.679145	24501.637249
HLA A*0201	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.389458	1.710232	-2.679227	24516.487475
HLA B*1801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.387355	1.708081	-2.679275	24398.069214
HLA A*2603	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.531997	1.852642	-2.679354	34040.568478
HLA B*5401	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.549526	1.870150	-2.679377	35442.660262
HLA B*0803	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.423138	1.743756	-2.679382	26493.425563
HLA A*3201	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.393861	1.714405	-2.679457	24766.303060
HLA A*0203	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.207392	1.527790	-2.679602	16120.999195
HLA A*0203	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.396941	1.717294	-2.679647	24942.579080
HLA A*3002	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.330286	1.650564	-2.679722	21393.727923
HLA A*3002	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.109630	1.429823	-2.679807	12871.521468
HLA B*2705	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-3.993767	1.313812	-2.679956	9857.513533
HLA A*2603	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.328087	1.648036	-2.680051	21285.671251
HLA A*0202	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.109442	1.429220	-2.680222	12865.951993
HLA B*1509	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.492422	1.811844	-2.680578	31075.782906

HLA A*0101	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.397912	1.717294	-2.680617	24998.370195
HLA B*3801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.398302	1.717294	-2.681007	25020.829854
HLA B*4801	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.407596	1.726550	-2.681046	25562.084862
HLA B*0801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.394667	1.713576	-2.681091	24812.301877
HLA B*4001	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.389221	1.708081	-2.681140	24503.095355
HLA A*0201	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.266740	1.585411	-2.681329	18481.616211
HLA B*0803	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.431150	1.749555	-2.681594	26986.704862
HLA B*1502	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.470847	1.789240	-2.681607	29569.689082
HLA A*0212	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.425396	1.743756	-2.681640	26631.520986
HLA B*2705	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.199249	1.517234	-2.682014	15821.535910
HLA A*2301	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.543869	1.861442	-2.682427	34983.942612
HLA B*4002	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.535202	1.852642	-2.682559	34292.685910
HLA A*0219	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.426322	1.743756	-2.682566	26688.346515
HLA A*6901	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.283043	1.600184	-2.682859	19188.588252
HLA B*7301	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.594073	1.911098	-2.682975	39271.053090
HLA A*2601	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.396208	1.713159	-2.683049	24900.514375
HLA B*0801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.393154	1.710050	-2.683104	24726.007008
HLA B*0801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.389038	1.705831	-2.683206	24492.757932
HLA A*3101	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.371926	1.688566	-2.683360	23546.501581
HLA B*7301	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.519387	1.835915	-2.683472	33066.415467
HLA A*0201	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.400933	1.717294	-2.683639	25172.893176
HLA A*0211	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.006666	1.322784	-2.683882	10154.675614
HLA B*1517	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.401295	1.717294	-2.684000	25193.874029
HLA A*2603	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.584644	1.900474	-2.684170	38427.671028
HLA A*8001	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.397397	1.713159	-2.684238	24968.770520
HLA A*0201	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.372883	1.688566	-2.684316	23598.403973
HLA A*2403	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.398086	1.713576	-2.684509	25008.379840
HLA A*2402	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.460779	1.776041	-2.684739	28892.107016
HLA B*1503	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.294212	1.609246	-2.684966	19688.493001
HLA A*0219	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.013879	1.328755	-2.685124	10324.736425
HLA A*6901	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.390969	1.705831	-2.685138	24601.918018
HLA A*0219	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.449575	1.764418	-2.685156	28156.231081
HLA A*0216	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.346888	1.661630	-2.685258	22227.362346
HLA A*3101	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.377535	1.692204	-2.685330	23852.538840
HLA B*4801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.391331	1.705831	-2.685500	24622.422980
HLA B*3801	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.476314	1.790732	-2.685582	29944.289278
HLA B*4601	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.395682	1.710050	-2.685632	24870.357830
HLA A*6802	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.399230	1.713576	-2.685654	25074.354189
HLA B*7301	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.538413	1.852707	-2.685706	34547.231305
HLA B*1503	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.115616	1.429823	-2.685794	13050.176131
HLA A*0101	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.374398	1.688566	-2.685832	23680.891568
HLA A*0212	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.374398	1.688566	-2.685832	23680.891568
HLA A*3002	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.429653	1.743756	-2.685897	26893.866053
HLA B*2705	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.105866	1.419915	-2.685951	12760.450595
HLA B*4801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.399657	1.713576	-2.686081	25099.054551
HLA A*2601	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.392073	1.705831	-2.686242	24664.551627
HLA A*3201	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.803379	1.117129	-2.686250	6358.859281
HLA B*0803	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.450730	1.764418	-2.686312	28231.273373
HLA B*3801	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.498214	1.811844	-2.686369	31492.965641
HLA B*1501	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.803675	1.117129	-2.686546	6363.195249
HLA B*1501	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.392409	1.705831	-2.686578	24683.639856
HLA B*5701	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.403905	1.717294	-2.686611	25345.754932
HLA A*0216	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.375190	1.688566	-2.686624	23724.104354
HLA B*5101	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.462732	1.776041	-2.686691	29022.287290
HLA A*0211	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.654271	0.967578	-2.686693	4510.986196
HLA B*5301	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.399859	1.713159	-2.686700	25110.734615
HLA A*0202	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.557136	1.870150	-2.686987	36069.182042
HLA A*2403	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.073744	1.386690	-2.687054	11850.695834
HLA A*0203	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-3.746855	1.059725	-2.687130	5582.841577
HLA A*0250	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.400740	1.713159	-2.687582	25161.728683
HLA B*7301	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.579821	1.892220	-2.687601	38003.235368
HLA B*3901	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.108060	1.420375	-2.687685	12825.090234
HLA B*4601	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.401483	1.713576	-2.687907	25204.780074
HLA B*3501	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.013174	1.325261	-2.687913	10307.993312
HLA A*0301	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.368224	1.679828	-2.688396	23346.597854

HLA B*5801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.338984	1.650564	-2.688420	21826.508143
HLA A*0219	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.345544	1.657009	-2.688535	22158.687049
HLA B*5801	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.345638	1.657009	-2.688629	22163.482609
HLA A*2601	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.679308	0.990658	-2.688650	4778.676269
HLA B*7301	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.543519	1.854767	-2.688752	34955.754346
HLA B*1501	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.406208	1.717294	-2.688913	25480.487141
HLA A*2603	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.243832	1.554677	-2.689155	17532.040640
HLA B*4001	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.369114	1.679828	-2.689286	23394.515611
HLA A*0201	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.395160	1.705831	-2.689329	24840.506574
HLA B*4403	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.589818	1.900474	-2.689344	38888.181060
HLA B*7301	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.581399	1.891829	-2.689570	38141.645498
HLA A*3201	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.518595	1.828963	-2.689633	33006.185926
HLA B*0803	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.381900	1.692204	-2.689696	24093.503408
HLA B*1501	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-3.794404	1.104589	-2.689815	6228.797063
HLA B*4403	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.600942	1.911098	-2.689845	39897.202184
HLA A*0219	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.369847	1.679828	-2.690019	23434.036217
HLA A*1101	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.433779	1.743756	-2.690023	27150.568847
HLA A*2902	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-3.997978	1.307776	-2.690202	9953.542132
HLA B*5801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.351836	1.661630	-2.690206	22482.051833
HLA A*8001	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.454696	1.764418	-2.690278	28490.259052
HLA A*3101	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.838791	1.148177	-2.690613	6899.071601
HLA B*0702	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.404417	1.713576	-2.690841	25375.664230
HLA A*0211	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.088992	1.398016	-2.690976	12274.166468
HLA A*0219	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.408419	1.717294	-2.691124	25610.531530
HLA B*0801	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.348514	1.657009	-2.691505	22310.729613
HLA A*3001	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.121368	1.429823	-2.691545	13224.154436
HLA B*5101	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.455881	1.764296	-2.691584	28568.046138
HLA A*6901	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.353297	1.661630	-2.691667	22557.830260
HLA B*4001	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.418364	1.726550	-2.691814	26203.781057
HLA B*1501	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.340624	1.648791	-2.691833	21909.083085
HLA B*0702	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.348847	1.657009	-2.691839	22327.875395
HLA B*3501	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.401941	1.710050	-2.691891	25231.383342
HLA B*3501	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.405580	1.713576	-2.692004	25443.708665
HLA A*0250	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.140657	1.448126	-2.692531	13824.746747
HLA A*0201	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.152372	1.459786	-2.692585	14202.726256
HLA B*7301	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-3.640170	0.947523	-2.692647	4366.866237
HLA B*2705	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.249687	1.556999	-2.692689	17769.998261
HLA A*0216	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.340753	1.648036	-2.692717	21915.602969
HLA B*5301	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.468518	1.775750	-2.692768	29411.584255
HLA A*3001	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.084749	1.391860	-2.692889	12154.828603
HLA A*8001	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.343563	1.650564	-2.692999	22057.861631
HLA B*0802	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.419572	1.726550	-2.693021	26276.746866
HLA A*0203	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.419593	1.726550	-2.693043	26278.026286
HLA A*6801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.485587	1.792274	-2.693313	30590.559970
HLA B*5101	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.407892	1.714405	-2.693488	25579.515096
HLA A*8001	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.410799	1.717294	-2.693504	25751.268099
HLA A*2602	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.564011	1.870150	-2.693861	36644.676058
HLA B*5301	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.437888	1.743756	-2.694132	27408.683912
HLA A*2403	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.443809	1.749555	-2.694253	27784.902980
HLA A*2403	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.458738	1.764418	-2.694319	28756.598401
HLA B*5401	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.441575	1.747156	-2.694419	27642.322174
HLA A*0203	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.279923	1.585411	-2.694512	19051.225071
HLA B*4002	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-3.572984	0.878392	-2.694592	3740.968196
HLA B*4403	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.632151	1.937546	-2.694605	42869.720386
HLA A*2602	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.486894	1.792274	-2.694620	30682.711787
HLA B*5301	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.586488	1.891829	-2.694659	38591.211251
HLA B*1509	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.832024	1.137355	-2.694669	6792.413797
HLA A*8001	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.404829	1.710050	-2.694779	25399.699523
HLA A*2402	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.556232	1.861442	-2.694790	35994.135067
HLA A*2301	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.470746	1.775750	-2.694996	29562.811226
HLA A*2902	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.405247	1.710050	-2.695197	25424.170205
HLA A*6901	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.032604	1.337377	-2.695228	10779.642775
HLA A*2902	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.408973	1.713576	-2.695397	25643.250244
HLA A*3002	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.513018	1.817618	-2.695399	32584.995425
HLA A*2301	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.471516	1.776041	-2.695476	29615.315338

HLA A*0212	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.295162	1.599646	-2.695516	19731.571135
HLA B*5801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.212777	1.517234	-2.695543	16322.135389
HLA B*4402	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.405912	1.710050	-2.695862	25463.124386
HLA A*0101	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.325538	1.629468	-2.696070	21161.096082
HLA B*5401	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.232696	1.536595	-2.696101	17088.183924
HLA A*8001	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.404410	1.708081	-2.696330	25375.252394
HLA A*0216	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.405186	1.708081	-2.697105	25420.594366
HLA B*1509	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.477797	1.780575	-2.697222	30046.682972
HLA B*1503	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.881396	1.183813	-2.697583	7610.202504
HLA B*4501	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.598299	1.900474	-2.697825	39655.120231
HLA A*0219	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.386453	1.688566	-2.697887	24347.437338
HLA A*0211	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.509980	1.811844	-2.698136	32357.859150
HLA B*4801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.377997	1.679828	-2.698170	23877.973191
HLA A*2403	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.386916	1.688566	-2.698350	24373.399406
HLA B*0803	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.386923	1.688566	-2.698357	24373.794982
HLA A*3301	1:360-368	9	AAFAAAAEL	1.357907	0.478008	-4.534297	1.835915	-2.698382	34221.335184
HLA A*3201	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.545337	1.846931	-2.698406	35102.429845
HLA A*2602	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.083116	0.384545	-2.698572	1210.922623
HLA A*0301	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.343848	1.645215	-2.698633	22072.305358
HLA B*4002	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.474784	1.776041	-2.698744	29839.015834
HLA A*0212	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.412422	1.713576	-2.698846	25847.712503
HLA A*3001	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.083508	1.384650	-2.698858	12120.158829
HLA A*0219	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.298627	1.599646	-2.698982	19889.650780
HLA A*6801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.413505	1.714405	-2.699101	25912.256087
HLA A*3301	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.546218	1.846931	-2.699287	35173.714724
HLA A*0212	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.391585	1.692204	-2.699380	24636.813278
HLA B*4402	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.407620	1.708081	-2.699539	25563.467780
HLA B*4501	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-3.595003	0.895455	-2.699549	3935.531469
HLA A*0203	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-3.706533	1.006851	-2.699682	5087.839967
HLA A*0250	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.573263	1.873578	-2.699685	37433.734759
HLA B*3801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.446844	1.747156	-2.699689	27979.787981
HLA A*6801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.344957	1.645215	-2.699742	22128.738296
HLA A*3201	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.561231	1.861442	-2.699789	36410.902698
HLA B*0801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.230830	1.530697	-2.700134	17014.939871
HLA B*7301	1:406-414	9	GAAVLDAAL	1.592227	0.308247	-4.600785	1.900474	-2.700311	39882.743562
HLA A*0101	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.361997	1.661630	-2.700367	23014.283964
HLA B*3901	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.329887	1.629468	-2.700419	21374.061559
HLA B*5301	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.553290	1.852707	-2.700583	35751.164040
HLA B*4601	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.406480	1.705831	-2.700649	25496.482366
HLA A*6802	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-3.394668	0.693953	-2.700715	2481.232736
HLA B*5701	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.408839	1.708081	-2.700759	25635.344016
HLA A*8001	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.357773	1.657009	-2.700764	22791.509686
HLA B*5701	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.392975	1.692204	-2.700771	24715.842961
HLA A*2602	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.348967	1.648036	-2.700931	22334.036603
HLA B*5701	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.389604	1.688566	-2.701038	24524.712006
HLA B*7301	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.574910	1.873578	-2.701332	37575.965442
HLA B*2705	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.414508	1.713159	-2.701350	25972.183175
HLA A*3301	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.165834	1.464436	-2.701398	14649.886688
HLA A*3201	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.390053	1.688566	-2.701486	24550.066214
HLA A*0212	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.411553	1.710050	-2.701503	25796.025944
HLA B*4801	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.358518	1.657009	-2.701509	22830.629175
HLA B*5701	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.407545	1.705831	-2.701713	25559.042706
HLA A*0216	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.412018	1.710232	-2.701786	25823.672369
HLA A*0203	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.303359	1.601532	-2.701827	20107.543675
HLA A*3301	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.593657	1.891829	-2.701827	39233.467077
HLA B*4402	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.415624	1.713576	-2.702048	26039.009651
HLA A*2403	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.256726	1.554677	-2.702049	18060.361641
HLA A*0250	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.491337	1.789240	-2.702097	30998.210046
HLA A*2403	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.302163	1.599646	-2.702518	20052.251031
HLA A*3301	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.595099	1.892220	-2.702879	39364.004464
HLA B*5801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.351728	1.648791	-2.702937	22476.457760
HLA A*0301	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.354937	1.651959	-2.702978	22643.171970
HLA B*0801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-3.925473	1.222401	-2.703072	8423.111544
HLA A*0206	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.452857	1.749555	-2.703301	28369.831176
HLA A*2403	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.429862	1.726550	-2.703312	26906.818033

HLA A*0202	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.411419	1.708081	-2.703338	25788.072613
HLA A*2402	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.090420	1.386690	-2.703730	12314.605281
HLA A*0211	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.447540	1.743756	-2.703784	28024.628669
HLA A*3001	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.031359	1.327486	-2.703873	10748.779206
HLA A*6901	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.124286	1.420375	-2.703911	13313.307797
HLA B*0803	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.418395	1.714405	-2.703990	26205.623996
HLA A*6901	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.031519	1.327486	-2.704032	10752.734113
HLA B*5801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.356182	1.651959	-2.704223	22708.188572
HLA A*3301	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.516168	1.811844	-2.704324	32822.248085
HLA A*2602	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.469437	1.764802	-2.704635	29473.863444
HLA B*1501	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.366297	1.661630	-2.704667	23243.259179
HLA A*0250	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.448867	1.743756	-2.705111	28110.419441
HLA A*0212	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.431979	1.726550	-2.705429	27038.290367
HLA A*2601	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.394059	1.688566	-2.705492	24777.560185
HLA A*0301	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.263364	1.556999	-2.706365	18338.496955
HLA B*1801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.386343	1.679828	-2.706515	24341.247428
HLA B*5101	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.395330	1.688566	-2.706763	24850.184135
HLA B*4403	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.292204	1.585411	-2.706792	19597.635050
HLA A*0206	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.261484	1.554677	-2.706807	18259.301067
HLA A*6901	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.363844	1.657009	-2.706835	23112.353034
HLA B*5101	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.420063	1.713159	-2.706904	26306.473915
HLA A*2501	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.420702	1.713576	-2.707126	26345.212119
HLA B*7301	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.577288	1.870150	-2.707138	37782.250803
HLA B*4001	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.413061	1.705831	-2.707230	25885.775147
HLA B*0802	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.417577	1.710232	-2.707345	26156.334614
HLA B*0702	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.356218	1.648791	-2.707427	22710.031378
HLA B*4402	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.417685	1.710232	-2.707453	26162.844556
HLA A*0250	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.577929	1.870150	-2.707780	37838.092625
HLA A*0301	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.355856	1.648036	-2.707819	22691.119010
HLA B*5101	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.451586	1.743756	-2.707830	28286.921159
HLA A*3001	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.293543	1.585411	-2.708132	19658.160310
HLA B*1502	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.457861	1.749555	-2.708306	28698.629295
HLA B*3901	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.418568	1.710232	-2.708337	26216.117041
HLA A*2403	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.337840	1.629468	-2.708372	21769.079359
HLA B*1502	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.473236	1.764802	-2.708435	29732.825656
HLA A*3301	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.353669	1.645215	-2.708453	22577.120090
HLA A*0201	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.388354	1.679828	-2.708526	24454.229863
HLA B*0702	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-2.977432	0.268538	-2.708894	949.362032
HLA A*3101	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.357223	1.648036	-2.709187	22762.675848
HLA B*4002	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.562007	1.852707	-2.709300	36475.963809
HLA A*0203	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-3.664435	0.955018	-2.709417	4617.802667
HLA A*0301	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.351819	1.642298	-2.709522	22481.200471
HLA A*0202	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.570998	1.861442	-2.709556	37239.021019
HLA B*0803	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.423169	1.713576	-2.709593	26495.288873
HLA A*0219	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.847244	1.137355	-2.709889	7034.675994
HLA B*5801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.146968	1.437023	-2.709945	14027.100255
HLA B*3801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.423190	1.713159	-2.710031	26496.578933
HLA B*5801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.353471	1.643417	-2.710054	22566.862685
HLA B*5801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.352362	1.642298	-2.710065	22509.312438
HLA B*1801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.423310	1.713159	-2.710151	26503.890463
HLA B*1503	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.372086	1.661630	-2.710456	23555.165284
HLA B*0802	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.390504	1.679828	-2.710676	24575.579584
HLA B*4402	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.390544	1.679828	-2.710716	24577.839858
HLA B*4601	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.170632	1.459786	-2.710846	14812.621101
HLA B*0702	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.416924	1.705831	-2.711092	26117.026383
HLA A*0101	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.356366	1.645215	-2.711151	22717.772799
HLA B*0801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.372995	1.661630	-2.711365	23604.532677
HLA A*3201	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.159552	1.448126	-2.711426	14439.486289
HLA B*7301	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.475788	1.764296	-2.711491	29908.024312
HLA A*3301	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-3.896001	1.184382	-2.711619	7870.468989
HLA B*3801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.400193	1.688566	-2.711627	25130.032200
HLA B*4501	1:93-101	9	IYRDVLARL	1.447955	0.489591	-4.649328	1.937546	-2.711782	44599.268509
HLA A*0203	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-3.187175	0.475212	-2.711963	1538.774865
HLA A*2301	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.492551	1.780575	-2.711977	31085.030691
HLA A*0301	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.367930	1.655822	-2.712108	23330.815378

HLA A*3002	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.524124	1.811844	-2.712280	33429.022686
HLA B*1503	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.207730	1.495432	-2.712298	16133.562734
HLA A*8001	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.229895	1.517234	-2.712661	16978.343806
HLA A*3101	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.392945	1.679828	-2.713117	24714.104792
HLA B*3901	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.423608	1.710050	-2.713558	26522.106375
HLA A*0212	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.430866	1.717294	-2.713571	26969.045238
HLA B*1501	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.143434	1.429823	-2.713612	13913.432185
HLA A*3201	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.018677	1.305053	-2.713624	10439.426044
HLA B*5301	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.504426	1.790732	-2.713694	31946.670152
HLA A*2902	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-3.628874	0.915076	-2.713797	4254.745281
HLA B*0702	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.361856	1.648036	-2.713820	23006.814893
HLA B*0803	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.231357	1.517234	-2.714122	17035.571331
HLA A*0201	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.350013	0.635887	-2.714126	2238.789134
HLA A*0203	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.427809	1.713576	-2.714233	26779.896351
HLA B*1501	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.357799	1.643417	-2.714382	22792.866021
HLA A*0212	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.394214	1.679828	-2.714386	24786.408659
HLA B*5401	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.532171	1.817618	-2.714552	34054.198728
HLA A*2601	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.394383	1.679828	-2.714555	24796.065144
HLA A*6801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.366598	1.651959	-2.714638	23259.359916
HLA A*3301	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.042867	1.328104	-2.714763	11037.403499
HLA A*2403	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.432151	1.717294	-2.714856	27048.970489
HLA B*3801	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.324340	1.609455	-2.714885	21102.792167
HLA B*5301	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.490949	1.776041	-2.714908	30970.552407
HLA A*2603	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.495676	1.780575	-2.715101	31309.498802
HLA B*3801	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.507449	1.792274	-2.715175	32169.875852
HLA A*2402	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.462398	1.747156	-2.715242	29000.000807
HLA B*0803	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.495951	1.780575	-2.715376	31329.322643
HLA A*0212	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.324845	1.609455	-2.715390	21127.351657
HLA B*1502	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.052829	1.337377	-2.715452	11293.504674
HLA A*6801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-3.352800	0.637330	-2.715469	2253.199673
HLA B*4001	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.137302	1.421817	-2.715486	13718.357606
HLA A*2301	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.507769	1.792234	-2.715535	32193.553384
HLA A*3301	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.536609	0.821048	-2.715561	3440.402774
HLA B*4001	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.366231	1.650564	-2.715667	23239.738629
HLA A*0219	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.423836	1.708081	-2.715755	26536.027748
HLA A*2501	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.405106	1.688566	-2.716540	25415.919028
HLA B*4801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.045320	1.328755	-2.716565	11099.918292
HLA B*1509	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.422414	1.705831	-2.716583	26449.317760
HLA A*3201	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.565752	1.848352	-2.717400	36791.869423
HLA A*6901	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.366417	1.648791	-2.717626	23249.672980
HLA B*5401	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.508471	1.790732	-2.717740	32245.670427
HLA A*0206	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-3.959752	1.241782	-2.717970	9114.892229
HLA A*3201	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.147804	1.429823	-2.717982	14054.141367
HLA B*4601	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.375338	1.657009	-2.718329	23732.191453
HLA A*3301	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.491870	1.773509	-2.718361	31036.300622
HLA B*1509	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.047148	1.328755	-2.718393	11146.735123
HLA A*2603	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.275499	1.556999	-2.718500	18858.138784
HLA B*3801	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.482984	1.764418	-2.718566	30407.743807
HLA B*1503	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.866970	1.148177	-2.718793	7361.568801
HLA A*2301	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.530644	1.811844	-2.718799	33934.659890
HLA B*5401	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.562639	1.843794	-2.718845	36529.084469
HLA A*0203	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.429275	1.710232	-2.719043	26870.451905
HLA B*0702	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.429407	1.710232	-2.719175	26878.593643
HLA A*3301	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.580636	1.861442	-2.719194	38074.643243
HLA A*3201	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.432426	1.713159	-2.719267	27066.096744
HLA A*2501	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.483696	1.764418	-2.719278	30457.628946
HLA A*0219	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.046828	1.327486	-2.719342	11138.536985
HLA B*7301	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.361654	1.642298	-2.719357	22996.113452
HLA A*0250	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.469357	1.749555	-2.719802	29468.442631
HLA A*0203	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.319650	1.599646	-2.720005	20876.147164
HLA A*6801	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.593596	1.873578	-2.720017	39227.948999
HLA A*0101	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.376045	1.655822	-2.720223	23770.867880
HLA B*3501	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.329542	1.609246	-2.720296	21357.070514
HLA A*0301	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.320487	1.600184	-2.720302	20916.391706
HLA B*5701	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.400174	1.679828	-2.720347	25128.944618

HLA A*2301	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.277494	1.556999	-2.720495	18944.953355
HLA A*2602	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.568987	1.848352	-2.720635	37066.970814
HLA B*4801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.150060	1.429220	-2.720840	14127.321325
HLA A*0203	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-3.673255	0.952354	-2.720901	4712.543119
HLA A*0206	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.438269	1.717294	-2.720974	27432.715468
HLA A*0206	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.431300	1.710050	-2.721250	26996.050165
HLA B*4001	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.378439	1.657009	-2.721430	23902.270856
HLA A*3002	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.513680	1.792234	-2.721446	32634.744666
HLA A*0203	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.427562	1.705831	-2.721731	26764.688662
HLA A*6901	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.636199	0.914377	-2.721823	4327.123191
HLA A*0201	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.377751	1.655822	-2.721929	23864.413437
HLA B*1503	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.322355	1.600184	-2.722170	21006.543945
HLA B*0702	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.448992	1.726550	-2.722442	28118.480532
HLA B*1503	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.142861	1.420375	-2.722486	13895.078390
HLA A*2501	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.384158	1.661630	-2.722528	24219.089378
HLA B*4001	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.371543	1.648791	-2.722753	23525.747147
HLA A*3002	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.436385	1.713576	-2.722808	27313.950124
HLA A*2603	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.466575	1.743756	-2.722819	29280.291385
HLA B*0802	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.373613	1.650564	-2.723049	23638.141129
HLA B*2705	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.411809	1.688566	-2.723243	25811.241777
HLA A*6901	1:201-209	9	PCDDALMKI	1.248268	0.016287	-3.987814	1.264555	-2.723258	9723.302270
HLA B*4601	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.403137	1.679828	-2.723309	25300.957073
HLA B*0801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.316981	1.593495	-2.723487	20748.243430
HLA A*3002	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.514275	1.790732	-2.723543	32679.442487
HLA A*3001	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.260349	1.536595	-2.723754	18211.652223
HLA A*6802	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.434033	1.710232	-2.723801	27166.436691
HLA B*1517	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.380941	1.657009	-2.723933	24040.382037
HLA B*1517	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.061353	1.337377	-2.723976	11517.352725
HLA B*1801	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.381125	1.657009	-2.724116	24050.528530
HLA A*0212	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.434399	1.710232	-2.724168	27189.373285
HLA A*2902	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.218157	1.493912	-2.724246	16525.602286
HLA B*0803	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.430116	1.705831	-2.724285	26922.543420
HLA A*3101	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.107910	1.383422	-2.724488	12820.650534
HLA A*3002	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.489304	1.764802	-2.724503	30853.491119
HLA A*2501	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.442108	1.717294	-2.724813	27676.289037
HLA A*8001	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.431171	1.705831	-2.725340	26988.018850
HLA A*0216	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.489762	1.764418	-2.725344	30886.056517
HLA B*1517	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.431216	1.705831	-2.725384	26990.793034
HLA A*2501	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.452002	1.726550	-2.725451	28314.020284
HLA B*2705	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-3.651335	0.925719	-2.725616	4480.584187
HLA B*4601	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.370841	1.645215	-2.725626	23487.723675
HLA B*5801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.863075	1.137355	-2.725720	7295.833751
HLA B*1801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.469477	1.743756	-2.725721	29476.574224
HLA A*0250	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.693348	0.967578	-2.725770	4935.692931
HLA A*0206	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.433918	1.708081	-2.725837	27159.236243
HLA A*0250	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.374633	1.648791	-2.725842	23693.706134
HLA A*0201	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-3.793121	1.067176	-2.725945	6210.425592
HLA A*2402	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.289889	1.563919	-2.725970	19493.482081
HLA A*6801	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.515264	1.789240	-2.726024	32753.956810
HLA A*2602	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.452744	1.726550	-2.726194	28362.465205
HLA B*3801	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.475774	1.749555	-2.726218	29907.053533
HLA A*2501	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.434352	1.708081	-2.726272	27186.431614
HLA A*0201	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-3.830915	1.104589	-2.726326	6775.091713
HLA A*0202	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.174504	1.448126	-2.726378	14945.273437
HLA B*1502	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-3.831178	1.104589	-2.726589	6779.198036
HLA B*0803	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.436645	1.710050	-2.726596	27330.357014
HLA A*2902	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.453212	1.726550	-2.726661	28393.015768
HLA B*5101	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.371877	1.645215	-2.726662	23543.826670
HLA B*5101	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.476453	1.749555	-2.726897	29953.848526
HLA A*0216	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.406854	1.679828	-2.727026	25518.423171
HLA B*7301	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-3.789719	1.062587	-2.727133	6161.966154
HLA A*0250	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.320649	1.593495	-2.727154	20924.200883
HLA B*1501	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.326805	1.599646	-2.727159	21222.890413
HLA A*2301	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.474319	1.747156	-2.727163	29807.070645
HLA A*2602	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.507828	1.780575	-2.727253	32197.907767

HLA A*1101	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.300709	1.573351	-2.727358	19985.213936
HLA A*0203	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.407213	1.679828	-2.727386	25539.553847
HLA A*0211	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.419635	1.692204	-2.727431	26280.585312
HLA A*0206	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.125527	1.398016	-2.727511	13351.390580
HLA B*0802	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.371116	1.643417	-2.727699	23502.595100
HLA B*3801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.376562	1.648791	-2.727771	23799.176230
HLA A*0250	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.503617	1.775750	-2.727867	31887.272626
HLA B*1501	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.282632	1.554677	-2.727954	19170.430425
HLA A*3101	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.337565	1.609455	-2.728110	21755.304827
HLA B*5301	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.598356	1.870150	-2.728206	39660.269281
HLA A*3001	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.292251	1.563919	-2.728331	19599.755585
HLA B*4501	1:375-383	9	VLGDAWELL	1.509402	0.401696	-4.639566	1.911098	-2.728468	43607.945429
HLA A*2601	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.384451	1.655822	-2.728629	24235.472741
HLA A*0101	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.377521	1.648791	-2.728730	23851.764615
HLA A*6901	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.380819	1.651959	-2.728860	24033.620086
HLA B*0802	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.434698	1.705831	-2.728866	27208.060323
HLA A*0250	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.590468	1.861442	-2.729026	38946.500213
HLA A*0201	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.113746	1.384650	-2.729096	12994.099354
HLA B*1517	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.417676	1.688566	-2.729109	26162.278410
HLA A*2403	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.330888	1.601532	-2.729356	21423.377299
HLA A*0201	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-3.454509	0.725139	-2.729370	2847.796063
HLA A*2902	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.329326	1.599646	-2.729680	21346.443536
HLA B*5101	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.456289	1.726550	-2.729739	28594.950493
HLA A*6901	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.377835	1.648036	-2.729799	23869.061628
HLA A*0219	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.443562	1.713576	-2.729986	27769.124571
HLA A*0219	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.440414	1.710050	-2.730364	27568.547101
HLA A*0216	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.447700	1.717294	-2.730405	28034.940055
HLA A*0219	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.440726	1.710232	-2.730495	27588.390229
HLA B*1801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.381545	1.650564	-2.730981	24073.829624
HLA A*2601	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.304348	1.573351	-2.730997	20153.392071
HLA A*0101	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.374422	1.643417	-2.731004	23682.172713
HLA B*3501	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.150953	1.419915	-2.731038	14156.393550
HLA A*1101	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.495615	1.764418	-2.731197	31305.095208
HLA B*1509	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.441307	1.710050	-2.731257	27625.279653
HLA A*6801	1:429-437	9	EAALKDALI	1.091740	0.176549	-3.999636	1.268289	-2.731347	9991.631201
HLA B*4402	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.267945	1.536595	-2.731350	18532.978984
HLA A*2902	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.437242	1.705831	-2.731411	27367.937795
HLA B*4801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.393062	1.661630	-2.731432	24720.790725
HLA A*3002	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.068960	1.337377	-2.731584	11720.882169
HLA A*2403	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.387541	1.655822	-2.731719	24408.498720
HLA B*2705	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.449015	1.717294	-2.731721	28120.001752
HLA B*0802	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.377086	1.645215	-2.731871	23827.905008
HLA A*0203	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.286696	1.554677	-2.732019	19350.690780
HLA B*1503	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.198863	1.466619	-2.732244	15807.504923
HLA B*5401	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.544106	1.811844	-2.732262	35003.063020
HLA A*2403	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.424489	1.692204	-2.732285	26575.966611
HLA B*0801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.382962	1.650564	-2.732398	24152.490617
HLA A*3002	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.521809	1.789240	-2.732570	33251.361863
HLA A*2601	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.384639	1.651959	-2.732680	24245.963908
HLA A*2301	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.497631	1.764802	-2.732829	31450.741356
HLA B*0702	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.795015	1.062125	-2.732890	6237.564474
HLA B*4002	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.606504	1.873578	-2.732926	40411.379187
HLA B*4403	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.425177	1.692204	-2.732973	26618.125514
HLA B*4403	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.594444	1.861442	-2.733002	39304.634864
HLA B*1509	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.383772	1.650564	-2.733208	24197.611203
HLA A*2402	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.383775	1.650564	-2.733211	24197.742110
HLA A*8001	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.446800	1.713576	-2.733224	27976.912145
HLA A*2603	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.413183	1.679828	-2.733356	25893.058209
HLA B*1501	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.413324	1.679828	-2.733497	25901.464287
HLA A*0216	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.384080	1.650564	-2.733516	24214.766019
HLA A*0216	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.389562	1.655822	-2.733739	24522.323955
HLA A*0216	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.443835	1.710050	-2.733785	27786.556475
HLA B*3801	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.448592	1.714405	-2.734188	28092.632384
HLA A*0216	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.335820	1.601532	-2.734288	21668.033856
HLA A*8001	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.460883	1.726550	-2.734332	28898.985171

HLA B*1517	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.498909	1.764418	-2.734491	31543.436582
HLA A*0219	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.461068	1.726550	-2.734518	28911.338695
HLA A*0201	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.385142	1.650564	-2.734578	24274.050110
HLA B*5801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.334344	1.599646	-2.734699	21594.543562
HLA B*0702	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.396436	1.661630	-2.734806	24913.584579
HLA A*2601	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.383622	1.648791	-2.734831	24189.234644
HLA A*0206	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-3.460110	0.725139	-2.734971	2884.762458
HLA A*3101	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.334638	1.599646	-2.734992	21609.151511
HLA A*0101	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.377368	1.642298	-2.735070	23843.378789
HLA A*0216	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.725748	0.990658	-2.735090	5317.990178
HLA A*0219	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.427417	1.692204	-2.735212	26755.712940
HLA B*3501	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.336759	1.601532	-2.735227	21714.973289
HLA B*2705	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.396864	1.661630	-2.735234	24938.126570
HLA B*0802	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.392287	1.657009	-2.735278	24676.696973
HLA B*0801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.391178	1.655822	-2.735356	24613.766205
HLA B*5301	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.500206	1.764802	-2.735404	31637.774236
HLA B*0801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.387381	1.651959	-2.735422	24399.521157
HLA A*3002	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.392447	1.657009	-2.735438	24685.776520
HLA B*4801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.387405	1.651959	-2.735445	24400.841180
HLA A*0219	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.607216	0.871584	-2.735632	4047.771726
HLA A*3001	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.266395	1.530697	-2.735698	18466.924480
HLA B*7301	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.579520	1.843794	-2.735726	37976.928536
HLA A*6801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-3.729065	0.993286	-2.735779	5358.768597
HLA A*2902	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.424404	1.688566	-2.735838	26570.791286
HLA A*0202	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.446224	1.710050	-2.736174	27939.855470
HLA B*4501	1:327-335	9	LNAEHIRML	1.465570	0.426650	-4.628577	1.892220	-2.736357	42518.416728
HLA A*2601	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.378691	1.642298	-2.736393	23916.110885
HLA B*3801	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.463164	1.726550	-2.736614	29051.191027
HLA A*6802	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.442477	1.705831	-2.736645	27699.805951
HLA B*5401	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.512451	1.775750	-2.736701	32542.539335
HLA A*2301	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.480489	1.743756	-2.736733	30233.543025
HLA B*7301	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.585222	1.848352	-2.736870	38478.845875
HLA B*5701	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.392693	1.655822	-2.736871	24699.802971
HLA A*0216	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.557952	0.821048	-2.736904	3613.699295
HLA A*0212	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.387769	1.650564	-2.737205	24421.310667
HLA A*0212	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.443081	1.705831	-2.737249	27738.344926
HLA B*2705	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.380744	1.643417	-2.737327	24029.459831
HLA B*1517	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.445439	1.708081	-2.737359	27889.416445
HLA A*0101	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.389425	1.651959	-2.737466	24514.630705
HLA A*1101	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.379922	1.642298	-2.737624	23984.004029
HLA A*6802	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.399366	1.661630	-2.737736	25082.223093
HLA A*2603	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.528531	1.790732	-2.737799	33770.019687
HLA A*2501	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.394916	1.657009	-2.737907	24826.534529
HLA B*5401	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.518833	1.780575	-2.738258	33024.225394
HLA A*0202	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.487824	1.749555	-2.738269	30748.514314
HLA A*2403	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.444164	1.705831	-2.738332	27807.609553
HLA A*2601	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.386493	1.648036	-2.738457	24349.676628
HLA A*0101	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.386559	1.648036	-2.738523	24353.365321
HLA B*5701	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.395588	1.657009	-2.738579	24864.976577
HLA A*2603	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.514359	1.775750	-2.738609	32685.807624
HLA A*0219	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.729267	0.990658	-2.738609	5361.262347
HLA B*1502	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.550762	1.811844	-2.738918	35543.659590
HLA B*4801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.389501	1.650564	-2.738936	24518.874958
HLA B*4403	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.122514	1.383422	-2.739093	13259.112671
HLA A*3002	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.296160	1.556999	-2.739162	19776.990215
HLA B*0801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.340735	1.601532	-2.739203	21914.654502
HLA B*0801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.382673	1.643417	-2.739256	24136.424500
HLA B*4403	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.594047	1.854767	-2.739280	39268.716188
HLA B*4403	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.530204	1.790732	-2.739472	33900.347276
HLA B*3501	1:200-208	9	NPCDDALMK	1.044498	0.110816	-3.894859	1.155314	-2.739544	7849.803083
HLA A*0216	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.168893	1.429220	-2.739673	14753.440008
HLA A*6901	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.009138	1.269415	-2.739723	10212.632704
HLA A*0203	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.078311	1.338560	-2.739752	11975.985190
HLA B*0803	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.453040	1.713159	-2.739881	28381.804958
HLA A*6901	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.383399	1.643417	-2.739982	24176.806036

HLA A*0216	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-3.997531	1.257536	-2.739995	9943.316352
HLA A*3301	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.613590	1.873578	-2.740012	41076.148887
HLA A*0101	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.349470	1.609455	-2.740015	22359.908054
HLA B*0803	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.392273	1.651959	-2.740314	24675.895997
HLA B*7301	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.601894	1.861442	-2.740452	39984.712991
HLA B*5401	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.516650	1.776041	-2.740609	32858.669045
HLA B*1509	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.396659	1.655822	-2.740837	24926.391945
HLA A*2602	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.454464	1.713576	-2.740888	28475.004352
HLA B*4402	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.304849	1.563919	-2.740929	20176.628338
HLA B*0803	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.467616	1.726550	-2.741066	29350.548126
HLA B*4801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.389947	1.648791	-2.741156	24544.090350
HLA B*1509	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.340967	1.599646	-2.741322	21926.394674
HLA B*0802	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.370822	1.629468	-2.741354	23486.707169
HLA A*2402	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.517160	1.775750	-2.741410	32897.265997
HLA B*1509	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.454999	1.713576	-2.741423	28510.148651
HLA B*0702	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.371142	1.629468	-2.741674	23503.993753
HLA A*6901	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.384104	1.642298	-2.741806	24216.076046
HLA A*0250	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.403499	1.661630	-2.741869	25322.044663
HLA B*0803	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.387595	1.645215	-2.742380	24411.535996
HLA B*4001	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.404018	1.661630	-2.742388	25352.337438
HLA B*3901	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.455982	1.713576	-2.742405	28574.692560
HLA B*3801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.448306	1.705831	-2.742475	28074.097182
HLA A*2602	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.554359	1.811844	-2.742515	35839.273911
HLA A*8001	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.398407	1.655822	-2.742585	25026.921792
HLA A*2301	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.533508	1.790732	-2.742776	34159.186785
HLA B*4601	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.404516	1.661630	-2.742886	25381.430625
HLA A*2902	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.422816	1.679828	-2.742989	26473.797108
HLA B*4601	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.391845	1.648791	-2.743055	24651.612071
HLA A*3002	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.453552	1.710050	-2.743502	28415.296951
HLA A*0201	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.391808	1.648036	-2.743771	24649.478363
HLA A*0201	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.396027	1.651959	-2.744068	24890.143941
HLA B*4601	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.394902	1.650564	-2.744338	24825.728689
HLA A*3002	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.345878	1.601532	-2.744346	22175.715987
HLA A*3101	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.346214	1.601532	-2.744682	22192.878072
HLA A*0212	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.400600	1.655822	-2.744777	25153.562678
HLA A*3201	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-3.978848	1.234017	-2.744831	9524.630842
HLA A*3301	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.492098	1.747156	-2.744942	31052.591481
HLA B*0702	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.455411	1.710050	-2.745361	28537.152862
HLA A*2602	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.598147	1.852707	-2.745439	39641.178245
HLA A*6901	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.193577	1.448126	-2.745451	15616.258324
HLA A*2602	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.374974	1.629468	-2.745506	23712.299573
HLA A*0216	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.472078	1.726550	-2.745528	29653.631625
HLA A*0201	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.407251	1.661630	-2.745621	25541.764601
HLA B*4601	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.401466	1.655822	-2.745644	25203.825607
HLA A*0101	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.345314	1.599646	-2.745668	22146.942311
HLA A*0301	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.345577	1.599646	-2.745931	22160.365377
HLA A*0201	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.394871	1.648791	-2.746081	24823.982793
HLA A*1101	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.460544	1.714405	-2.746140	28876.480934
HLA A*2902	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.463467	1.717294	-2.746173	29071.472223
HLA A*8001	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.345925	1.599646	-2.746279	22178.115480
HLA A*3301	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.590302	1.843794	-2.746508	38931.543652
HLA B*0801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.310513	1.563919	-2.746594	20441.520772
HLA B*5801	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.356126	1.609455	-2.746671	22705.240392
HLA B*1501	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.347036	1.600184	-2.746851	22234.939234
HLA B*5801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.320280	1.573351	-2.746929	20906.436404
HLA B*2705	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.356410	1.609455	-2.746955	22720.108031
HLA A*2402	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.395116	1.648036	-2.747079	24837.953402
HLA B*4601	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.884573	1.137355	-2.747218	7666.068878
HLA B*5401	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.464602	1.717294	-2.747307	29147.534627
HLA A*3002	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.075454	1.328104	-2.747350	11897.460635
HLA A*2402	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.348892	1.601532	-2.747360	22330.170548
HLA A*0211	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.409133	1.661630	-2.747503	25652.685425
HLA A*2601	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.341125	1.593495	-2.747630	21934.343612
HLA A*8001	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.377159	1.629468	-2.747691	23831.901439
HLA A*0219	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.396777	1.648791	-2.747986	24933.135308

HLA B*4002	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.462414	1.714405	-2.748010	29001.099035
HLA A*0206	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.348286	1.600184	-2.748101	22299.024923
HLA A*2902	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.086849	1.338560	-2.748290	12213.757101
HLA A*0203	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.005863	1.257536	-2.748326	10135.904985
HLA A*0219	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.333869	1.585411	-2.748458	21570.957986
HLA B*3801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.462055	1.713576	-2.748479	28977.104379
HLA A*1101	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.440722	1.692204	-2.748517	27588.091731
HLA A*0206	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.196664	1.448126	-2.748538	15727.663468
HLA B*2705	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.350071	1.601532	-2.748540	22390.896451
HLA B*4501	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.404373	1.655822	-2.748551	25373.056053
HLA B*4402	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.390894	1.642298	-2.748596	24597.659390
HLA B*4001	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.321948	1.573351	-2.748597	20986.892890
HLA B*7301	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.601356	1.852642	-2.748713	39935.208017
HLA A*0203	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.396857	1.648036	-2.748820	24937.721836
HLA A*8001	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.410479	1.661630	-2.748849	25732.328703
HLA A*0202	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.560700	1.811844	-2.748856	36366.412659
HLA B*1801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.350391	1.601532	-2.748859	22407.376501
HLA B*0801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.397663	1.648791	-2.748872	24984.039032
HLA A*0201	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.348528	1.599646	-2.748882	22311.453816
HLA B*0801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.215930	1.466619	-2.749311	16441.066456
HLA B*1517	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.134285	1.384650	-2.749635	13623.396008
HLA A*2902	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.359159	1.609455	-2.749704	22864.372637
HLA A*3101	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.405536	1.655822	-2.749714	25441.093494
HLA B*0802	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.359009	1.609246	-2.749763	22856.457609
HLA B*4601	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.351500	1.601532	-2.749968	22464.666125
HLA B*1509	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.393450	1.643417	-2.750033	24742.867138
HLA A*0219	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.411952	1.661630	-2.750322	25819.760976
HLA A*3301	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.603071	1.852707	-2.750364	40093.232734
HLA B*4002	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.542708	1.792234	-2.750474	34890.573362
HLA B*5701	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.399570	1.648791	-2.750780	25094.031079
HLA A*0211	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.008485	1.257536	-2.750948	10197.284968
HLA A*3101	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.287596	1.536595	-2.751001	19390.826737
HLA B*0803	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.360616	1.609455	-2.751161	22941.191502
HLA B*5101	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.407018	1.655822	-2.751196	25528.088630
HLA B*5101	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.515666	1.764418	-2.751247	32784.271221
HLA A*0250	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-3.458033	0.706599	-2.751434	2870.999473
HLA A*3001	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.245447	1.493912	-2.751535	17597.321350
HLA A*3101	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.306376	1.554677	-2.751698	20247.702889
HLA A*3301	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.403748	1.651959	-2.751788	25336.569710
HLA A*3201	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.431686	1.679828	-2.751858	27020.012278
HLA B*0702	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.394195	1.642298	-2.751897	24785.335949
HLA B*1501	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.361457	1.609246	-2.752211	22985.665686
HLA A*2402	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.409255	1.657009	-2.752246	25659.902906
HLA B*0802	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.361713	1.609455	-2.752258	22999.223822
HLA B*1509	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.394702	1.642298	-2.752405	24814.315436
HLA A*2501	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.444760	1.692204	-2.752556	27845.846584
HLA A*2501	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.465730	1.713159	-2.752571	29223.321752
HLA B*3901	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.409586	1.657009	-2.752577	25679.483602
HLA A*0201	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.394940	1.642298	-2.752642	24827.877653
HLA B*0803	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.408698	1.655822	-2.752876	25627.024304
HLA B*4501	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.543610	1.790732	-2.752878	34963.130288
HLA B*4501	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.644765	1.891829	-2.752936	44133.161134
HLA A*0211	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.533740	1.780575	-2.753165	34177.486629
HLA A*2902	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.401255	1.648036	-2.753219	25191.557103
HLA B*5301	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.445578	1.692204	-2.753374	27898.319707
HLA B*3501	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.402486	1.648791	-2.753695	25263.070988
HLA A*3101	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.310720	1.556999	-2.753721	20451.254689
HLA B*0803	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.347327	1.593495	-2.753832	22249.860019
HLA B*4002	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.624144	1.870150	-2.753994	42086.577096
HLA A*0212	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.402963	1.648791	-2.754172	25290.830322
HLA B*4601	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.397623	1.643417	-2.754206	24981.741403
HLA A*2403	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.434098	1.679828	-2.754271	27170.552091
HLA A*3301	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.526255	1.771882	-2.754372	33593.454277
HLA B*5701	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.396800	1.642298	-2.754503	24934.484199
HLA B*1801	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.464757	1.710232	-2.754525	29157.943691

HLA A*2402	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.535401	1.780575	-2.754827	34308.458705
HLA A*6801	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.528369	1.773509	-2.754860	33757.416288
HLA A*8001	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.364345	1.609455	-2.754889	23139.000896
HLA A*6801	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.607655	1.852707	-2.754948	40518.645627
HLA B*4001	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.403008	1.648036	-2.754971	25293.430047
HLA A*0219	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.403064	1.648036	-2.755028	25296.714292
HLA A*0201	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.398473	1.643417	-2.755056	25030.713079
HLA B*3801	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.463258	1.708081	-2.755177	29057.478256
HLA B*0802	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.403999	1.648791	-2.755208	25351.240235
HLA A*2501	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.291886	1.536595	-2.755291	19583.327436
HLA A*6901	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.139981	1.384650	-2.755331	13803.223899
HLA A*0250	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.340758	1.585411	-2.755347	21915.840092
HLA B*4801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.397656	1.642298	-2.755358	24983.633553
HLA A*0203	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.355543	1.600184	-2.755359	22674.798276
HLA B*4403	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.411245	1.655822	-2.755423	25777.750894
HLA B*1502	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.529688	0.774156	-2.755532	3386.005868
HLA B*3801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.341024	1.585411	-2.755612	21929.241724
HLA B*5701	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.417257	1.661630	-2.755627	26137.097302
HLA A*0219	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.406295	1.650564	-2.755730	25485.587976
HLA A*6801	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.602728	1.846931	-2.755797	40061.577845
HLA A*0216	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.365291	1.609455	-2.755836	23189.503239
HLA B*3501	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.461738	1.705831	-2.755907	28955.949111
HLA B*3501	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-3.604664	0.848752	-2.755913	4024.060224
HLA A*2902	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.056259	1.299885	-2.756374	11383.058926
HLA A*0301	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.365858	1.609455	-2.756403	23219.757043
HLA A*0206	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.537051	1.780575	-2.756476	34439.001112
HLA B*1509	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-3.987607	1.230828	-2.756779	9718.674397
HLA B*0803	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.313878	1.556999	-2.756879	20600.495431
HLA A*3002	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.366335	1.609455	-2.756879	23245.271162
HLA B*7301	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.569069	1.811844	-2.757225	37073.989965
HLA B*5701	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.400715	1.643417	-2.757297	25160.231383
HLA B*3501	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.437242	1.679828	-2.757414	27367.937795
HLA A*0211	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-3.511921	0.754283	-2.757637	3250.280938
HLA B*3501	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.367378	1.609455	-2.757923	23301.173200
HLA A*2403	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.275259	1.517234	-2.758025	18847.735570
HLA A*0203	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.406913	1.648791	-2.758122	25521.874700
HLA A*2403	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.415237	1.657009	-2.758228	26015.776776
HLA A*0203	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.142950	1.384650	-2.758300	13897.935176
HLA B*5801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.367742	1.609246	-2.758496	23320.720193
HLA B*4002	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.605489	1.846931	-2.758558	40317.045155
HLA B*1501	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.400879	1.642298	-2.758581	25169.761172
HLA B*4601	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.410550	1.651959	-2.758590	25736.505313
HLA B*4801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.406741	1.648036	-2.758705	25511.797543
HLA B*5701	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.388173	1.629468	-2.758705	24444.045295
HLA B*4601	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.401039	1.642298	-2.758741	25179.022137
HLA A*0206	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.016285	1.257536	-2.758749	10382.091359
HLA B*1503	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.921417	1.162617	-2.758800	8344.827062
HLA A*2601	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.402249	1.643417	-2.758832	25249.271047
HLA A*2403	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.368287	1.609455	-2.758832	23350.008271
HLA B*0803	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.469143	1.710232	-2.758912	29453.938890
HLA A*0212	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.207044	1.448126	-2.758918	16108.096864
HLA A*0301	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.907222	1.148177	-2.759044	8076.473128
HLA B*0702	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.411034	1.651959	-2.759074	25765.203019
HLA B*4601	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.352614	1.593495	-2.759119	22522.345909
HLA B*4601	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.332641	1.573351	-2.759289	21510.011981
HLA A*0216	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.359488	1.600184	-2.759304	22881.696317
HLA B*5801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.316335	1.556999	-2.759337	20717.398813
HLA A*1101	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.192224	1.432365	-2.759858	15567.672301
HLA B*0801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.369112	1.609246	-2.759866	23394.389050
HLA A*2402	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.415709	1.655822	-2.759887	26044.081398
HLA A*2301	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.389385	1.629468	-2.759918	24512.376244
HLA B*1503	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.408816	1.648791	-2.760025	25633.957210
HLA A*2601	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.369755	1.609455	-2.760300	23429.092492
HLA B*4801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.360010	1.599646	-2.760364	22909.193638
HLA B*7301	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-3.369942	0.609548	-2.760394	2343.913186

HLA B*4001	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.389900	1.629468	-2.760432	24541.434878
HLA B*4002	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-3.550114	0.789406	-2.760709	3549.066435
HLA A*0301	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.180786	1.419915	-2.760872	15163.043753
HLA B*5801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.346792	1.585411	-2.761380	22222.432742
HLA A*2301	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.278619	1.517234	-2.761385	18994.109774
HLA B*4402	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.413350	1.651959	-2.761391	25903.005698
HLA B*0802	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.278654	1.517234	-2.761420	18995.651177
HLA B*4601	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.390913	1.629468	-2.761445	24598.723978
HLA B*0801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.298193	1.536595	-2.761597	19869.754589
HLA B*4501	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.553953	1.792234	-2.761719	35805.747238
HLA B*0702	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.412535	1.650564	-2.761971	25854.425371
HLA B*1502	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.318988	1.556999	-2.761989	20844.323031
HLA B*3901	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.467837	1.705831	-2.762006	29365.477543
HLA A*0219	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.417828	1.655822	-2.762006	26171.479805
HLA B*1517	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.371668	1.609455	-2.762213	23532.493514
HLA B*3801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.472329	1.710050	-2.762280	29670.801840
HLA B*1517	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.418228	1.655822	-2.762406	26195.560293
HLA A*0219	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.372100	1.609455	-2.762645	23555.929882
HLA A*8001	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.410916	1.648036	-2.762880	25758.234617
HLA A*6802	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-3.830962	1.067986	-2.762976	6775.824802
HLA B*0803	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.411785	1.648791	-2.762995	25809.845455
HLA A*0206	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.362665	1.599646	-2.763019	23049.670483
HLA B*4001	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.327058	1.563919	-2.763139	21235.293892
HLA B*4001	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.415286	1.651959	-2.763327	26018.732535
HLA A*1101	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.469165	1.705831	-2.763333	29455.373008
HLA B*5401	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.535244	1.771882	-2.763361	34296.025426
HLA B*5401	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.555764	1.792234	-2.763530	35955.405786
HLA B*1517	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.364234	1.600184	-2.764050	23133.118211
HLA B*7301	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.540387	1.776041	-2.764346	34704.581780
HLA B*1517	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.349912	1.585411	-2.764501	22382.660972
HLA B*0702	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.444380	1.679828	-2.764552	27821.453118
HLA B*2705	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.420467	1.655822	-2.764645	26330.963506
HLA B*4801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.420713	1.655822	-2.764891	26345.924752
HLA B*0802	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.426594	1.661630	-2.764964	26705.099967
HLA B*5301	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-3.688442	0.923460	-2.764982	4880.253797
HLA B*5301	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.594023	1.828963	-2.765061	39266.591851
HLA A*1101	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.453754	1.688566	-2.765188	28428.520257
HLA B*1501	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.417748	1.651959	-2.765789	26166.666364
HLA A*0203	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.427588	1.661630	-2.765958	26766.281443
HLA A*0301	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.225882	1.459786	-2.766096	16822.184942
HLA A*2403	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.928748	1.162617	-2.766131	8486.873600
HLA A*6802	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.196082	1.429823	-2.766259	15706.576557
HLA A*2602	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.483602	1.717294	-2.766308	30451.038764
HLA B*4403	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.658260	1.891829	-2.766431	45526.103114
HLA A*2902	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.422316	1.655822	-2.766494	26443.308752
HLA B*0801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.366539	1.599646	-2.766894	23256.214364
HLA B*5701	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.418864	1.651959	-2.766905	26233.993245
HLA B*1501	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-3.450750	0.683810	-2.766939	2823.252421
HLA A*0101	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.367131	1.600184	-2.766947	23287.940998
HLA B*5401	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.977293	1.210192	-2.767101	9490.580847
HLA B*3901	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.409622	1.642298	-2.767324	25681.567534
HLA A*6801	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.615754	1.848352	-2.767402	41281.321837
HLA B*7301	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.559899	1.792274	-2.767625	36299.386755
HLA A*2301	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.418192	1.650564	-2.767628	26193.434653
HLA A*0216	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.481283	1.713576	-2.767707	30288.876919
HLA A*2601	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.367502	1.599646	-2.767857	23307.855166
HLA B*0702	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.411508	1.643417	-2.768091	25793.374561
HLA B*2705	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-3.830906	1.062587	-2.768319	6774.945104
HLA B*4001	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.410749	1.642298	-2.768452	25748.342724
HLA A*3201	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.105904	1.337377	-2.768527	12761.555165
HLA B*4001	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.305142	1.536595	-2.768547	20190.277118
HLA A*2603	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.460779	1.692204	-2.768575	28892.107016
HLA A*0206	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.478873	1.710232	-2.768641	30121.222823
HLA B*4403	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.621435	1.852642	-2.768792	41824.874817
HLA A*6801	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.586531	1.817618	-2.768913	38594.969369

HLA B*0802	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.425015	1.655822	-2.769193	26608.191291
HLA A*0219	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.475029	1.705831	-2.769198	29855.808838
HLA A*6802	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.378672	1.609455	-2.769217	23915.075840
HLA A*6901	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-3.557224	0.787998	-2.769226	3607.643963
HLA B*1502	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.305990	1.536595	-2.769395	20229.746652
HLA B*4501	1:59-67	9	LALLDALRW	1.480034	0.393544	-4.643130	1.873578	-2.769552	43967.299753
HLA B*5401	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.543159	1.773509	-2.769650	34926.832983
HLA A*3201	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.581672	1.811844	-2.769828	38165.588690
HLA B*1502	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.560618	1.790732	-2.769886	36359.527472
HLA A*0202	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.363433	1.593495	-2.769938	23090.482217
HLA B*1509	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.427012	1.657009	-2.770004	26730.828303
HLA B*0803	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.420666	1.650564	-2.770102	26343.074335
HLA B*5801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.370293	1.600184	-2.770109	23458.135953
HLA B*4002	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.618601	1.848352	-2.770249	41552.883929
HLA A*2603	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.534699	1.764418	-2.770280	34253.007682
HLA A*0211	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.497004	1.726550	-2.770453	31405.345428
HLA B*4001	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.370157	1.599646	-2.770512	23450.776564
HLA B*5301	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.517789	1.747156	-2.770634	32944.996701
HLA B*5401	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.560054	1.789240	-2.770815	36312.349862
HLA A*6901	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.298707	1.527790	-2.770917	19893.309544
HLA B*0803	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.372486	1.601532	-2.770954	23576.838490
HLA B*7301	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.600090	1.828963	-2.771127	39818.929348
HLA A*0250	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.583108	1.811844	-2.771263	38291.951568
HLA B*4403	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.547019	1.775750	-2.771269	35238.662103
HLA B*1501	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.005299	1.234017	-2.771282	10122.753335
HLA B*4403	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.641480	1.870150	-2.771331	43800.639950
HLA A*2402	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.288722	1.517234	-2.771487	19441.140063
HLA B*3801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.413811	1.642298	-2.771513	25930.486213
HLA B*3901	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.420345	1.648791	-2.771554	26323.557272
HLA B*4801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.415042	1.643417	-2.771625	26004.097773
HLA A*6801	1:157-165	9	RLRMPDDDL	1.319169	0.572660	-4.663589	1.891829	-2.771760	46088.132384
HLA A*2403	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.420554	1.648791	-2.771763	26336.234594
HLA A*0101	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.373414	1.601532	-2.771882	23627.273852
HLA B*5301	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.564380	1.792234	-2.772146	36675.813530
HLA B*0802	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.420302	1.648036	-2.772266	26320.994062
HLA A*1101	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.402066	1.629468	-2.772598	25238.618826
HLA A*1101	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.420674	1.648036	-2.772637	26343.501878
HLA A*2403	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.416144	1.643417	-2.772727	26070.160131
HLA A*2402	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.584574	1.811844	-2.772729	38421.434851
HLA A*2602	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.601708	1.828963	-2.772746	39967.627926
HLA B*1801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.366386	1.593495	-2.772891	23248.037922
HLA B*4801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.267031	1.493912	-2.773120	18494.018324
HLA A*1101	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.490458	1.717294	-2.773163	30935.554820
HLA A*3101	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.101928	1.328755	-2.773173	12645.274855
HLA A*0203	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.957050	1.183813	-2.773237	9058.361122
HLA A*0101	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.346829	1.573351	-2.773478	22224.356360
HLA B*0801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.078659	1.305053	-2.773606	11985.577765
HLA A*6801	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.520802	1.747156	-2.773646	33174.280173
HLA B*7301	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.591380	1.817618	-2.773762	39028.336216
HLA B*5301	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.462412	1.688566	-2.773846	29000.942143
HLA B*4002	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.635299	1.861442	-2.773857	43181.622933
HLA B*4002	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.617727	1.843794	-2.773933	41469.343723
HLA A*0206	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-3.897340	1.123062	-2.774278	7894.776115
HLA A*2301	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.524004	1.749555	-2.774448	33419.800745
HLA B*3801	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.555440	1.780575	-2.774865	35928.572767
HLA B*3501	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.425579	1.650564	-2.775015	26642.761096
HLA A*3101	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.161756	1.386690	-2.775065	14512.945341
HLA B*5801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.329819	1.554677	-2.775142	21370.708514
HLA B*4002	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.592903	1.817618	-2.775284	39165.394365
HLA B*4402	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.432376	1.657009	-2.775367	27063.022002
HLA A*2301	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.455321	1.679828	-2.775494	28531.286917
HLA A*6801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.912879	1.137355	-2.775524	8182.373735
HLA A*0203	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.426171	1.650564	-2.775607	26679.107731
HLA B*3801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.420826	1.645215	-2.775611	26352.767010
HLA B*1801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.312348	1.536595	-2.775753	20528.071435

HLA A*2301	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.423834	1.648036	-2.775797	26535.884191
HLA B*4601	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.376036	1.600184	-2.775851	23770.353495
HLA B*3901	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.427837	1.651959	-2.775878	26781.634922
HLA B*5701	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.385130	1.609246	-2.775884	24273.393519
HLA B*0702	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.332937	1.556999	-2.775938	21524.679193
HLA B*4002	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.489109	1.713159	-2.775950	30839.640370
HLA B*4601	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.385328	1.609246	-2.776082	24284.426601
HLA B*4002	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.547980	1.771882	-2.776098	35316.719065
HLA B*0802	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.369605	1.593495	-2.776110	23420.981974
HLA B*1501	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.205418	1.429220	-2.776199	16047.906631
HLA A*0203	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.418860	1.642298	-2.776562	26233.709400
HLA A*0216	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.889460	1.112802	-2.776658	7752.819016
HLA A*2301	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.541082	1.764418	-2.776664	34760.199689
HLA A*2501	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.487021	1.710232	-2.776789	30691.676560
HLA A*3201	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.552816	1.775750	-2.777066	35712.116593
HLA B*4402	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.438725	1.661630	-2.777094	27461.521724
HLA B*5701	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.744713	0.967578	-2.777134	5555.364686
HLA A*3002	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.526708	1.749555	-2.777153	33628.547809
HLA B*7301	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.569457	1.792234	-2.777223	37107.098159
HLA A*1101	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.420702	1.643417	-2.777285	26345.212119
HLA A*2501	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.487342	1.710050	-2.777293	30714.432276
HLA B*7301	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.624273	1.846931	-2.777342	42099.101564
HLA B*5101	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.305199	1.527790	-2.777409	20192.898740
HLA A*3301	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.626084	1.848352	-2.777732	42275.064667
HLA B*1801	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.483621	1.705831	-2.777790	30452.356686
HLA A*0301	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.242279	1.464436	-2.777843	17469.459132
HLA A*6802	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-3.451018	0.673165	-2.777852	2824.994135
HLA B*0801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.305659	1.527790	-2.777869	20214.321399
HLA A*3001	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.926083	1.148177	-2.777906	8434.967586
HLA B*4601	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.387485	1.609455	-2.778030	24405.329791
HLA A*0301	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.295270	1.517234	-2.778035	19736.482045
HLA A*0101	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.387330	1.609246	-2.778083	24396.617358
HLA B*1801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.426164	1.648036	-2.778128	26678.674742
HLA A*0101	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.295674	1.517234	-2.778439	19754.855407
HLA B*5801	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.101228	1.322784	-2.778445	12624.905238
HLA A*0212	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.426770	1.648036	-2.778734	26715.937538
HLA B*1801	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.488797	1.710050	-2.778747	30817.458759
HLA B*5701	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.378597	1.599646	-2.778951	23910.936105
HLA A*0212	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.421259	1.642298	-2.778961	26379.012131
HLA B*4403	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.625894	1.846931	-2.778963	42256.543749
HLA B*5801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.927268	1.148177	-2.779090	8457.997617
HLA A*0203	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.431119	1.651959	-2.779160	26984.806993
HLA B*3901	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.440830	1.661630	-2.779200	27594.958017
HLA B*5801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.372749	1.593495	-2.779254	23591.128204
HLA A*0301	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.364775	1.585411	-2.779363	23161.920075
HLA B*3901	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.430125	1.650564	-2.779561	26923.126018
HLA A*6901	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.021604	1.241782	-2.779822	10510.033015
HLA A*3002	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.428746	1.648791	-2.779956	26837.764416
HLA B*4403	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.597653	1.817618	-2.780035	39596.168398
HLA B*4501	1:74-82	9	EGPEVGGPY	0.862924	0.998518	-4.641981	1.861442	-2.780539	43851.140798
HLA A*0101	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.366071	1.585411	-2.780660	23231.190942
HLA A*8001	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.424111	1.643417	-2.780694	26552.829230
HLA B*0702	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.389959	1.609246	-2.780713	24544.754263
HLA B*0702	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.335437	1.554677	-2.780759	21648.935147
HLA B*1517	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-3.990971	1.210192	-2.780780	9794.256981
HLA B*7301	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.554392	1.773509	-2.780883	35841.988425
HLA A*0212	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.424430	1.643417	-2.781013	26572.372528
HLA B*4501	1:17-25	9	GTPHVGLVR	1.315761	0.554389	-4.651167	1.870150	-2.781018	44788.589170
HLA B*5101	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.491090	1.710050	-2.781040	30980.606874
HLA B*3501	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.436937	1.655822	-2.781115	27348.697085
HLA A*2301	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.494283	1.713159	-2.781124	31209.216860
HLA A*0101	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.335916	1.554677	-2.781238	21672.840477
HLA B*0801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.423594	1.642298	-2.781296	26521.245499
HLA B*5301	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.553335	1.771882	-2.781452	35754.839016
HLA B*5101	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.410921	1.629468	-2.781453	25758.513317

HLA B*4402	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.432449	1.650564	-2.781885	27067.561029
HLA A*3201	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.430739	1.648791	-2.781948	26961.167813
HLA B*5401	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.546326	1.764296	-2.782030	35182.468964
HLA A*2902	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.339092	1.556999	-2.782094	21831.940452
HLA A*0202	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.051616	1.269415	-2.782201	11262.022786
HLA A*0250	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.051903	1.269415	-2.782488	11269.458247
HLA B*1502	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.444201	1.661630	-2.782571	27810.016635
HLA A*2601	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.384271	1.601532	-2.782739	24225.379279
HLA A*2603	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.594615	1.811844	-2.782771	39320.160190
HLA B*0803	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.430823	1.648036	-2.782787	26966.419174
HLA A*6901	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.376325	1.593495	-2.782830	23786.175940
HLA B*0801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.212237	1.429220	-2.783017	16301.838802
HLA B*1801	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.496938	1.713576	-2.783362	31400.588604
HLA A*3002	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.445035	1.661630	-2.783405	27863.477387
HLA B*4001	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.392661	1.609246	-2.783414	24697.932318
HLA A*0201	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.384947	1.601532	-2.783415	24263.153003
HLA A*2301	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.491499	1.708081	-2.783418	31009.783291
HLA A*2501	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.338099	1.554677	-2.783421	21782.037728
HLA A*8001	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.356789	1.573351	-2.783437	22739.905687
HLA A*2402	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.493707	1.710232	-2.783476	31167.878852
HLA B*0803	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.425807	1.642298	-2.783509	26656.745801
HLA A*2403	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.425817	1.642298	-2.783519	26657.322647
HLA A*0101	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.377107	1.593495	-2.783612	23829.065193
HLA B*1517	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.445320	1.661630	-2.783689	27881.722696
HLA B*2705	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.431923	1.648036	-2.783886	27034.780015
HLA A*2301	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.472475	1.688566	-2.783909	29680.755486
HLA B*5801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.348032	1.563919	-2.784113	22286.000121
HLA B*5301	1:310-318	9	ADVNSSPAR	1.184766	0.627078	-4.596037	1.811844	-2.784193	39449.065240
HLA A*2402	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.533778	1.749555	-2.784222	34180.445100
HLA B*4002	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.341303	1.556999	-2.784305	21943.363807
HLA B*0802	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.426641	1.642298	-2.784344	26707.989556
HLA A*0211	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.385894	1.601532	-2.784362	24316.108879
HLA A*0301	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.315137	1.530697	-2.784440	20660.317391
HLA A*2602	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.492720	1.708081	-2.784640	31097.141043
HLA B*0801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.278624	1.493912	-2.784712	18994.315287
HLA A*0201	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.384903	1.600184	-2.784718	24260.659173
HLA A*0206	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.464548	1.679828	-2.784720	29143.908099
HLA B*4403	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.637578	1.852707	-2.784871	43408.818085
HLA B*4801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.394272	1.609246	-2.785026	24789.761179
HLA A*6802	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.433828	1.648791	-2.785038	27153.653535
HLA A*6802	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.122477	1.337377	-2.785100	13257.965036
HLA B*3901	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.171807	1.386690	-2.785116	14852.742659
HLA A*3001	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.123840	1.338560	-2.785280	13299.630359
HLA B*4402	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.414807	1.629468	-2.785339	25990.033649
HLA A*6901	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.387001	1.601532	-2.785469	24378.146734
HLA B*5301	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.566137	1.780575	-2.785563	36824.526457
HLA A*2902	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.427971	1.642298	-2.785673	26789.894679
HLA B*1503	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.113807	1.328104	-2.785703	12995.927195
HLA A*2402	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.493888	1.708081	-2.785808	31180.864894
HLA B*4403	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.575187	1.789240	-2.785948	37599.960354
HLA A*0202	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-3.845722	1.059725	-2.785997	7010.058351
HLA A*0211	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.441976	1.655822	-2.786154	27667.905670
HLA B*4501	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.114977	1.328755	-2.786222	13030.987051
HLA B*2705	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.379870	1.593495	-2.786375	23981.149682
HLA A*0212	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.438917	1.651959	-2.786958	27473.706657
HLA A*2501	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.492984	1.705831	-2.787152	31115.988746
HLA A*1101	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.112539	1.325261	-2.787278	12958.017072
HLA B*5401	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.552153	1.764802	-2.787351	35657.676127
HLA B*3801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.467200	1.679828	-2.787373	29322.456949
HLA B*1509	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.497934	1.710232	-2.787702	31472.697724
HLA A*2602	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.563508	1.775750	-2.787758	36602.276468
HLA A*2501	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.435893	1.648036	-2.787857	27283.084599
HLA A*0211	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.438480	1.650564	-2.787916	27446.075435
HLA A*0216	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.493750	1.705831	-2.787918	31170.914066
HLA B*0803	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.467752	1.679828	-2.787925	29359.758997

HLA B*0802	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.373475	1.585411	-2.788063	23630.597430
HLA A*6802	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.436244	1.648036	-2.788207	27305.085636
HLA A*0203	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-3.788620	1.000328	-2.788292	6146.384847
HLA B*5301	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.305640	1.517234	-2.788406	20213.446560
HLA B*5101	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.502055	1.713576	-2.788479	31772.761834
HLA B*4001	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-3.694396	0.905846	-2.788550	4947.616201
HLA B*1501	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.373980	1.585411	-2.788569	23658.098787
HLA B*4001	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.175430	1.386690	-2.788739	14977.163206
HLA A*0216	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.437672	1.648791	-2.788881	27395.045736
HLA B*5401	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.477468	1.688566	-2.788901	30023.934696
HLA A*0212	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.450554	1.661630	-2.788924	28219.821092
HLA A*0250	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.610082	0.821048	-2.789034	4074.575638
HLA B*4402	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.434566	1.645215	-2.789351	27199.818787
HLA A*6802	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.441340	1.651959	-2.789380	27627.372028
HLA A*2403	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-3.366539	0.577123	-2.789417	2325.623824
HLA B*4501	1:273-281	9	RGFIPEGLL	1.457510	0.395197	-4.642604	1.852707	-2.789896	43914.051782
HLA A*3002	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.565747	1.775750	-2.789997	36791.471345
HLA A*0211	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.469874	1.679828	-2.790046	29503.536133
HLA A*0201	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-3.990934	1.200757	-2.790177	9793.409244
HLA B*1801	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.435590	1.645215	-2.790375	27264.051040
HLA A*0206	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-3.852991	1.062587	-2.790404	7128.381585
HLA A*2403	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.452382	1.661630	-2.790752	28338.845626
HLA B*0702	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.390725	1.599646	-2.791079	24588.080172
HLA A*2902	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.384637	1.593495	-2.791142	24245.832741
HLA B*4001	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.348244	1.556999	-2.791245	22296.853594
HLA A*0212	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.251081	1.459786	-2.791294	17827.097097
HLA A*2902	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.443503	1.651959	-2.791544	27765.369128
HLA A*0206	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.518288	1.726550	-2.791737	32982.802878
HLA A*8001	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.443976	1.651959	-2.792016	27795.577270
HLA A*0219	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.346822	1.554677	-2.792145	22223.995669
HLA A*0211	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.440938	1.648791	-2.792147	27601.826012
HLA A*0211	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.556934	1.764418	-2.792516	36052.404741
HLA A*0201	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.401842	1.609246	-2.792596	25225.651036
HLA A*1101	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.438003	1.645215	-2.792788	27415.950494
HLA B*4402	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.441652	1.648791	-2.792861	27647.257497
HLA B*4601	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.347626	1.554677	-2.792948	22265.152169
HLA B*3901	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.448841	1.655822	-2.793019	28108.746674
HLA B*1509	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.378496	1.585411	-2.793084	23905.374465
HLA A*6802	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.378503	1.585411	-2.793091	23905.762444
HLA B*1501	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-3.686647	0.893488	-2.793159	4860.124577
HLA B*1517	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.473170	1.679828	-2.793343	29728.322161
HLA A*3002	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.481943	1.688566	-2.793377	30334.956445
HLA B*4801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.357334	1.563919	-2.793415	22768.464331
HLA B*4501	1:340-348	9	FTVRLRDHL	1.515241	0.339526	-4.648343	1.854767	-2.793577	44498.287896
HLA B*0702	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.063096	1.269415	-2.793681	11563.677881
HLA B*4501	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.586049	1.792274	-2.793775	38552.190221
HLA B*4002	1:380-388	9	WELLKFFND	0.942251	-0.784797	-2.951310	0.157454	-2.793856	893.943940
HLA A*0201	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.387355	1.593495	-2.793861	24398.069214
HLA B*1517	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.287841	1.493912	-2.793929	19401.739638
HLA A*0216	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.348657	1.554677	-2.793980	22318.093441
HLA B*3901	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.442141	1.648036	-2.794104	27678.385276
HLA B*7301	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.543669	1.749555	-2.794114	34967.859274
HLA B*2705	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.403473	1.609246	-2.794227	25320.537824
HLA B*4403	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.638036	1.843794	-2.794242	43454.635442
HLA A*2301	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.450317	1.655822	-2.794495	28204.406027
HLA A*0250	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.575089	1.780575	-2.794514	37591.418036
HLA A*0203	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.708939	0.914083	-2.794856	5116.103422
HLA A*2402	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.394552	1.599646	-2.794906	24805.725391
HLA B*1502	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.575545	1.780575	-2.794970	37630.891635
HLA A*2601	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.352233	1.556999	-2.795234	22502.615926
HLA A*0206	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.560036	1.764418	-2.795617	36310.778330
HLA B*1502	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.096369	1.300706	-2.795664	12484.449358
HLA B*4402	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.404974	1.609246	-2.795728	25408.220345
HLA B*1801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.439230	1.643417	-2.795813	27493.481521
HLA A*2301	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.405656	1.609455	-2.796200	25448.113770

HLA B*4501	1:198-206	9	LVNPCDDAL	1.410722	0.441920	-4.648989	1.852642	-2.796347	44564.538136
HLA A*2501	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.476175	1.679828	-2.796348	29934.733082
HLA B*5701	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.216315	1.419915	-2.796401	16455.659802
HLA B*4002	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.585821	1.789240	-2.796581	38531.964910
HLA A*6802	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.440092	1.643417	-2.796675	27548.122110
HLA B*1509	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.458380	1.661630	-2.796750	28732.961480
HLA A*6802	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.181656	1.384650	-2.797006	15193.425393
HLA B*5301	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.523776	1.726550	-2.797226	33402.267996
HLA A*2902	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.382776	1.585411	-2.797365	24142.170501
HLA A*3301	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.097356	1.299885	-2.797472	12512.848193
HLA A*6802	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.439829	1.642298	-2.797531	27531.435550
HLA A*2402	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.486102	1.688566	-2.797536	30626.824095
HLA B*5701	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.370975	1.573351	-2.797624	23494.967552
HLA B*1502	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.541503	1.743756	-2.797747	34793.876733
HLA B*4403	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.571285	1.773509	-2.797776	37263.607126
HLA A*3101	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.383251	1.585411	-2.797840	24168.567428
HLA A*2301	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.352661	1.554677	-2.797983	22524.782908
HLA B*4001	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.391610	1.593495	-2.798116	24638.279429
HLA B*4801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.218068	1.419915	-2.798153	16522.205371
HLA B*3901	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.441725	1.643417	-2.798308	27651.894512
HLA B*5401	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.525169	1.726550	-2.798619	33509.596685
HLA B*4801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.392158	1.593495	-2.798663	24669.355664
HLA A*0211	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.353464	1.554677	-2.798787	22566.496435
HLA B*4501	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.563607	1.764802	-2.798805	36610.594011
HLA B*4501	1:276-284	9	IPEGLLNYL	1.660827	0.186104	-4.645749	1.846931	-2.798818	44233.313159
HLA B*1517	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.228053	1.429220	-2.798834	16906.485152
HLA A*2603	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.526015	1.726550	-2.799465	33574.922230
HLA A*2602	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.564039	1.764418	-2.799621	36647.055058
HLA A*2601	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.385069	1.585411	-2.799658	24269.979534
HLA B*5401	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.549256	1.749555	-2.799701	35420.616921
HLA B*4001	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.401318	1.601532	-2.799786	25195.237027
HLA A*2402	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.479737	1.679828	-2.799910	30181.249066
HLA B*5401	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.564417	1.764418	-2.799999	36678.988261
HLA B*5701	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.393748	1.593495	-2.800254	24759.872713
HLA B*5801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.260079	1.459786	-2.800293	18200.325599
HLA A*2402	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.409833	1.609455	-2.800378	25694.074678
HLA B*3501	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-3.715523	0.915076	-2.800446	5194.246695
HLA A*2402	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.510605	1.710050	-2.800555	32404.456616
HLA A*2501	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.449401	1.648791	-2.800610	28144.961502
HLA A*3002	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.506538	1.705831	-2.800707	32102.420912
HLA A*2301	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.518015	1.717294	-2.800721	32962.111108
HLA B*3501	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.917950	1.117129	-2.800821	8278.458975
HLA B*4801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.401255	1.600184	-2.801071	25191.557103
HLA A*0203	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.410514	1.609246	-2.801268	25734.416923
HLA A*3001	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.265866	1.464436	-2.801430	18444.459752
HLA A*2402	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.514608	1.713159	-2.801449	32704.556619
HLA B*1502	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.494189	1.692204	-2.801985	31202.464054
HLA A*2403	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.071437	1.269415	-2.802021	11787.905814
HLA A*0203	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.445639	1.643417	-2.802222	27902.244080
HLA A*0301	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.366165	1.563919	-2.802246	23236.218612
HLA A*1101	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.411717	1.609455	-2.802262	25805.796549
HLA A*0202	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.140902	1.338560	-2.802342	13832.527132
HLA B*4801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.403875	1.601532	-2.802343	25343.972465
HLA A*2301	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.528910	1.726550	-2.802359	33799.445923
HLA B*0801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.387882	1.585411	-2.802471	24427.653086
HLA B*0702	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.458380	1.655822	-2.802558	28732.961480
HLA A*0250	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.415334	0.612666	-2.802668	2602.157458
HLA B*4403	1:349-357	9	DTHGHHIAL	1.488707	0.303527	-4.594998	1.792234	-2.802764	39354.848469
HLA A*3301	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.298218	1.495432	-2.802786	19870.937049
HLA B*7301	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.567725	1.764802	-2.802924	36959.443434
HLA A*3201	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.567810	1.764802	-2.803008	36966.642209
HLA A*1101	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.240113	1.437023	-2.803091	17382.539859
HLA A*8001	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.451952	1.648791	-2.803161	28310.803776
HLA A*0211	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.513441	1.710232	-2.803209	32616.741498
HLA B*0803	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.412460	1.609246	-2.803214	25849.949932

HLA A*3001	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.298672	1.495432	-2.803240	19891.695301
HLA B*5101	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.483264	1.679828	-2.803436	30427.325910
HLA A*0201	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.331405	1.527790	-2.803615	21448.890060
HLA A*2301	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.517322	1.713576	-2.803746	32909.548258
HLA A*2601	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.358424	1.554677	-2.803746	22825.689262
HLA A*0211	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.331623	1.527790	-2.803833	21459.684134
HLA B*5301	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.568202	1.764296	-2.803906	37000.054868
HLA A*3301	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.377262	1.573351	-2.803911	23837.574943
HLA B*0702	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.397595	1.593495	-2.804100	24980.119674
HLA B*4402	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.403795	1.599646	-2.804149	25339.311219
HLA A*2403	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.456118	1.651959	-2.804158	28583.659950
HLA B*0802	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.403870	1.599646	-2.804224	25343.698250
HLA B*1801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.321553	1.517234	-2.804319	20967.827379
HLA B*3501	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.189010	1.384650	-2.804360	15452.885464
HLA B*1517	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-3.988204	1.183813	-2.804391	9732.038122
HLA B*4801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.389851	1.585411	-2.804439	24538.646941
HLA A*2402	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.518468	1.713576	-2.804892	32996.545105
HLA B*4002	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.634070	1.828963	-2.805108	43059.618736
HLA B*4601	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.405132	1.599646	-2.805486	25417.431543
HLA A*2301	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.497981	1.692204	-2.805777	31476.103185
HLA B*5101	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.511653	1.705831	-2.805821	32482.736831
HLA A*3301	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.549656	1.743756	-2.805899	35453.207579
HLA A*0206	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.369849	1.563919	-2.805930	23434.162993
HLA B*7301	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.581703	1.775750	-2.805952	38168.272915
HLA A*2601	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.342610	1.536595	-2.806014	22009.466580
HLA A*0212	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.360867	1.554677	-2.806190	22954.475042
HLA A*2402	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.300298	1.493912	-2.806386	19966.302276
HLA A*0219	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.458503	1.651959	-2.806543	28741.045608
HLA A*2501	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.416057	1.609455	-2.806602	26064.942296
HLA A*6801	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.650512	1.843794	-2.806718	44721.038098
HLA B*5701	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.416177	1.609455	-2.806721	26072.134719
HLA B*3801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.499104	1.692204	-2.806900	31557.603421
HLA A*2603	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.635922	1.828963	-2.806959	43243.573394
HLA A*2402	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.533773	1.726550	-2.807223	34180.075277
HLA A*0211	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-3.514092	0.706599	-2.807493	3266.568915
HLA A*0301	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.362395	1.554677	-2.807717	23035.334885
HLA A*0211	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.401295	1.593495	-2.807800	25193.874029
HLA B*0702	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.417372	1.609455	-2.807917	26144.026761
HLA B*4501	1:250-258	9	VLGEGTKKL	1.458243	0.385551	-4.651750	1.843794	-2.807956	44848.720221
HLA A*8001	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.393676	1.585411	-2.808264	24755.720668
HLA B*5101	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.945664	1.137355	-2.808309	8823.970063
HLA B*1503	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.336120	1.527790	-2.808330	21683.043425
HLA B*5401	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.552301	1.743756	-2.808545	35669.831155
HLA B*1501	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.245613	1.437023	-2.808591	17604.081817
HLA B*3501	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.381966	1.573351	-2.808615	24097.153293
HLA A*0211	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.519030	1.710050	-2.808980	33039.236026
HLA A*3201	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.589623	1.780575	-2.809048	38870.723377
HLA A*0202	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.589705	1.780575	-2.809130	38878.084095
HLA B*4002	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.582649	1.773509	-2.809140	38251.577601
HLA A*3301	1:140-148	9	TDAQRAAYL	1.463082	0.301720	-4.574161	1.764802	-2.809359	37511.174469
HLA B*5101	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.517463	1.708081	-2.809382	32920.232213
HLA A*1101	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.465459	1.655822	-2.809637	29205.146489
HLA B*4601	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.395254	1.585411	-2.809843	24845.882531
HLA B*4601	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.366856	1.556999	-2.809858	23273.205396
HLA B*5401	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-3.035008	0.225072	-2.809937	1083.947725
HLA A*0211	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.523569	1.713576	-2.809993	33386.369955
HLA B*1509	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.303921	1.493912	-2.810009	20133.558810
HLA A*2402	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.229928	1.419915	-2.810013	16979.629768
HLA A*0202	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.409713	1.599646	-2.810068	25686.986549
HLA B*0802	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.411607	1.601532	-2.810075	25799.235877
HLA B*4501	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.658662	1.848352	-2.810310	45568.238390
HLA A*2301	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.520712	1.710232	-2.810481	33167.461045
HLA B*3901	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.367556	1.556999	-2.810558	23310.755484
HLA B*7301	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.599970	1.789240	-2.810730	39807.944648
HLA A*2403	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-3.068484	0.257713	-2.810770	1170.802930

HLA A*0216	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.864936	1.054023	-2.810913	7327.160780
HLA B*3801	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.328181	1.517234	-2.810947	21290.277874
HLA A*2603	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.524643	1.713576	-2.811067	33469.013842
HLA B*4403	1:402-410	9	LGPDGAAVL	1.624819	0.223533	-4.659431	1.848352	-2.811079	45648.921486
HLA B*4402	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.411464	1.600184	-2.811279	25790.723451
HLA A*0101	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.368350	1.556999	-2.811352	23353.419186
HLA B*1801	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.440834	1.629468	-2.811367	27595.256590
HLA B*3501	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.404916	1.593495	-2.811421	25404.784186
HLA A*3002	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.271366	1.459786	-2.811580	18679.535969
HLA A*0212	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.411898	1.600184	-2.811714	25816.548488
HLA B*4801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.342748	1.530697	-2.812051	22016.492759
HLA B*3501	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.339879	1.527790	-2.812090	21871.542633
HLA B*4501	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.641123	1.828963	-2.812161	43764.637350
HLA B*4501	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.525336	1.713159	-2.812177	33522.470265
HLA A*0211	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.529617	1.717294	-2.812322	33854.528986
HLA A*0219	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.455740	1.643417	-2.812322	28558.774645
HLA A*0219	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.726730	0.914083	-2.812646	5330.029535
HLA A*2902	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.456162	1.643417	-2.812745	28586.598155
HLA A*2403	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.376968	1.563919	-2.813049	23821.460563
HLA A*0203	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.925881	1.112802	-2.813079	8431.044126
HLA B*3501	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.412901	1.599646	-2.813256	25876.254235
HLA B*0802	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.465401	1.651959	-2.813441	29201.196841
HLA A*0216	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.407213	1.593495	-2.813718	25539.553847
HLA B*0802	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.371095	1.556999	-2.814096	23501.450810
HLA A*0250	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-3.769457	0.955018	-2.814439	5881.083558
HLA B*4001	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.331691	1.517234	-2.814457	21463.051139
HLA A*0206	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.462504	1.648036	-2.814467	29007.061572
HLA A*2501	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.387875	1.573351	-2.814523	24427.256637
HLA B*0702	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.387896	1.573351	-2.814545	24428.446004
HLA B*0801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.234705	1.419915	-2.814790	17167.407635
HLA B*5301	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.564638	1.749555	-2.815083	36697.645354
HLA A*1101	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.400755	1.585411	-2.815343	25162.545429
HLA B*3801	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.525677	1.710232	-2.815445	33548.776744
HLA B*1503	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.400926	1.585411	-2.815515	25172.484632
HLA B*0702	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-3.717881	0.902312	-2.815570	5222.536153
HLA A*2902	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.370258	1.554677	-2.815581	23456.232441
HLA A*2601	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.309588	1.493912	-2.815676	20397.996148
HLA B*5401	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.508072	1.692204	-2.815868	32216.028324
HLA A*3101	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.343662	1.527790	-2.815872	22062.874085
HLA A*0201	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.370719	1.554677	-2.816041	23481.117173
HLA B*4002	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.144849	1.328755	-2.816094	13958.818667
HLA A*0219	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.458460	1.642298	-2.816163	28738.246998
HLA A*6801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.459901	1.643417	-2.816483	28833.708757
HLA A*2402	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.580986	1.764418	-2.816568	38105.346576
HLA B*3501	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.460072	1.643417	-2.816655	28845.098069
HLA B*1801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.312116	1.495432	-2.816683	20517.079974
HLA A*2902	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.591005	0.774156	-2.816849	3899.460864
HLA A*3101	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.001380	1.184382	-2.816998	10031.819592
HLA A*0219	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.265387	1.448126	-2.817261	18424.115354
HLA B*5401	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.527380	1.710050	-2.817330	33680.619123
HLA A*2501	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.473558	1.655822	-2.817736	29754.870451
HLA A*0206	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.531372	1.713576	-2.817796	33991.618291
HLA A*2301	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.523635	1.705831	-2.817804	33391.427602
HLA A*6802	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.411308	1.593495	-2.817814	25781.516447
HLA B*3901	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.156540	1.338560	-2.817980	14339.688025
HLA B*4403	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.532427	1.714405	-2.818022	34074.285659
HLA B*1502	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.466336	1.648036	-2.818299	29264.138722
HLA B*0801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.418688	1.600184	-2.818504	26223.351179
HLA A*0101	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.382574	1.563919	-2.818655	24130.940957
HLA A*0216	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.462142	1.643417	-2.818725	28982.905188
HLA B*3501	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.382715	1.563919	-2.818796	24138.774972
HLA B*0803	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.248649	1.429823	-2.818826	17727.557918
HLA A*3002	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.529229	1.710232	-2.818998	33824.322844
HLA A*0250	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.511584	1.692204	-2.819380	32477.641119
HLA A*3002	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.412876	1.593495	-2.819381	25874.714416

HLA B*3501	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.404822	1.585411	-2.819410	25399.287298
HLA A*2501	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.462884	1.643417	-2.819467	29032.494563
HLA A*0216	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.279298	1.459786	-2.819512	19023.829493
HLA B*4801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.356121	1.536595	-2.819526	22704.994728
HLA B*1502	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.546237	1.726550	-2.819687	35175.237044
HLA A*1101	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.499536	1.679828	-2.819709	31589.032118
HLA B*1801	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.468767	1.648791	-2.819977	29428.455114
HLA A*2403	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.405423	1.585411	-2.820012	25434.487944
HLA A*2403	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.313941	1.493912	-2.820030	20603.504704
HLA A*2402	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.374779	1.554677	-2.820101	23701.654647
HLA B*4001	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.420319	1.600184	-2.820134	26321.990836
HLA B*7301	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.610900	1.790732	-2.820168	40822.496364
HLA B*5701	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.420471	1.600184	-2.820287	26331.248402
HLA A*0101	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.348220	1.527790	-2.820430	22295.647391
HLA B*0802	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.384553	1.563919	-2.820633	24241.111179
HLA A*0212	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.414276	1.593495	-2.820781	25958.276743
HLA A*2402	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.538178	1.717294	-2.820884	34528.546691
HLA B*1509	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.430339	1.609246	-2.821093	26936.383534
HLA B*5801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.251156	1.429823	-2.821333	17830.183528
HLA B*7301	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.568583	1.747156	-2.821427	37032.496005
HLA B*1503	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-3.505272	0.683810	-2.821462	3200.898171
HLA A*2501	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.415037	1.593495	-2.821542	26003.816416
HLA B*1801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.150379	1.328755	-2.821624	14137.719255
HLA A*2603	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.510370	1.688566	-2.821804	32386.930906
HLA A*0250	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.510464	1.688566	-2.821898	32393.940052
HLA B*1502	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.586434	1.764418	-2.822016	38586.409744
HLA A*0202	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.422295	1.600184	-2.822110	26442.021285
HLA A*2301	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.386035	1.563919	-2.822116	24324.003008
HLA B*0802	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.422304	1.600184	-2.822120	26442.593484
HLA A*3101	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.259480	1.437023	-2.822457	18175.235165
HLA A*8001	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.464938	1.642298	-2.822640	29170.092297
HLA A*8001	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.377375	1.554677	-2.822697	23843.765762
HLA A*0212	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.207519	1.384650	-2.822869	16125.709376
HLA B*5701	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.386834	1.563919	-2.822915	24368.784834
HLA B*5401	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.537335	1.714405	-2.822930	34461.552144
HLA B*0801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.282900	1.459786	-2.823113	19182.257001
HLA B*4402	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.377798	1.554677	-2.823120	23866.995654
HLA B*5701	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.380692	1.556999	-2.823694	24026.600074
HLA B*7301	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.604431	1.780575	-2.823857	40219.014694
HLA A*0202	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.208628	1.384650	-2.823978	16166.938469
HLA A*3201	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.204467	0.380458	-2.824009	1601.280052
HLA A*6901	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.388058	1.563919	-2.824139	24437.566414
HLA A*0301	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.319996	1.495432	-2.824564	20892.755601
HLA A*8001	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.388542	1.563919	-2.824623	24464.815727
HLA B*3801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.476603	1.651959	-2.824644	29964.221329
HLA A*0212	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.433913	1.609246	-2.824667	27158.942387
HLA B*2705	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.352574	1.527790	-2.824784	22520.274666
HLA B*0803	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.486741	1.661630	-2.825111	30671.924329
HLA A*3201	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.538695	1.713576	-2.825119	34569.666190
HLA A*2301	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.535248	1.710050	-2.825199	34296.396503
HLA B*5301	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.481156	1.655822	-2.825334	30280.029800
HLA A*3002	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.589851	1.764418	-2.825432	38891.126502
HLA B*4002	1:364-372	9	AAAELVQTR	0.986953	0.803779	-4.616407	1.790732	-2.825675	41343.453557
HLA B*0803	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.469150	1.643417	-2.825733	29454.416921
HLA A*3301	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.590050	1.764296	-2.825754	38909.014332
HLA B*1501	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.389879	1.563919	-2.825960	24540.240009
HLA B*4601	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.390163	1.563919	-2.826244	24556.309225
HLA A*3101	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-3.988965	1.162617	-2.826348	9749.111437
HLA B*4501	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.602531	1.775750	-2.826781	40043.376770
HLA B*3501	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.478971	1.651959	-2.827012	30128.067604
HLA B*0803	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.363668	1.536595	-2.827073	23102.977291
HLA A*2501	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.436387	1.609246	-2.827141	27314.097890
HLA A*1101	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.479413	1.651959	-2.827454	30158.725219
HLA A*0202	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-3.581879	0.754283	-2.827596	3818.380173
HLA B*5301	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.429186	1.601532	-2.827654	26864.928558

HLA A*3002	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.554606	1.726550	-2.828056	35859.637777
HLA A*0201	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.392303	1.563919	-2.828384	24677.631478
HLA B*4002	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.323870	1.495432	-2.828438	21079.971762
HLA B*4801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.385516	1.556999	-2.828517	24294.938960
HLA A*0206	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.010444	1.181912	-2.828532	10243.397511
HLA B*1509	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.258049	1.429220	-2.828829	18115.453160
HLA B*4501	1:434-442	9	DALIEGLAL	1.463983	0.353635	-4.646468	1.817618	-2.828850	44306.598782
HLA B*4402	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.030067	1.200757	-2.829310	10716.844402
HLA B*1517	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.472851	1.643417	-2.829434	29706.457743
HLA B*0803	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.393422	1.563919	-2.829503	24741.260916
HLA B*5701	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.415077	1.585411	-2.829666	26006.208048
HLA A*0301	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.366316	1.536595	-2.829720	23244.265149
HLA A*2301	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.486833	1.657009	-2.829824	30678.396349
HLA B*4402	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.357656	1.527790	-2.829866	22785.345543
HLA B*3501	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.472202	1.642298	-2.829905	29662.135255
HLA B*5301	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.152795	1.322784	-2.830011	14216.563324
HLA A*2603	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.323983	1.493912	-2.830071	21085.446407
HLA A*0206	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.153034	1.322784	-2.830251	14224.410312
HLA A*0202	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.431805	1.601532	-2.830273	27027.468246
HLA B*1509	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.479075	1.648791	-2.830284	30135.239996
HLA B*4501	1:53-61	9	DSEESYLAL	1.497889	0.291351	-4.619569	1.789240	-2.830329	41645.603377
HLA A*1101	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.439610	1.609246	-2.830364	27517.587426
HLA A*0101	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.367030	1.536595	-2.830435	23282.524266
HLA B*5401	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.475825	1.645215	-2.830610	29910.613210
HLA B*5401	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.543770	1.713159	-2.830611	34975.994627
HLA A*3002	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.605191	0.774156	-2.831035	4028.939598
HLA B*4501	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.607091	1.776041	-2.831051	40466.071434
HLA B*4601	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.361819	1.530697	-2.831122	23004.823550
HLA B*3501	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-3.754604	0.923460	-2.831144	5683.343502
HLA A*3101	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.395412	1.563919	-2.831493	24854.889866
HLA A*0206	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-3.757419	0.925719	-2.831700	5720.297139
HLA B*4403	1:206-214	9	LMKITHVLR	1.064507	0.764456	-4.660671	1.828963	-2.831708	45779.500451
HLA B*3501	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.431909	1.600184	-2.831724	27033.902498
HLA A*3201	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.493531	1.661630	-2.831901	31155.235310
HLA B*5801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.363066	1.530697	-2.832370	23071.003393
HLA A*0202	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.016210	1.183813	-2.832397	10380.294204
HLA A*6802	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.171153	1.338560	-2.832594	14830.421678
HLA A*2601	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.396565	1.563919	-2.832646	24920.998568
HLA B*3501	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.171252	1.338560	-2.832693	14833.791760
HLA A*3201	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.161563	1.328755	-2.832808	14506.508668
HLA B*0803	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.406309	1.573351	-2.832958	25486.415235
HLA A*0202	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.597639	1.764418	-2.833221	39594.883153
HLA B*2705	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.433720	1.600184	-2.833536	27146.897056
HLA B*5101	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.490618	1.657009	-2.833609	30946.937252
HLA B*1517	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.485724	1.651959	-2.833764	30600.159985
HLA B*1501	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.361612	1.527790	-2.833822	22993.874245
HLA A*6802	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-3.739868	0.905846	-2.834022	5493.737898
HLA B*4402	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.391046	1.556999	-2.834048	24606.310500
HLA A*2403	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.361885	1.527790	-2.834095	23008.308514
HLA A*1101	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.298660	1.464436	-2.834224	19891.157248
HLA A*0301	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.362197	1.527790	-2.834407	23024.869300
HLA B*1517	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.301073	1.466619	-2.834454	20001.979222
HLA A*0202	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.483386	1.648791	-2.834595	30435.886754
HLA A*2602	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.514479	1.679828	-2.834651	32694.827025
HLA A*0219	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.443905	1.609246	-2.834659	27791.066507
HLA A*2403	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.428502	1.593495	-2.835007	26822.668972
HLA A*0250	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.599481	1.764418	-2.835063	39763.175675
HLA A*6801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-3.438283	0.603125	-2.835158	2743.363410
HLA B*4403	1:283-291	9	YLALLGWSI	1.492210	0.300064	-4.627442	1.792274	-2.835168	42407.462130
HLA A*0203	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.222095	1.386690	-2.835405	16676.120838
HLA B*1517	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.477757	1.642298	-2.835459	30043.919762
HLA B*5801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.329589	1.493912	-2.835677	21359.381427
HLA A*0203	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.058543	1.222401	-2.836142	11443.073395
HLA A*8001	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.393217	1.556999	-2.836219	24729.618926
HLA B*4402	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.409723	1.573351	-2.836371	25687.542410

HLA B*3801	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.466315	1.629468	-2.836847	29262.713915
HLA A*3201	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.492775	1.655822	-2.836952	31101.010622
HLA A*0216	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.479366	1.642298	-2.837068	30155.462289
HLA B*2705	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.367768	1.530697	-2.837071	23322.108021
HLA B*2705	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.373839	1.536595	-2.837244	23650.420771
HLA B*1503	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.259175	1.421817	-2.837358	18162.457278
HLA A*2402	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.543192	1.705831	-2.837361	34929.478388
HLA B*5101	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.392092	1.554677	-2.837415	24665.619110
HLA A*0250	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.564204	1.726550	-2.837653	36660.935642
HLA A*0203	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.401612	1.563919	-2.837693	25212.280719
HLA B*5801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.267083	1.429220	-2.837863	18496.219568
HLA A*3201	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.548265	1.710232	-2.838033	35339.844837
HLA A*0202	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.564631	1.726550	-2.838081	36697.049769
HLA A*0206	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.487075	1.648791	-2.838284	30695.495685
HLA B*5701	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-3.975747	1.137355	-2.838392	9456.857218
HLA A*3001	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.270758	1.432365	-2.838392	18653.381254
HLA A*2501	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.490404	1.651959	-2.838444	30931.705827
HLA A*0203	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.802505	0.963515	-2.838990	6346.075080
HLA B*2705	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.424736	1.585411	-2.839325	26591.067068
HLA A*2902	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.276460	1.437023	-2.839437	18899.911341
HLA A*2902	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.439751	1.600184	-2.839567	27526.520902
HLA A*2403	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.449194	1.609246	-2.839948	28131.565712
HLA A*6901	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.370735	1.530697	-2.840038	23482.006401
HLA A*1101	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.260298	1.419915	-2.840383	18209.484845
HLA A*3301	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.377001	1.536595	-2.840406	23823.264832
HLA A*0101	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.371212	1.530697	-2.840515	23507.808682
HLA B*1502	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.082343	1.241782	-2.840561	12087.680341
HLA B*4002	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-3.889713	1.048747	-2.840966	7757.350064
HLA A*3001	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.178785	1.337733	-2.841051	15093.314686
HLA A*1101	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.154867	1.313812	-2.841055	14284.560066
HLA A*0206	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.434601	1.593495	-2.841106	27202.026096
HLA B*3801	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.491694	1.650564	-2.841129	31023.710455
HLA B*5101	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.179889	1.338560	-2.841329	15131.740502
HLA B*5101	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.491945	1.650564	-2.841381	31041.673981
HLA B*5701	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.358788	1.517234	-2.841554	22844.837379
HLA A*2602	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.335514	1.493912	-2.841603	21652.800397
HLA A*0219	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.443388	1.601532	-2.841856	27758.009933
HLA A*0250	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-3.954766	1.112802	-2.841964	9010.853542
HLA A*0212	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.042735	1.200757	-2.841978	11034.060183
HLA A*0212	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.756493	0.914377	-2.842116	5708.117332
HLA B*3501	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.302015	1.459786	-2.842229	20045.417927
HLA A*0206	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.443858	1.601532	-2.842326	27788.059738
HLA A*2902	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.451879	1.609246	-2.842633	28306.056267
HLA A*2403	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.262626	1.419915	-2.842711	18307.371699
HLA A*0301	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.336684	1.493912	-2.842773	21711.214396
HLA B*4402	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.436269	1.593495	-2.842775	27306.710577
HLA A*8001	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.442980	1.600184	-2.842795	27731.893037
HLA B*5301	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.607627	1.764418	-2.843208	40516.015296
HLA B*1801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.499036	1.655822	-2.843214	31552.652839
HLA B*5401	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.551458	1.708081	-2.843377	35600.622214
HLA A*0206	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.549244	1.705831	-2.843413	35419.658826
HLA A*6802	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.005947	1.162401	-2.843546	10137.879205
HLA B*1501	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.157470	1.313812	-2.843658	14370.441100
HLA A*0206	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.479691	0.635887	-2.843804	3017.801469
HLA B*5701	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.371821	1.527790	-2.844031	23540.770001
HLA A*1101	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.401065	1.556999	-2.844066	25180.520555
HLA B*2705	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.398849	1.554677	-2.844172	25052.388600
HLA B*4402	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-3.949329	1.105060	-2.844269	8898.754440
HLA A*2501	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.445886	1.601532	-2.844354	27918.098127
HLA B*1801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.453618	1.609246	-2.844372	28419.601538
HLA A*0250	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.494990	1.650564	-2.844426	31260.078619
HLA B*0802	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.372610	1.527790	-2.844820	23583.599508
HLA B*4001	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.372666	1.527790	-2.844877	23586.661739
HLA A*2403	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.274714	1.429823	-2.844891	18824.094723
HLA B*1501	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.311643	1.466619	-2.845024	20494.782079

HLA B*3901	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.454339	1.609246	-2.845093	28466.841052
HLA A*0202	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.555348	1.710232	-2.845117	35920.993152
HLA B*5401	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.558807	1.713576	-2.845231	36208.186833
HLA A*0219	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.445421	1.600184	-2.845236	27888.209442
HLA A*6802	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.409704	1.563919	-2.845785	25686.430700
HLA A*0216	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.497800	1.651959	-2.845841	31462.994184
HLA B*4501	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.267849	1.421817	-2.846032	18528.868724
HLA A*2602	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.507797	1.661630	-2.846167	32195.643414
HLA B*1801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.446422	1.600184	-2.846237	27952.555083
HLA A*0202	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.114559	1.268289	-2.846270	13018.444768
HLA A*2601	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.374248	1.527790	-2.846458	23672.693884
HLA A*2301	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.508204	1.661630	-2.846573	32225.789770
HLA A*6802	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-3.895620	1.048747	-2.846873	7863.574315
HLA B*4601	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.374692	1.527790	-2.846902	23696.910859
HLA A*0211	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.552776	1.705831	-2.846944	35708.832368
HLA A*0219	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.440590	1.593495	-2.847095	27579.735080
HLA B*1801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.184851	1.337733	-2.847118	15305.622485
HLA B*4501	1:374-382	9	VVLGDAWEL	1.258066	0.515443	-4.620732	1.773509	-2.847223	41757.275392
HLA B*5101	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.499207	1.651959	-2.847248	31565.116134
HLA A*2501	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.404422	1.556999	-2.847423	25375.938790
HLA B*5701	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-3.995760	1.148177	-2.847582	9902.839613
HLA B*3901	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.448083	1.599646	-2.848437	28059.672502
HLA B*5301	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.558525	1.710050	-2.848475	36184.688588
HLA A*2902	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.412420	1.563919	-2.848501	25847.572670
HLA A*0216	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.376350	1.527790	-2.848561	23787.591469
HLA A*2402	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.510264	1.661630	-2.848634	32379.047429
HLA B*4402	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.504144	0.655319	-2.848825	3192.597031
HLA A*3201	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.575469	1.726550	-2.848919	37624.377673
HLA A*0201	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.297213	1.448126	-2.849087	19824.980460
HLA B*0803	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.376985	1.527790	-2.849195	23822.362680
HLA A*2403	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-3.717999	0.868794	-2.849205	5223.949011
HLA A*2602	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.562582	1.713159	-2.849423	36524.341938
HLA A*6802	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.150271	1.300706	-2.849565	14134.201452
HLA B*5101	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.511303	1.661630	-2.849672	32456.563908
HLA A*0202	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.563344	1.713576	-2.849767	36588.418094
HLA B*7301	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.564359	1.714405	-2.849954	36674.027864
HLA B*7301	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.621970	1.771882	-2.850088	41876.495736
HLA B*1517	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.298237	1.448126	-2.850111	19871.797064
HLA A*8001	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.443722	1.593495	-2.850227	27779.341947
HLA A*6801	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.479916	1.629468	-2.850448	30193.660685
HLA A*2402	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.287862	1.437023	-2.850839	19402.684312
HLA B*4403	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.631685	1.780575	-2.851111	42823.824725
HLA B*1509	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.281001	1.429823	-2.851179	19098.590697
HLA B*4001	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.249279	1.398016	-2.851263	17753.278864
HLA B*5101	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.460657	1.609246	-2.851411	28883.980398
HLA B*1503	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-3.882604	1.031013	-2.851591	7631.393514
HLA A*3002	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.280877	1.429220	-2.851657	19093.115455
HLA A*0203	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.382452	1.530697	-2.851755	24124.153535
HLA A*3101	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-3.961429	1.109528	-2.851901	9150.168052
HLA B*3801	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.461209	1.609246	-2.851963	28920.724646
HLA A*8001	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.461315	1.609246	-2.852069	28927.766110
HLA B*5401	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.558194	1.705831	-2.852362	36157.097636
HLA A*6802	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.453942	1.601532	-2.852410	28440.826531
HLA A*8001	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.389282	1.536595	-2.852687	24506.542132
HLA A*2603	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.570075	1.717294	-2.852780	37159.931747
HLA A*3301	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.628572	1.775750	-2.852822	42517.956690
HLA B*4501	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.409894	1.556999	-2.852895	25697.688986
HLA B*0702	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.453254	1.600184	-2.853069	28395.780758
HLA A*0203	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.907316	1.054023	-2.853293	8078.221030
HLA B*1509	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.505283	1.651959	-2.853324	32009.814674
HLA B*0702	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.282611	1.429220	-2.853391	19169.497059
HLA B*1501	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.348878	1.495432	-2.853446	22329.445738
HLA A*0301	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.283398	1.429823	-2.853575	19204.269685
HLA A*2602	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.542271	1.688566	-2.853705	34855.482750
HLA B*1502	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.564086	1.710232	-2.853855	36651.020403

HLA B*1509	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.273781	1.419915	-2.853867	18783.709110
HLA B*1503	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.237376	1.383422	-2.853954	17273.330548
HLA B*0803	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.453834	1.599646	-2.854189	28433.749773
HLA A*0219	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.314141	1.459786	-2.854354	20612.981210
HLA B*0702	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.440087	1.585411	-2.854676	27547.824047
HLA B*5101	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.464179	1.609455	-2.854724	29119.165155
HLA B*7301	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.598513	1.743756	-2.854757	39674.647250
HLA A*3201	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-3.450877	0.595974	-2.854902	2824.077310
HLA A*0101	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.348951	1.493912	-2.855039	22333.190846
HLA B*0803	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.409770	1.554677	-2.855092	25690.321895
HLA A*0202	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.572537	1.717294	-2.855243	37371.210715
HLA A*0216	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.464710	1.609246	-2.855464	29154.789037
HLA A*0211	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.503906	1.648036	-2.855870	31908.498000
HLA A*0250	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.566184	1.710232	-2.855953	36828.511005
HLA B*1501	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.386773	1.530697	-2.856076	24365.357432
HLA B*2705	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-3.633526	0.777400	-2.856125	4300.565292
HLA B*1509	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.504780	1.648036	-2.856744	31972.777833
HLA B*4001	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.276706	1.419915	-2.856792	18910.650265
HLA B*3901	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.350913	1.493912	-2.857001	22434.303823
HLA B*4501	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.442453	1.585411	-2.857042	27698.307462
HLA B*5101	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.456689	1.599646	-2.857043	28621.260827
HLA B*5801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.352548	1.495432	-2.857116	22518.934552
HLA A*0301	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.289636	1.432365	-2.857270	19482.095989
HLA B*0802	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.430685	1.573351	-2.857333	26957.813313
HLA A*8001	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.351314	1.493912	-2.857403	22455.067200
HLA B*0802	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.412119	1.554677	-2.857442	25829.680306
HLA B*4501	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.549778	1.692204	-2.857574	35463.182474
HLA A*2301	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.506376	1.648791	-2.857585	32090.439882
HLA B*4002	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.638273	1.780575	-2.857699	43478.385490
HLA B*5701	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.195287	1.337377	-2.857911	15677.882656
HLA A*2602	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.467715	1.609246	-2.858469	29357.217778
HLA B*1801	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.510539	1.651959	-2.858580	32399.548462
HLA B*3901	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.458792	1.600184	-2.858607	28760.176734
HLA A*2501	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.458331	1.599646	-2.858686	28729.697380
HLA B*0801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.245538	1.386690	-2.858848	17601.034524
HLA A*0250	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.576261	1.717294	-2.858967	37693.034470
HLA A*3301	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.280938	1.421817	-2.859121	19095.801226
HLA B*4001	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.390144	1.530697	-2.859447	24555.246473
HLA A*0250	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.319258	1.459786	-2.859472	20857.295095
HLA A*2602	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.569532	1.710050	-2.859482	37113.522564
HLA A*3001	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.160595	1.300814	-2.859781	14474.211490
HLA A*3001	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.827367	0.967578	-2.859789	6719.971887
HLA B*1517	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.289680	1.429823	-2.859858	19484.098616
HLA A*2301	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.090966	1.230828	-2.860137	12330.070975
HLA A*3201	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.624562	1.764418	-2.860144	42127.124317
HLA B*5101	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.503749	1.643417	-2.860332	31896.934459
HLA B*1503	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.731964	0.871584	-2.860380	5394.662358
HLA B*5401	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.510978	1.650564	-2.860414	32432.342026
HLA A*0201	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.391256	1.530697	-2.860559	24618.160803
HLA A*3301	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.577997	1.717294	-2.860703	37844.029388
HLA A*0202	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-3.867628	1.006851	-2.860777	7372.728327
HLA A*2403	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.391486	1.530697	-2.860789	24631.216052
HLA B*4001	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.290435	1.429220	-2.861215	19517.963599
HLA A*6801	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.633603	1.771882	-2.861720	43013.287075
HLA A*1101	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.398356	1.536595	-2.861760	25023.943326
HLA B*5101	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.418832	1.556999	-2.861833	26232.006398
HLA B*7301	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.550619	1.688566	-2.862053	35531.932003
HLA A*1101	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.462182	1.599646	-2.862536	28985.570814
HLA B*3801	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.524201	1.661630	-2.862571	33434.991180
HLA B*3801	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.506343	1.643417	-2.862926	32088.009494
HLA A*3001	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.284784	1.421817	-2.862967	19265.664466
HLA B*2705	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.462638	1.599646	-2.862992	29016.007675
HLA A*0202	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.524746	1.661630	-2.863116	33476.981591
HLA A*6801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-2.727249	-0.136008	-2.863258	533.641133
HLA A*0201	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.292580	1.429220	-2.863360	19614.605759

HLA B*5101	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.505713	1.642298	-2.863415	32041.520393
HLA A*2601	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.300995	1.437023	-2.863973	19998.408660
HLA B*1509	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.391822	1.527790	-2.864032	24650.278482
HLA B*5101	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.513123	1.648791	-2.864333	32592.929045
HLA B*0801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-3.757846	0.893488	-2.864358	5725.932116
HLA B*5701	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.419076	1.554677	-2.864398	26246.769424
HLA A*2601	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.395137	1.530697	-2.864440	24839.162767
HLA B*0702	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.392245	1.527790	-2.864455	24674.294122
HLA A*2603	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.526201	1.661630	-2.864570	33589.274589
HLA B*3801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.512693	1.648036	-2.864657	32560.677696
HLA B*5101	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-3.551265	0.686428	-2.864837	3558.486943
HLA B*5101	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.466566	1.601532	-2.865034	29279.657779
HLA B*5401	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-3.927282	1.062125	-2.865156	8458.272163
HLA A*0203	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.263291	1.398016	-2.865275	18335.421727
HLA A*3301	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.495103	1.629468	-2.865635	31268.197124
HLA B*5401	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.522660	1.657009	-2.865651	33316.544466
HLA A*0212	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.429698	1.563919	-2.865779	26896.630559
HLA A*0203	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-3.252843	0.387024	-2.865819	1789.959438
HLA B*5701	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.303004	1.437023	-2.865982	20091.124666
HLA B*4501	1:325-333	9	DALNAEHIR	1.176166	0.604409	-4.646593	1.780575	-2.866018	44319.304374
HLA A*2501	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.508342	1.642298	-2.866045	32236.077351
HLA B*1502	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.459783	1.593495	-2.866288	28825.910453
HLA B*0803	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.466662	1.600184	-2.866478	29286.152887
HLA A*2403	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.286887	1.420375	-2.866511	19359.172131
HLA B*1502	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.580164	1.713576	-2.866587	38033.263846
HLA B*3501	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.296555	1.429823	-2.866732	19794.972928
HLA B*4501	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.616320	1.749555	-2.866764	41335.178835
HLA B*1517	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.430910	1.563919	-2.866991	26971.817472
HLA A*3201	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.510464	1.643417	-2.867047	32393.940052
HLA A*3002	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.584625	1.717294	-2.867331	38426.007948
HLA B*4403	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.573195	1.705831	-2.867364	37427.862361
HLA B*5801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.265483	1.398016	-2.867467	18428.202376
HLA B*1509	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.440867	1.573351	-2.867516	27597.346691
HLA B*5301	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.422245	1.554677	-2.867568	26439.017439
HLA B*4001	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.361535	1.493912	-2.867623	22989.769599
HLA B*1517	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.175618	1.307776	-2.867842	14983.646593
HLA A*2602	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.109959	1.241782	-2.868177	12881.273851
HLA A*3301	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.511834	1.643417	-2.868416	32496.270706
HLA B*1801	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.510783	1.642298	-2.868486	32417.782499
HLA A*3002	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.520621	1.651959	-2.868661	33160.463924
HLA B*5701	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.405315	1.536595	-2.868720	25428.159234
HLA B*4601	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.174039	1.305053	-2.868986	14929.273258
HLA A*6901	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-3.576438	0.707098	-2.869340	3770.836993
HLA B*5101	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.137683	1.268289	-2.869394	13730.385672
HLA A*2301	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.511721	1.642298	-2.869423	32487.833343
HLA B*3801	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.526452	1.657009	-2.869443	33608.723643
HLA B*7301	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-3.742730	0.872828	-2.869902	5530.057009
HLA B*5101	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.443428	1.573351	-2.870077	27760.562902
HLA B*4601	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.336912	1.466619	-2.870293	21722.610546
HLA B*0801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.318436	1.448126	-2.870310	20817.839981
HLA B*4002	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.614158	1.743756	-2.870402	41129.960718
HLA A*3301	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.262302	1.391860	-2.870442	18293.709162
HLA B*3901	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.175768	1.305053	-2.870715	14988.835322
HLA B*4501	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.642674	1.771882	-2.870792	43921.179465
HLA B*2705	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.300819	1.429823	-2.870997	19990.296118
HLA B*0802	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.401732	1.530697	-2.871035	25219.237856
HLA A*2902	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.401873	1.530697	-2.871176	25227.425182
HLA B*4002	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.635802	1.764418	-2.871383	43231.643950
HLA B*5101	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.435590	1.563919	-2.871671	27264.051040
HLA B*1501	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.892227	1.020365	-2.871862	7802.384333
HLA A*8001	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.308970	1.437023	-2.871947	20368.994499
HLA A*0212	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.473863	1.601532	-2.872332	29775.803983
HLA A*0250	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.586030	1.713576	-2.872454	38550.521753
HLA A*3002	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.552614	1.679828	-2.872786	35695.505378
HLA B*4001	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.256398	1.383422	-2.872976	18046.688182

HLA B*0702	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.259750	1.386690	-2.873060	18186.546174
HLA A*2601	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.302290	1.429220	-2.873070	20058.109831
HLA B*0802	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.409697	1.536595	-2.873101	25686.013821
HLA A*3101	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.295133	1.421817	-2.873317	19730.290230
HLA A*1101	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.474855	1.601532	-2.873323	29843.859000
HLA B*1801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.446769	1.573351	-2.873418	27974.944639
HLA B*4402	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.390772	1.517234	-2.873537	24590.740691
HLA B*4601	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.367474	1.493912	-2.873563	23306.342100
HLA A*3001	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.293989	1.420375	-2.873614	19678.376907
HLA B*3501	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.430795	1.556999	-2.873796	26964.668607
HLA B*3501	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-3.268148	0.394299	-2.873849	1854.162251
HLA B*4403	1:20-28	9	HVGLVRTAL	1.472888	0.303153	-4.650178	1.776041	-2.874138	44686.696399
HLA A*6801	1:319-327	9	FDQKKADAL	1.490473	0.285277	-4.650183	1.775750	-2.874433	44687.179902
HLA A*2603	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.587776	1.713159	-2.874617	38705.789255
HLA B*5401	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-3.615176	0.740545	-2.874631	4122.646218
HLA A*3002	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.522923	1.648036	-2.874887	33336.737330
HLA A*0250	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.402688	1.527790	-2.874898	25274.827379
HLA A*3002	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.460326	1.585411	-2.874915	28861.956262
HLA A*0250	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.838471	0.963515	-2.874956	6893.997511
HLA B*0702	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.259795	1.384650	-2.875145	18188.415627
HLA B*3801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.476720	1.601532	-2.875189	29972.327581
HLA B*4801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.403034	1.527790	-2.875244	25294.935273
HLA A*2902	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.295185	1.419915	-2.875270	19732.638620
HLA B*5101	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.460697	1.585411	-2.875286	28886.636926
HLA A*1101	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.023611	1.148177	-2.875433	10558.702184
HLA A*0216	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.439530	1.563919	-2.875611	27512.526410
HLA A*2301	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.477425	1.601532	-2.875893	30021.011167
HLA B*3501	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.117684	1.241782	-2.875902	13112.452258
HLA B*4001	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.324138	1.448126	-2.876012	21092.976367
HLA A*1101	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.335843	1.459786	-2.876057	21669.206104
HLA A*6901	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.371649	1.495432	-2.876217	23531.475070
HLA A*1101	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.406985	1.530697	-2.876289	25526.155245
HLA B*3801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.476037	1.599646	-2.876391	29925.179935
HLA A*2603	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.584797	1.708081	-2.876716	38441.186218
HLA B*0803	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.462210	1.585411	-2.876799	28987.452579
HLA B*5301	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.032139	1.155314	-2.876825	10768.102255
HLA A*0201	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.110903	1.234017	-2.876886	12909.318213
HLA B*5101	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.470671	1.593495	-2.877176	29557.693860
HLA B*4501	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.590880	1.713576	-2.877303	38983.389516
HLA B*5301	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.275677	1.398016	-2.877661	18865.893932
HLA A*2301	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.200640	1.322784	-2.877856	15872.288048
HLA A*3201	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.898261	1.020365	-2.877896	7911.536146
HLA B*4601	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.315215	1.437023	-2.878192	20664.006131
HLA B*1509	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.478419	1.600184	-2.878235	30089.789408
HLA B*1503	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.592452	0.714055	-2.878397	3912.477462
HLA A*1101	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-3.995558	1.117129	-2.878429	9898.233384
HLA A*3001	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.276573	1.398016	-2.878557	18904.819807
HLA A*0101	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.373994	1.495432	-2.878562	23658.866725
HLA A*2602	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.488132	1.609455	-2.878677	30770.313371
HLA A*3301	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.593112	1.714405	-2.878707	39184.256265
HLA A*0211	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.521044	1.642298	-2.878746	33192.770649
HLA B*1801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.178677	1.299885	-2.878792	15089.559108
HLA B*4501	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.586937	1.708081	-2.878857	38631.107727
HLA A*2601	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.374337	1.495432	-2.878905	23677.560916
HLA B*3501	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.409612	1.530697	-2.878915	25681.011802
HLA A*0250	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.589014	1.710050	-2.878964	38816.297363
HLA B*4501	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.626284	1.747156	-2.879128	42294.508927
HLA A*0250	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-3.057662	0.178488	-2.879174	1141.989399
HLA A*2301	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.531139	1.651959	-2.879180	33973.417967
HLA B*4403	1:187-195	9	LTRASGDPL	1.250089	0.497067	-4.626472	1.747156	-2.879316	42312.817577
HLA B*4403	1:409-417	9	VLDAALAAL	1.329115	0.442767	-4.651254	1.771882	-2.879372	44797.555215
HLA A*6802	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.410249	1.530697	-2.879552	25718.689832
HLA B*7301	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.589898	1.710232	-2.879666	38895.334663
HLA A*0301	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.316711	1.437023	-2.879689	20735.339190
HLA A*0206	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.541456	1.661630	-2.879826	34790.112316

HLA A*0212	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.407967	1.527790	-2.880178	25583.943714
HLA B*2705	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.344663	1.464436	-2.880227	22113.779102
HLA B*5301	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.264896	1.384650	-2.880246	18403.295590
HLA B*3901	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.481805	1.601532	-2.880273	30325.275573
HLA B*3801	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.473807	1.593495	-2.880312	29771.938223
HLA B*7301	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.593906	1.713576	-2.880330	39255.971892
HLA B*3501	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.028512	1.148177	-2.880334	10678.532313
HLA B*7301	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.588464	1.708081	-2.880384	38767.190356
HLA B*7301	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.573122	1.692204	-2.880918	37421.585989
HLA A*2602	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.538077	1.657009	-2.881068	34520.515414
HLA B*4403	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.594232	1.713159	-2.881073	39285.502487
HLA A*0206	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-3.503679	0.622434	-2.881245	3189.179086
HLA B*4601	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.091628	1.210192	-2.881436	12348.895948
HLA A*2301	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.525035	1.643417	-2.881618	33499.265136
HLA A*2501	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.467243	1.585411	-2.881831	29325.312450
HLA B*3801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.268544	1.386690	-2.881854	18558.563274
HLA A*2301	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.302259	1.420375	-2.881884	20056.699223
HLA B*1509	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.475489	1.593495	-2.881995	29887.482884
HLA B*4001	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.209492	1.327486	-2.882006	16199.156304
HLA B*5301	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.595642	1.713576	-2.882066	39413.227797
HLA B*4501	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.646492	1.764418	-2.882074	44308.995784
HLA B*1503	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-3.488421	0.606197	-2.882225	3079.082687
HLA B*5701	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.376372	1.493912	-2.882460	23788.749691
HLA B*4501	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-3.725856	0.843357	-2.882499	5319.313750
HLA A*1101	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.349158	1.466619	-2.882539	22343.825545
HLA A*3001	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.266155	1.383422	-2.882733	18456.737082
HLA A*0211	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.703883	0.821048	-2.882835	5056.886701
HLA B*0702	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.447044	1.563919	-2.883125	27992.657182
HLA B*7301	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.596495	1.713159	-2.883336	39490.703138
HLA B*4403	1:136-144	9	DRHLTDAQR	1.200835	0.563583	-4.647765	1.764418	-2.883347	44439.107507
HLA A*2402	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.184212	1.300706	-2.883506	15283.116979
HLA A*2603	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.589432	1.705831	-2.883601	38853.693918
HLA A*3201	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.600898	1.717294	-2.883603	39893.101446
HLA A*3101	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.313443	1.429823	-2.883620	20579.888162
HLA A*0203	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.313429	1.429220	-2.884209	20579.220163
HLA A*2501	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-3.904619	1.020365	-2.884254	8028.206283
HLA B*4002	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.457720	1.573351	-2.884369	28689.315423
HLA B*4601	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.379898	1.495432	-2.884466	23982.706556
HLA A*0219	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.448545	1.563919	-2.884626	28089.592988
HLA A*0250	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.564485	1.679828	-2.884658	36684.743160
HLA B*2705	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.378684	1.493912	-2.884772	23915.722738
HLA A*0212	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.756686	0.871584	-2.885101	5710.650077
HLA B*5401	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.565024	1.679828	-2.885196	36730.218754
HLA A*0219	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.413021	1.527790	-2.885231	25883.394591
HLA B*1801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.485045	1.599646	-2.885399	30552.355301
HLA B*2705	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.449391	1.563919	-2.885472	28144.352464
HLA B*7301	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.333625	1.448126	-2.885499	21558.824964
HLA A*0250	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.095726	1.210192	-2.885534	12465.957247
HLA B*4002	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.635137	1.749555	-2.885581	43165.507003
HLA B*5401	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-3.672146	0.786321	-2.885825	4700.525143
HLA B*3801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.541898	1.655822	-2.886075	34825.513918
HLA B*7301	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.612626	1.726550	-2.886076	40985.140716
HLA A*3301	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.270079	1.383422	-2.886657	18624.240263
HLA A*3101	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.334830	1.448126	-2.886705	21618.739693
HLA B*3901	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.480205	1.593495	-2.886710	30213.758727
HLA A*3201	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.592616	1.705831	-2.886785	39139.553480
HLA A*2902	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.128642	1.241782	-2.886860	13447.511303
HLA A*0201	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.209666	1.322784	-2.886883	16205.642640
HLA B*1501	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.194785	1.307776	-2.887009	15659.742619
HLA A*0211	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.530575	1.643417	-2.887158	33929.336408
HLA B*5801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.335364	1.448126	-2.887238	21645.304783
HLA B*7301	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.593405	1.705831	-2.887574	39210.763037
HLA B*0702	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.424400	1.536595	-2.887804	26570.503797
HLA B*1509	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.489417	1.601532	-2.887885	30861.504030
HLA B*1502	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.598017	1.710050	-2.887968	39629.385009

HLA A*2501	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.381891	1.493912	-2.887979	24092.982041
HLA B*5801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.354864	1.466619	-2.888245	22639.374880
HLA B*5401	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.517836	1.629468	-2.888369	32948.561469
HLA B*5101	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.158166	1.269415	-2.888750	14393.471312
HLA B*5801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.353476	1.464436	-2.889040	22567.106855
HLA B*7301	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.606558	1.717294	-2.889263	40416.407785
HLA A*3001	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-3.750394	0.860662	-2.889732	5628.512417
HLA B*1509	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.420488	1.530697	-2.889791	26332.245565
HLA B*4402	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.349822	1.459786	-2.890036	22378.060111
HLA A*1101	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.445002	1.554677	-2.890325	27861.367131
HLA B*1501	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.338684	1.448126	-2.890558	21811.399264
HLA A*2402	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.532883	1.642298	-2.890585	34110.066025
HLA A*0202	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.596467	1.705831	-2.890635	39488.139537
HLA B*3501	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.190607	1.299885	-2.890723	15509.837065
HLA A*3001	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.113234	1.222401	-2.890833	12978.783720
HLA A*0202	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.538874	1.648036	-2.890837	34583.882485
HLA A*2602	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.596782	1.705831	-2.890950	39516.775861
HLA A*2402	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.534374	1.643417	-2.890957	34227.445139
HLA B*4403	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.634759	1.743756	-2.891003	43127.926554
HLA B*1502	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.539856	1.648791	-2.891065	34662.176673
HLA B*4601	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.320296	1.429220	-2.891077	20907.228130
HLA B*5301	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.520574	1.629468	-2.891106	33156.876230
HLA A*2902	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.008344	1.117129	-2.891215	10193.975534
HLA A*3001	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-3.918495	1.027215	-2.891280	8288.855745
HLA B*4403	1:92-100	9	EIYRDVLAR	0.990352	0.759203	-4.641088	1.749555	-2.891533	43761.086067
HLA B*0801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.387144	1.495432	-2.891712	24386.192929
HLA A*3301	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.605007	1.713159	-2.891848	40272.357237
HLA A*2902	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.419731	1.527790	-2.891942	26286.415136
HLA A*3201	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.549026	1.657009	-2.892017	35401.842980
HLA B*5401	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.543998	1.651959	-2.892039	34994.353420
HLA A*2402	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.544118	1.651959	-2.892158	35004.009846
HLA B*4403	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.547516	0.655319	-2.892197	3527.894576
HLA B*1801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.456170	1.563919	-2.892250	28587.062110
HLA A*0250	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.598276	1.705831	-2.892444	39652.974991
HLA B*5401	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.548328	1.655822	-2.892506	35345.007199
HLA A*0301	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.314745	1.421817	-2.892928	20641.660226
HLA A*0202	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.457004	1.563919	-2.893084	28642.016620
HLA A*0203	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.777319	0.883995	-2.893324	5988.509277
HLA A*2501	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.323200	1.429823	-2.893378	21047.495316
HLA A*2603	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.457645	1.563919	-2.893726	28684.349260
HLA B*4001	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.194526	1.300706	-2.893820	15650.426469
HLA A*0211	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.323043	1.429220	-2.893823	21039.867769
HLA A*8001	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.323783	1.429823	-2.893960	21075.752693
HLA A*6802	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-3.953821	1.059725	-2.894096	8991.278253
HLA A*0212	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.006910	1.112802	-2.894108	10160.390531
HLA B*4801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.389949	1.495432	-2.894517	24544.223131
HLA B*0801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.331734	1.437023	-2.894711	21465.141270
HLA B*5701	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.425457	1.530697	-2.894760	26635.267163
HLA B*1503	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.117200	1.222401	-2.894799	13097.847393
HLA B*3801	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.494985	1.600184	-2.894801	31259.740394
HLA A*0203	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.347917	0.452989	-2.894928	2228.011611
HLA A*3101	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.324286	1.429220	-2.895066	21100.166564
HLA A*0201	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.390631	1.495432	-2.895199	24582.759996
HLA A*6801	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.639298	1.743756	-2.895542	43581.059507
HLA B*4001	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.325416	1.429823	-2.895593	21155.144002
HLA A*3001	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.223951	1.328104	-2.895847	16747.543967
HLA A*8001	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.423777	1.527790	-2.895987	26532.439067
HLA A*0212	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.223871	1.327486	-2.896385	16744.463770
HLA A*3001	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.219525	1.322784	-2.896741	16577.716060
HLA B*3501	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.390884	1.493912	-2.896973	24597.127113
HLA B*7301	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.607194	1.710050	-2.897145	40475.704926
HLA A*3201	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.482726	1.585411	-2.897315	30389.653913
HLA B*4402	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.392790	1.495432	-2.897358	24705.282130
HLA A*3301	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.577208	1.679828	-2.897380	37775.301917
HLA A*1101	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.461362	1.563919	-2.897443	28930.896199

HLA A*0101	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.317529	1.419915	-2.897614	20774.413168
HLA B*0803	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.391681	1.493912	-2.897769	24642.278464
HLA B*3901	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.425593	1.527790	-2.897803	26643.625917
HLA B*5401	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.546258	1.648036	-2.898222	35176.949733
HLA A*0206	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.541681	1.643417	-2.898264	34808.185231
HLA B*4001	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.393805	1.495432	-2.898373	24763.087678
HLA B*5301	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.606922	1.708081	-2.898841	40450.312482
HLA B*1517	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.285691	1.386690	-2.899001	19305.937393
HLA A*2501	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.430095	1.530697	-2.899398	26921.232620
HLA B*5301	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.238043	1.338560	-2.899484	17299.889838
HLA A*8001	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.319462	1.419915	-2.899548	20867.114108
HLA A*3002	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.499778	1.600184	-2.899594	31606.639019
HLA A*3001	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.213454	1.313812	-2.899642	16347.585882
HLA B*5101	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.499922	1.600184	-2.899737	31617.071033
HLA A*6901	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.366560	1.466619	-2.899941	23257.346714
HLA B*4501	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.550520	1.650564	-2.899956	35523.859520
HLA A*3002	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.592167	1.692204	-2.899963	39099.131904
HLA B*1503	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-3.847686	0.947523	-2.900163	7041.834315
HLA B*5301	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.606088	1.705831	-2.900257	40372.701776
HLA B*5401	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.509505	1.609246	-2.900259	32322.517873
HLA A*0301	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.201124	1.300814	-2.900309	15889.986576
HLA B*4501	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.158090	1.257536	-2.900554	14390.979781
HLA B*4501	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.548662	1.648036	-2.900625	35372.169816
HLA B*2705	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.322460	1.421817	-2.900644	21011.658506
HLA B*4002	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.627228	1.726550	-2.900678	42386.590078
HLA A*6801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.337770	1.437023	-2.900747	21765.546597
HLA B*4501	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.610855	1.710050	-2.900805	40818.300522
HLA A*0211	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.165750	1.264555	-2.901194	14647.033812
HLA B*4501	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.284678	1.383422	-2.901257	19260.974907
HLA A*0216	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.024677	1.123062	-2.901615	10584.667177
HLA A*2602	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.550417	1.648791	-2.901626	35515.404600
HLA A*0203	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.239444	1.337733	-2.901710	17355.759790
HLA B*1509	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.458726	1.556999	-2.901727	28755.820562
HLA B*4403	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.619078	1.717294	-2.901784	41598.542685
HLA B*4403	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.615432	1.713576	-2.901856	41250.737322
HLA A*2601	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.135892	1.234017	-2.901876	13673.900920
HLA B*4403	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.612133	1.710232	-2.901901	40938.604891
HLA B*1502	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.607742	1.705831	-2.901911	40526.756890
HLA A*0206	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.553875	1.651959	-2.901916	35799.355540
HLA A*0202	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-3.608593	0.706599	-2.901994	4060.624314
HLA B*7301	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.102769	1.200757	-2.902012	12669.789200
HLA B*5301	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.582156	1.679828	-2.902328	38208.145550
HLA A*0211	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.554329	1.651959	-2.902369	35836.753475
HLA A*2602	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.612659	1.710232	-2.902428	40988.244984
HLA B*0702	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.350626	1.448126	-2.902500	22419.501923
HLA A*0216	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-3.609612	0.706599	-2.903014	4070.169422
HLA A*0206	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-3.951777	1.048747	-2.903030	8949.059302
HLA B*4402	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.433753	1.530697	-2.903056	27148.953198
HLA A*3002	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.502849	1.599646	-2.903204	31830.912830
HLA B*3501	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.398840	1.495432	-2.903408	25051.846484
HLA B*0702	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.434145	1.530697	-2.903449	27173.492043
HLA B*5801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.208571	1.305053	-2.903519	16164.839533
HLA B*4801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.370150	1.466619	-2.903531	23450.395969
HLA B*5801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.173066	1.269415	-2.903651	14895.873669
HLA B*1509	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.351777	1.448126	-2.903651	22479.011403
HLA B*5401	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.565284	1.661630	-2.903654	36752.281789
HLA B*4001	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.368155	1.464436	-2.903719	23342.935369
HLA A*0203	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.871411	0.967578	-2.903833	7437.224684
HLA A*0250	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.551890	1.648036	-2.903853	35636.077415
HLA A*3301	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.596140	1.692204	-2.903936	39458.456621
HLA A*0212	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.232071	1.328104	-2.903967	17063.611190
HLA A*6802	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.016774	1.112802	-2.903972	10393.780455
HLA A*0206	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.325888	1.421817	-2.904072	21178.160357
HLA A*2301	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.503836	1.599646	-2.904190	31903.319777
HLA B*2705	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-3.657284	0.752921	-2.904362	4542.380783

HLA A*0212	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.435156	1.530697	-2.904459	27236.778023
HLA B*1501	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.517151	0.612666	-2.904485	3289.658790
HLA B*7301	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.549942	1.645215	-2.904727	35476.614649
HLA B*4501	1:220-228	9	PSTPRQLAL	1.513261	0.230495	-4.648520	1.743756	-2.904763	44516.346370
HLA A*0101	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.371708	1.466619	-2.905089	23534.657852
HLA A*2501	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.325477	1.419915	-2.905562	21158.119833
HLA A*2402	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.505910	1.600184	-2.905726	32056.084352
HLA A*8001	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.436518	1.530697	-2.905822	27322.374053
HLA A*0211	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.243767	1.337733	-2.906033	17529.385142
HLA A*2501	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.469966	1.563919	-2.906046	29509.761613
HLA B*4501	1:473-481	9	RDRSMQRLR	1.081313	0.624518	-4.611891	1.705831	-2.906060	40915.799494
HLA B*4002	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.623411	1.717294	-2.906116	42015.599694
HLA A*2601	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.326116	1.419915	-2.906201	21189.276709
HLA A*0203	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-3.893064	0.986777	-2.906287	7817.425584
HLA B*4403	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.633408	1.726550	-2.906857	42993.977550
HLA B*5301	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.492333	1.585411	-2.906922	31069.395134
HLA B*4002	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.443586	1.536595	-2.906990	27770.626891
HLA A*8001	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.327415	1.420375	-2.907040	21252.762923
HLA B*3901	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.291753	1.384650	-2.907103	19577.289580
HLA B*4501	1:2-10	9	TATETVRVR	1.064509	0.662041	-4.633856	1.726550	-2.907306	43038.425707
HLA A*0301	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.221122	1.313812	-2.907311	16638.813223
HLA B*2705	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-3.835088	0.927578	-2.907510	6840.500262
HLA A*2603	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.617673	1.710050	-2.907623	41464.184119
HLA A*2402	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.556504	1.648791	-2.907714	36016.730172
HLA B*1502	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.517202	1.609455	-2.907747	32900.469624
HLA B*0803	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.374422	1.466619	-2.907803	23682.172713
HLA A*2403	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.138632	1.230828	-2.907804	13760.427555
HLA B*2705	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.056142	1.148177	-2.907964	11379.980288
HLA B*1501	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.208684	1.300706	-2.907978	16169.037678
HLA A*3002	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.517228	1.609246	-2.907982	32902.427549
HLA A*2402	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.337838	1.429823	-2.908015	21768.961591
HLA A*0206	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.550426	1.642298	-2.908128	35516.173146
HLA A*0201	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.294854	1.386690	-2.908164	19717.592414
HLA A*0250	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.564081	1.655822	-2.908259	36650.623849
HLA B*2705	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-3.958638	1.050133	-2.908505	9091.548968
HLA B*4002	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.616806	1.708081	-2.908726	41381.493842
HLA B*5801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.295458	1.386690	-2.908767	19745.025668
HLA A*6901	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.872355	0.963515	-2.908840	7453.416578
HLA A*6801	1:224-232	9	RQLALHQAL	1.264243	0.500053	-4.673328	1.764296	-2.909031	47133.286697
HLA A*6801	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.626333	1.717294	-2.909039	42299.314181
HLA B*1502	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.463718	1.554677	-2.909041	29088.305353
HLA B*0702	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.338991	1.429823	-2.909169	21826.862382
HLA A*2402	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.437028	1.527790	-2.909238	27354.467878
HLA B*0702	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.346963	1.437023	-2.909940	22231.210601
HLA B*5101	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.347069	1.437023	-2.910046	22236.623337
HLA A*0216	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.247923	1.337733	-2.910190	17697.948299
HLA A*6802	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.405670	1.495432	-2.910238	25448.939813
HLA A*3201	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.602446	1.692204	-2.910242	40035.578841
HLA B*1502	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.560973	1.650564	-2.910409	36389.241460
HLA A*2603	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.620807	1.710232	-2.910576	41764.504889
HLA A*0101	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.375291	1.464436	-2.910854	23729.623821
HLA B*1502	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.239958	1.328755	-2.911203	17376.334485
HLA B*5701	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.359845	1.448126	-2.911720	22900.519746
HLA B*4002	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.217034	1.305053	-2.911981	16482.923491
HLA A*6802	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.074627	1.162617	-2.912010	11874.826085
HLA B*1502	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.591911	1.679828	-2.912083	39076.082806
HLA A*0202	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-3.090607	0.178488	-2.912118	1231.988209
HLA A*0301	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.360426	1.448126	-2.912300	22931.140851
HLA A*6801	1:179-187	9	AGSVPDFAL	1.284688	0.428471	-4.625471	1.713159	-2.912312	42215.415198
HLA B*1801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.497868	1.585411	-2.912457	31467.930699
HLA B*4002	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.622905	1.710232	-2.912674	41966.758661
HLA B*5401	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.408409	1.495432	-2.912977	25609.977335
HLA A*0216	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.443938	1.530697	-2.913241	27793.171439
HLA B*5801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.221019	1.307776	-2.913243	16634.853073
HLA A*0101	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.346399	1.432365	-2.914034	22202.364919

HLA B*1501	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.549978	0.635887	-2.914091	3547.953007
HLA A*3101	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.298843	1.384650	-2.914193	19899.552518
HLA B*1501	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.298961	1.384650	-2.914311	19904.935965
HLA A*3201	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.523771	1.609455	-2.914316	33401.906593
HLA B*5301	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.565031	1.650564	-2.914466	36730.814878
HLA B*1502	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.445501	1.530697	-2.914804	27893.339566
HLA B*4002	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.560198	1.645215	-2.914983	36324.335033
HLA A*2601	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.381733	1.466619	-2.915114	24084.250819
HLA B*4801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.375007	1.459786	-2.915220	23714.095573
HLA A*2602	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.508826	1.593495	-2.915331	32272.022459
HLA B*2705	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.375124	1.459786	-2.915338	23720.510972
HLA A*3002	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.443851	1.527790	-2.916061	27787.608750
HLA B*5701	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.411569	1.495432	-2.916137	25797.002838
HLA A*3002	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.572013	1.655822	-2.916191	37326.153073
HLA B*4403	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-3.811673	0.895455	-2.916218	6481.460764
HLA A*3001	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.241652	1.325261	-2.916392	17444.243755
HLA A*2602	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.559815	1.643417	-2.916398	36292.317920
HLA A*3002	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.883995	0.967578	-2.916417	7655.873409
HLA A*2602	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.572269	1.655822	-2.916447	37348.169972
HLA B*4002	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.518116	1.601532	-2.916584	32969.779818
HLA A*2403	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.376419	1.459786	-2.916632	23791.323720
HLA B*2705	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.412124	1.495432	-2.916692	25829.959779
HLA B*1801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.473774	1.556999	-2.916776	29769.683428
HLA A*2602	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.186247	1.269415	-2.916831	15354.885818
HLA A*1101	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.444706	1.527790	-2.916917	27842.382012
HLA B*0702	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.410897	1.493912	-2.916986	25757.119847
HLA B*4002	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.471671	1.554677	-2.916994	29625.891453
HLA A*2301	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.244817	1.327486	-2.917330	17571.826355
HLA B*1502	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.304266	1.386690	-2.917576	20149.576466
HLA A*3101	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.222762	1.305053	-2.917709	16701.761865
HLA B*4403	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.628241	1.710050	-2.918191	42485.536599
HLA B*1801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-3.610923	0.692320	-2.918603	4082.474680
HLA A*2301	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.348563	1.429823	-2.918740	22313.264427
HLA B*5101	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.378740	1.459786	-2.918954	23918.828093
HLA B*1502	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.482937	1.563919	-2.919018	30404.453935
HLA B*7301	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.580699	1.661630	-2.919069	38080.205099
HLA A*2602	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.473781	1.554677	-2.919104	29770.166584
HLA B*4002	1:87-95	9	QSQRAEIYR	1.003259	0.710317	-4.632733	1.713576	-2.919157	42927.275255
HLA A*3002	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.305873	1.386690	-2.919183	20224.275358
HLA A*6801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.219088	1.299885	-2.919203	16561.043299
HLA A*0216	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-3.626360	0.707098	-2.919261	4230.187487
HLA B*4402	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.086422	1.167129	-2.919292	12201.737356
HLA B*5401	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.562815	1.643417	-2.919398	36543.908849
HLA B*5401	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.568216	1.648791	-2.919426	37001.255884
HLA A*3002	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.304106	1.384650	-2.919456	20142.165355
HLA B*5101	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.436812	1.517234	-2.919578	27340.856678
HLA B*0802	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.188995	1.269415	-2.919580	15452.383882
HLA A*3002	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.189019	1.269415	-2.919604	15453.219861
HLA A*0201	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.129850	1.210192	-2.919658	13484.956607
HLA B*3501	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.224896	1.305053	-2.919843	16784.005747
HLA B*5401	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.562312	1.642298	-2.920015	36501.625851
HLA B*7301	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.248806	1.328755	-2.920051	17733.984659
HLA B*0802	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.386707	1.466619	-2.920088	24361.666923
HLA A*2601	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.384583	1.464436	-2.920147	24242.816081
HLA A*2402	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.450977	1.530697	-2.920280	28247.314375
HLA B*1801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.349543	1.429220	-2.920323	22363.658272
HLA A*0101	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.368778	1.448126	-2.920652	23376.424282
HLA B*0801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.385105	1.464436	-2.920668	24271.949082
HLA B*4001	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.259358	1.338560	-2.920798	18170.122932
HLA A*0250	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.521036	1.600184	-2.920852	33192.231946
HLA A*2601	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.189470	1.268289	-2.921181	15469.279440
HLA B*3801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.495136	1.573351	-2.921784	31270.565418
HLA A*2902	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.342212	1.420375	-2.921837	21989.353153
HLA A*3002	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.564161	1.642298	-2.921864	36657.365847
HLA A*0201	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.837202	0.914377	-2.922826	6873.887188

HLA A*0202	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.123694	1.200757	-2.922937	13295.170237
HLA B*7301	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.566367	1.643417	-2.922950	36844.054861
HLA B*0803	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.387691	1.464436	-2.923255	24416.951209
HLA A*2602	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.615622	1.692204	-2.923418	41268.817398
HLA B*4501	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.028502	1.105060	-2.923442	10678.301237
HLA A*0301	1:376-384	9	LGDAWELLK	0.881918	0.032559	-3.838466	0.914477	-2.923989	6893.922920
HLA B*4402	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.417950	1.493912	-2.924039	26178.843250
HLA A*0203	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.419901	1.495432	-2.924468	26296.656005
HLA A*6901	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.047533	1.123062	-2.924471	11156.629138
HLA B*4002	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-3.769439	0.844865	-2.924574	5880.829035
HLA B*0802	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.354465	1.429823	-2.924642	22618.563445
HLA B*1502	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.524406	1.599646	-2.924760	33450.731408
HLA A*6901	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.346714	1.421817	-2.924897	22218.465807
HLA A*0212	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.262708	1.337733	-2.924975	18310.838457
HLA A*0212	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.420890	1.495432	-2.925458	26356.616561
HLA A*3301	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.614198	1.688566	-2.925632	41133.743537
HLA A*0211	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.534997	1.609246	-2.925751	34276.549500
HLA A*0203	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.347593	1.421817	-2.925776	22263.465905
HLA B*5301	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.535291	1.609455	-2.925836	34299.736381
HLA A*0206	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.148237	1.222401	-2.925836	14068.138100
HLA B*4002	1:144-152	9	RAAYLAEGR	0.951129	0.758921	-4.636168	1.710050	-2.926119	43268.144381
HLA B*4501	1:289-297	9	WSIADDHDL	1.275539	0.438866	-4.640621	1.714405	-2.926216	43713.999635
HLA B*4601	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.346237	1.419915	-2.926322	22194.078715
HLA A*2603	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.583622	1.657009	-2.926613	38337.345445
HLA A*3002	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.570324	1.643417	-2.926907	37181.247155
HLA B*1517	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.463620	1.536595	-2.927024	29081.696795
HLA A*6801	1:428-436	9	IEAALKDAL	1.293005	0.395561	-4.615641	1.688566	-2.927075	41270.603514
HLA A*2902	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.422548	1.495432	-2.927116	26457.475026
HLA B*1501	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.391627	1.464436	-2.927190	24639.212479
HLA B*1801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.421472	1.493912	-2.927561	26392.001713
HLA B*4501	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.376153	1.448126	-2.928027	23776.784113
HLA B*0803	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.459120	1.530697	-2.928424	28781.967497
HLA A*0250	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.112332	1.183813	-2.928519	12951.849614
HLA A*0101	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.388380	1.459786	-2.928593	24455.685148
HLA A*3101	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.065958	1.137355	-2.928603	11640.125376
HLA A*0301	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.357905	1.429220	-2.928685	22798.415506
HLA B*5301	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.585746	1.657009	-2.928737	38525.294970
HLA A*2501	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.456663	1.527790	-2.928873	28619.557661
HLA B*5801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.349275	1.420375	-2.928900	22349.870244
HLA A*2301	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.315600	1.386690	-2.928910	20682.347824
HLA B*4403	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.579964	1.650564	-2.929400	38015.778628
HLA A*8001	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.377666	1.448126	-2.929540	23859.766152
HLA B*7301	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.585516	1.655822	-2.929694	38504.875462
HLA A*2402	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.377988	1.448126	-2.929862	23877.456487
HLA A*0216	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.140065	1.210192	-2.929873	13805.912421
HLA B*0801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.267717	1.337733	-2.929984	18523.256183
HLA A*2403	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.367354	1.437023	-2.930332	23299.912666
HLA B*0802	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.424301	1.493912	-2.930390	26564.467257
HLA A*6901	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.394879	1.464436	-2.930442	24824.385681
HLA B*5801	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.352282	1.421817	-2.930466	22505.172541
HLA A*2902	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.394925	1.464436	-2.930489	24827.071770
HLA B*5701	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.397308	1.466619	-2.930689	24963.638073
HLA B*7301	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.581435	1.650564	-2.930870	38144.740754
HLA A*0203	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.253794	1.322784	-2.931011	17938.837058
HLA B*1801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.351507	1.420375	-2.931132	22465.030722
HLA B*5101	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.329194	1.398016	-2.931178	21339.977529
HLA A*0201	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.397858	1.466619	-2.931239	24995.259905
HLA B*1503	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.323116	1.391860	-2.931256	21043.396589
HLA A*2301	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.516704	1.585411	-2.931293	32862.757820
HLA A*0301	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.318079	1.386690	-2.931388	20800.728442
HLA A*0203	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.608828	0.677348	-2.931479	4062.821661
HLA A*0203	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.398400	1.466619	-2.931781	25026.515617
HLA A*2601	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.361638	1.429823	-2.931815	22995.242623
HLA B*5801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.316547	1.384650	-2.931897	20727.488364
HLA B*2705	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.398591	1.466619	-2.931972	25037.484664

HLA B*4002	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.580309	1.648036	-2.932273	38046.022841
HLA A*2301	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.525865	1.593495	-2.932370	33563.299500
HLA B*5401	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-3.598786	0.666384	-2.932402	3969.959354
HLA B*1502	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.584489	1.651959	-2.932530	38413.952774
HLA A*2301	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.541949	1.609246	-2.932703	34829.659012
HLA B*1801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.352654	1.419915	-2.932739	22524.417342
HLA B*3501	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.370002	1.437023	-2.932980	23442.404896
HLA B*5101	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.427083	1.493912	-2.933171	26735.166980
HLA A*0216	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.610524	0.677348	-2.933176	4078.721831
HLA B*1501	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-3.900864	0.967687	-2.933177	7959.101552
HLA A*0216	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.197750	1.264555	-2.933194	15767.021864
HLA A*2603	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.319906	1.386690	-2.933216	20888.460997
HLA B*5701	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.319906	1.386690	-2.933216	20888.460997
HLA B*5801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.233967	1.300706	-2.933261	17138.270025
HLA A*2603	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.542722	1.609455	-2.933267	34891.705905
HLA B*4403	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.613120	1.679828	-2.933292	41031.729439
HLA A*2603	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.506665	1.573351	-2.933313	32111.800491
HLA B*5401	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.526962	1.593495	-2.933467	33648.201635
HLA B*4001	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.353854	1.420375	-2.933479	22586.771190
HLA B*3501	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.134285	1.200757	-2.933528	13623.396008
HLA B*1517	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.464285	1.530697	-2.933588	29126.254933
HLA A*3101	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.241502	1.307776	-2.933726	17438.205029
HLA B*1502	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.589721	1.655822	-2.933899	38879.556406
HLA A*0219	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.464910	1.530697	-2.934213	29168.198675
HLA B*5301	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.498300	1.563919	-2.934381	31499.270089
HLA B*5301	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.242202	1.307776	-2.934426	17466.340652
HLA A*2501	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.430043	1.495432	-2.934611	26918.028711
HLA A*0203	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.203013	1.268289	-2.934724	15959.251407
HLA B*3801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.471342	1.536595	-2.934747	29603.461758
HLA A*0202	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.577137	1.642298	-2.934840	37769.171609
HLA A*2403	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.272327	1.337377	-2.934950	18720.912904
HLA B*3801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.491994	1.556999	-2.934996	31045.200754
HLA A*6801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-3.725893	0.790719	-2.935175	5319.774201
HLA B*5401	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.260577	1.325261	-2.935317	18221.211464
HLA B*4001	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.401969	1.466619	-2.935350	25233.021383
HLA B*0702	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.430833	1.495432	-2.935401	26967.002722
HLA B*4501	1:394-402	9	DPKAAAKEL	1.567209	0.150085	-4.652711	1.717294	-2.935417	44948.064368
HLA B*4001	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.395386	1.459786	-2.935600	24853.410826
HLA B*1509	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.163118	1.227496	-2.935622	14558.554645
HLA B*3901	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.466319	1.530697	-2.935622	29263.030533
HLA A*2403	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.365141	1.429220	-2.935921	23181.475659
HLA B*4002	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-3.573825	0.637857	-2.935968	3748.220500
HLA A*0202	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-3.990187	1.054023	-2.936164	9776.575688
HLA B*3801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.490951	1.554677	-2.936274	30970.719955
HLA B*4601	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.400900	1.464436	-2.936464	25170.986693
HLA B*2705	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.369034	1.432365	-2.936669	23390.212908
HLA B*4501	1:226-234	9	LALHQALIR	1.054870	0.655362	-4.647089	1.710232	-2.936857	44369.923151
HLA A*2902	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.403492	1.466619	-2.936873	25321.633698
HLA B*4402	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.385015	1.448126	-2.936890	24266.959870
HLA A*6901	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.369286	1.432365	-2.936920	23403.756443
HLA A*3001	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.244730	1.307776	-2.936954	17568.309426
HLA A*8001	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.323727	1.386690	-2.937036	21073.016451
HLA A*2601	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.397017	1.459786	-2.937230	24946.897425
HLA B*5401	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-3.653769	0.716494	-2.937275	4505.766776
HLA A*0301	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.329539	1.391860	-2.937680	21356.954975
HLA A*0202	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.589792	1.651959	-2.937832	38885.866940
HLA A*6801	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.617753	1.679828	-2.937925	41471.811586
HLA B*3501	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.207378	1.269415	-2.937963	16120.475927
HLA A*3201	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.260970	1.322784	-2.938186	18237.680883
HLA A*0101	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.322907	1.384650	-2.938257	21033.267050
HLA B*5301	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.600177	1.661630	-2.938546	39826.900538
HLA B*2705	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.367951	1.429220	-2.938731	23331.951360
HLA B*1502	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.929448	0.990658	-2.938790	8500.566722
HLA A*8001	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.368235	1.429220	-2.939016	23347.229375
HLA B*5801	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.207566	1.268289	-2.939277	16127.454236

HLA B*5801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.371727	1.432365	-2.939361	23535.676433
HLA B*5301	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.588507	1.648791	-2.939716	38770.965611
HLA A*2301	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.539926	1.600184	-2.939742	34667.802686
HLA A*0216	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.267894	1.328104	-2.939789	18530.773365
HLA A*6901	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.337810	1.398016	-2.939794	21767.548425
HLA A*0250	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.591972	1.651959	-2.940013	39081.579522
HLA A*2602	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.002451	1.062125	-2.940326	10056.597732
HLA A*0212	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.369568	1.429220	-2.940348	23418.954783
HLA A*2403	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.388596	1.448126	-2.940470	24467.860012
HLA B*5401	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.210277	1.269415	-2.940862	16228.453068
HLA B*4601	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.389080	1.448126	-2.940954	24495.143104
HLA B*7301	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.598109	1.657009	-2.941100	39637.747124
HLA A*0203	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.009307	1.067986	-2.941320	10216.611422
HLA A*2602	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.593812	1.651959	-2.941852	39247.477993
HLA A*0250	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.585354	1.643417	-2.941936	38490.504953
HLA A*0206	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.551260	1.609246	-2.942014	35584.447874
HLA B*1501	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.269783	1.327486	-2.942296	18611.549449
HLA A*0101	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.371558	1.429220	-2.942338	23526.510790
HLA B*4801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.362787	1.420375	-2.942411	23056.155596
HLA B*4403	1:476-484	9	SMQRLRAAR	0.945431	0.762650	-4.651156	1.708081	-2.943075	44787.377679
HLA A*8001	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.281805	1.338560	-2.943245	19133.959276
HLA A*0101	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.365188	1.421817	-2.943371	23183.983979
HLA A*2602	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.814995	0.871584	-2.943411	6531.231357
HLA B*3501	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.657960	0.714055	-2.943906	4549.463547
HLA A*0250	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.586284	1.642298	-2.943986	38573.052171
HLA A*2403	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.439446	1.495432	-2.944014	27507.168702
HLA B*1509	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.403809	1.459786	-2.944023	25340.133729
HLA B*5701	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.342046	1.398016	-2.944030	21980.908618
HLA B*5701	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.373322	1.429220	-2.944102	23622.289361
HLA B*1801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.178662	1.234192	-2.944470	15089.069319
HLA B*3901	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.381653	1.437023	-2.944631	24079.821260
HLA A*2601	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.392773	1.448126	-2.944648	24704.346578
HLA A*0219	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.373884	1.429220	-2.944664	23652.851873
HLA B*5101	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.364584	1.419915	-2.944669	23151.772721
HLA B*4801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.410110	1.464436	-2.945674	25710.482161
HLA A*6801	1:62-70	9	LDALRWLGL	1.379202	0.313002	-4.637968	1.692204	-2.945764	43447.818518
HLA A*0216	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.367601	1.421817	-2.945784	23313.151670
HLA B*5101	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-3.946345	1.000328	-2.946017	8837.824572
HLA B*7301	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.594183	1.648036	-2.946147	39281.039606
HLA B*3801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.366299	1.419915	-2.946385	23243.384923
HLA B*1502	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.555971	1.609246	-2.946725	35972.527160
HLA B*4001	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.383796	1.437023	-2.946773	24198.920302
HLA A*2601	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.368689	1.421817	-2.946872	23371.619149
HLA B*5401	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.556462	1.609455	-2.947007	36013.223106
HLA A*0301	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.367671	1.420375	-2.947296	23316.935624
HLA B*4001	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.379762	1.432365	-2.947396	23975.182597
HLA A*3101	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.275005	1.327486	-2.947519	18836.726657
HLA B*5701	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.377384	1.429823	-2.947562	23844.281736
HLA A*6801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-3.938409	0.990658	-2.947751	8677.783610
HLA B*0801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.339727	1.391860	-2.947867	21863.853015
HLA A*2603	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.596772	1.648791	-2.947981	39515.920744
HLA A*0202	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.591486	1.643417	-2.948069	39037.838626
HLA B*1517	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.065272	1.117129	-2.948143	11621.752130
HLA A*2603	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.541658	1.593495	-2.948163	34806.302198
HLA A*2402	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.533738	1.585411	-2.948327	34177.301733
HLA B*4002	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.335049	1.386690	-2.948359	21629.619243
HLA A*0211	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.335484	1.386690	-2.948793	21651.277641
HLA A*0101	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.369170	1.420375	-2.948795	23397.553290
HLA A*3001	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.058378	1.109528	-2.948850	11438.740812
HLA B*4402	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.413677	1.464436	-2.949240	25922.491425
HLA B*5101	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.479956	1.530697	-2.949259	30196.437667
HLA A*0201	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.413773	1.464436	-2.949337	25928.241813
HLA B*1503	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.131419	1.181912	-2.949507	13533.776784
HLA A*8001	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.444970	1.495432	-2.949537	27859.257034
HLA A*3101	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.274799	1.325261	-2.949538	18827.761186

HLA B*5301	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.601523	1.651959	-2.949563	39950.550161
HLA B*7301	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.409614	1.459786	-2.949828	25681.150734
HLA A*0219	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.150624	1.200757	-2.949866	14145.675776
HLA B*0801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.275337	1.325261	-2.950076	18851.100687
HLA B*4601	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.334729	1.384650	-2.950079	21613.711214
HLA A*6801	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.598201	1.648036	-2.950164	39646.111003
HLA A*3001	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.181012	1.230828	-2.950184	15170.920715
HLA A*0201	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.562867	0.612666	-2.950202	3654.829600
HLA B*4801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.287643	1.337377	-2.950267	19392.924895
HLA A*3201	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.505067	1.554677	-2.950390	31993.887039
HLA A*3301	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.444314	1.493912	-2.950402	27817.239130
HLA B*0802	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.446180	1.495432	-2.950747	27936.983739
HLA B*4002	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.184987	1.234192	-2.950795	15310.425738
HLA A*2602	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.552794	1.601532	-2.951262	35710.377848
HLA A*2601	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.383709	1.432365	-2.951344	24194.076988
HLA B*1502	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.593673	1.642298	-2.951375	39234.952846
HLA B*4002	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.631239	1.679828	-2.951411	42779.829633
HLA A*1101	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.445388	1.493912	-2.951476	27886.097312
HLA B*3501	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.114625	1.162401	-2.952224	13020.416911
HLA A*2403	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.047298	1.094888	-2.952410	11150.595157
HLA B*0802	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.373150	1.420375	-2.952775	23612.962243
HLA B*3801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.291579	1.338560	-2.953019	19569.453737
HLA A*2902	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.374964	1.421817	-2.953148	23711.786454
HLA B*1503	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.261000	1.307776	-2.953224	18238.963558
HLA B*1503	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.338122	1.384650	-2.953472	21783.216144
HLA A*1101	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.449375	1.495432	-2.953943	28143.286680
HLA A*0301	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.337368	1.383422	-2.953946	21745.420795
HLA B*1502	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.597484	1.643417	-2.954067	39580.748218
HLA A*0219	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.449525	1.495432	-2.954093	28153.032499
HLA B*0702	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.421113	1.466619	-2.954494	26370.165748
HLA A*2402	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.548243	1.593495	-2.954749	35338.124217
HLA B*1501	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.376717	1.421817	-2.954900	23807.675307
HLA B*3801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.485663	1.530697	-2.954966	30595.856157
HLA B*5701	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.419541	1.464436	-2.955105	26274.898926
HLA B*5401	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.554970	1.599646	-2.955325	35889.719870
HLA B*3501	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-3.749750	0.794424	-2.955325	5620.175400
HLA A*0216	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.419943	1.464436	-2.955506	26299.216846
HLA B*1517	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.376076	1.420375	-2.955700	23772.539710
HLA A*6901	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.347816	1.391860	-2.955956	22274.910920
HLA A*0216	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.278807	1.322784	-2.956023	19002.332036
HLA A*0201	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.388934	1.432365	-2.956569	24486.928489
HLA A*2403	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.354669	1.398016	-2.956654	22629.211612
HLA A*0201	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.024738	1.067986	-2.956752	10586.156090
HLA B*5101	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.404885	1.448126	-2.956759	25402.997567
HLA B*1509	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.354841	1.398016	-2.956825	22638.150148
HLA B*5301	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.600294	1.643417	-2.956877	39837.674951
HLA B*5401	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.558750	1.601532	-2.957218	36203.485964
HLA A*6901	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.258160	1.300706	-2.957454	18120.059868
HLA B*0801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.286342	1.328755	-2.957587	19334.889786
HLA A*8001	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.422196	1.464436	-2.957760	26436.013934
HLA B*5301	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.095181	1.137355	-2.957825	12450.321110
HLA A*2902	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.286086	1.328104	-2.957981	19323.491790
HLA B*7301	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.567385	1.609246	-2.958139	36930.462561
HLA A*0211	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.522101	1.563919	-2.958182	33273.675233
HLA B*5101	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.453674	1.495432	-2.958242	28423.291703
HLA A*2902	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.406473	1.448126	-2.958347	25496.068570
HLA B*4002	1:36-44	9	HTGGTFVFR	1.068867	0.581697	-4.608931	1.650564	-2.958366	40637.846973
HLA B*3501	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.345163	1.386690	-2.958473	22139.275638
HLA B*1509	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.259276	1.300706	-2.958570	18166.682815
HLA B*1503	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.063411	1.104589	-2.958822	11572.063721
HLA A*6802	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.076013	1.117129	-2.958885	11912.789119
HLA A*6801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.673119	0.714055	-2.959064	4711.064679
HLA A*2402	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.568350	1.609246	-2.959104	37012.667487
HLA A*0201	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.380927	1.421817	-2.959111	24039.601715
HLA A*0201	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.380345	1.420375	-2.959969	24007.370549

HLA A*0219	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.358104	1.398016	-2.960088	22808.901554
HLA A*6802	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-3.832922	0.872828	-2.960094	6806.465362
HLA A*0201	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.358128	1.398016	-2.960112	22810.135523
HLA B*1501	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.108403	1.148177	-2.960226	12835.224054
HLA B*5301	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.559972	1.599646	-2.960327	36305.474911
HLA B*1801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.488271	1.527790	-2.960481	30780.136314
HLA A*0202	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.638088	0.677348	-2.960740	4345.985224
HLA A*6802	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.084114	1.123062	-2.961053	12137.087369
HLA B*4601	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.390910	1.429823	-2.961088	24598.590902
HLA B*1503	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.078231	1.117129	-2.961102	11973.782575
HLA B*0802	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.425941	1.464436	-2.961505	26664.967040
HLA A*0203	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.171774	1.210192	-2.961582	14851.617778
HLA A*1101	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.391108	1.429220	-2.961888	24609.771797
HLA B*0802	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.399086	1.437023	-2.962064	25066.080936
HLA A*2902	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.394481	1.432365	-2.962116	24801.699831
HLA A*0301	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.287495	1.325261	-2.962235	19386.316466
HLA B*4002	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-3.857864	0.895455	-2.962409	7208.813193
HLA B*3501	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.926041	0.963515	-2.962526	8434.146246
HLA A*1101	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.354540	1.391860	-2.962680	22622.479430
HLA B*4402	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.429320	1.466619	-2.962701	26873.214004
HLA B*5401	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.562947	1.600184	-2.962762	36554.981642
HLA A*2602	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.499661	1.536595	-2.963066	31598.090754
HLA A*2601	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.383502	1.420375	-2.963127	24182.561650
HLA B*5301	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.605787	1.642298	-2.963489	40344.754738
HLA B*1509	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.221174	1.257536	-2.963638	16640.793652
HLA A*0201	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.301409	1.337733	-2.963676	20017.459023
HLA A*2602	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.527909	1.563919	-2.963989	33721.640977
HLA A*3201	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.615953	1.651959	-2.963994	41300.309029
HLA B*5101	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.393323	1.429220	-2.964103	24735.639961
HLA B*0801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.205907	1.241782	-2.964125	16065.974813
HLA A*0202	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.386145	1.421817	-2.964329	24330.188532
HLA A*3002	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.412619	1.448126	-2.964494	25859.461166
HLA B*0802	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.412674	1.448126	-2.964548	25862.678993
HLA B*7301	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.594065	1.629468	-2.964598	39270.415740
HLA A*0203	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.429204	1.464436	-2.964768	26866.091274
HLA A*6802	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.431406	1.466619	-2.964787	27002.623019
HLA B*0803	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.384921	1.419915	-2.965007	24261.709176
HLA B*7301	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.351895	1.386690	-2.965204	22485.092674
HLA B*4501	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.132796	1.167129	-2.965666	13576.749576
HLA B*4501	1:272-280	9	DRGFIPEGL	1.324386	0.355442	-4.645562	1.679828	-2.965734	44214.173515
HLA B*3901	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.461362	1.495432	-2.965930	28930.896199
HLA A*3201	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.608611	1.642298	-2.966313	40607.958879
HLA B*1503	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.293853	1.327486	-2.966367	19672.203321
HLA B*5801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.358278	1.391860	-2.966418	22818.034510
HLA A*0202	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.294640	1.328104	-2.966536	19707.887834
HLA A*0216	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.461985	1.495432	-2.966552	28972.401873
HLA B*1501	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.364627	1.398016	-2.966611	23154.027305
HLA A*3301	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.566271	1.599646	-2.966626	36835.883555
HLA A*2602	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-3.662311	0.695627	-2.966684	4595.274252
HLA B*0801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.274785	1.307776	-2.967009	18827.150059
HLA B*4601	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.365139	1.398016	-2.967123	23181.350250
HLA B*4601	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.399646	1.432365	-2.967280	25098.375645
HLA B*4402	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.396518	1.429220	-2.967299	24918.302317
HLA A*3001	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.194860	1.227496	-2.967363	15662.453813
HLA B*4801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.399751	1.432365	-2.967386	25104.486463
HLA A*2603	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.552860	1.585411	-2.967449	35715.787555
HLA A*1101	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.415629	1.448126	-2.967503	26039.291388
HLA B*4501	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.427513	1.459786	-2.967726	26761.648161
HLA A*2601	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.354524	1.386690	-2.967833	22621.622750
HLA A*3002	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.295589	1.327486	-2.968103	19751.008404
HLA A*2603	1:149-157	9	AEGRQPVVR	1.045430	0.597987	-4.611670	1.643417	-2.968253	40894.997889
HLA B*1502	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.568649	1.600184	-2.968464	37038.105997
HLA B*5801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.352040	1.383422	-2.968619	22492.635734
HLA A*2902	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.366748	1.398016	-2.968732	23267.414466
HLA B*4402	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.355452	1.386690	-2.968762	22670.014723

HLA B*4403	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.611083	1.642298	-2.968785	40839.725923
HLA B*3801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.496611	1.527790	-2.968821	31376.985035
HLA A*2301	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.496700	1.527790	-2.968911	31383.436046
HLA B*1503	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-3.894760	0.925719	-2.969041	7848.019690
HLA A*0202	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.578430	1.609246	-2.969184	37881.718831
HLA A*1101	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.307746	1.338560	-2.969186	20311.664256
HLA B*4501	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.570831	1.601532	-2.969299	37224.720178
HLA B*4501	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.296797	1.327486	-2.969310	19806.006128
HLA A*0212	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.436469	1.466619	-2.969850	27319.270198
HLA A*3301	1:415-423	9	AALTSVTDW	1.150326	0.497710	-4.618007	1.648036	-2.969970	41496.049320
HLA B*0802	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.399303	1.429220	-2.970083	25078.559675
HLA B*0801	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.293002	1.322784	-2.970219	19633.715373
HLA A*3002	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.299010	1.328755	-2.970255	19907.197447
HLA B*4801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.368553	1.398016	-2.970537	23364.286903
HLA A*0301	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.368602	1.398016	-2.970586	23366.941416
HLA B*1801	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.501409	1.530697	-2.970712	31725.528020
HLA B*5301	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.579964	1.609246	-2.970718	38015.778628
HLA B*5701	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.403137	1.432365	-2.970772	25300.957073
HLA A*0250	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.525470	1.554677	-2.970793	33532.808971
HLA B*2705	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.309787	1.338560	-2.971228	20407.378132
HLA B*3501	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.437912	1.466619	-2.971293	27410.166732
HLA A*8001	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.393147	1.421817	-2.971330	24725.605716
HLA A*0202	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.228899	1.257536	-2.971363	16939.443631
HLA A*3002	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.272430	1.300814	-2.971616	18725.369669
HLA B*3901	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.431406	1.459786	-2.971620	27002.623019
HLA B*7301	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.573211	1.601532	-2.971680	37429.279752
HLA A*2603	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.391928	1.419915	-2.972013	24656.280200
HLA A*0206	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.467694	1.495432	-2.972262	29355.788440
HLA A*0212	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.394162	1.421817	-2.972345	24783.458817
HLA B*4501	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.602369	1.629468	-2.972901	40028.432074
HLA B*3901	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.310739	1.337733	-2.973005	20452.139820
HLA B*4801	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.394940	1.421817	-2.973123	24827.877653
HLA A*0211	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.183479	1.210192	-2.973287	15257.342587
HLA A*0203	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.393939	1.420375	-2.973563	24770.724892
HLA A*0301	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.215455	1.241782	-2.973674	16423.109512
HLA B*1501	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.406104	1.432365	-2.973739	25474.422612
HLA A*2902	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.433577	1.459786	-2.973790	27137.939970
HLA A*0219	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.440947	1.466619	-2.974328	27602.423310
HLA B*0803	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.394890	1.420375	-2.974515	24825.057176
HLA A*2601	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.303300	1.328755	-2.974545	20104.824370
HLA B*5401	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.529586	1.554677	-2.974909	33852.148130
HLA B*1503	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-3.858197	0.883265	-2.974932	7214.353162
HLA B*4001	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.079993	1.105060	-2.974933	12022.463896
HLA A*6801	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.511570	1.536595	-2.974975	32476.586933
HLA A*2603	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.604514	1.629468	-2.975046	40226.630729
HLA B*1517	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.470685	1.495432	-2.975253	29558.653299
HLA B*0803	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.423528	1.448126	-2.975402	26517.228447
HLA B*0702	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.440362	1.464436	-2.975926	27565.266155
HLA A*2403	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.442651	1.466619	-2.976032	27710.897284
HLA A*0211	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.939616	0.963515	-2.976101	8701.947356
HLA A*0212	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.374168	1.398016	-2.976152	23668.340018
HLA B*5301	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.549573	1.573351	-2.976222	35446.495287
HLA A*6901	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-3.983091	1.006851	-2.976240	9618.145045
HLA B*1501	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.396746	1.420375	-2.976371	24931.381858
HLA A*2603	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.628474	1.651959	-2.976514	42508.297056
HLA B*1501	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.314338	1.337733	-2.976605	20622.350510
HLA A*0250	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.585943	1.609246	-2.976697	38542.806025
HLA A*3002	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.470633	1.493912	-2.976721	29555.135509
HLA B*7301	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.625584	1.648791	-2.976793	42226.378896
HLA B*4402	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.375136	1.398016	-2.977120	23721.152608
HLA A*8001	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.443849	1.466619	-2.977230	27787.458423
HLA A*0216	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.397609	1.420375	-2.977233	24980.930526
HLA B*7301	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.513885	1.536595	-2.977289	32650.108161
HLA B*5401	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.562737	1.585411	-2.977326	36537.385381
HLA B*1502	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.304947	1.327486	-2.977461	20181.213299

HLA A*6801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.247000	1.269415	-2.977584	17660.360903
HLA B*4402	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.278410	1.300706	-2.977704	18984.966689
HLA B*5401	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.551138	1.573351	-2.977787	35574.438871
HLA B*1509	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.364563	1.386690	-2.977873	23150.645512
HLA B*4801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.407892	1.429823	-2.978070	25579.515096
HLA A*0301	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.362742	1.384650	-2.978092	23053.785824
HLA A*0206	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.509019	1.530697	-2.978322	32286.341856
HLA A*2403	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.283442	1.305053	-2.978390	19206.243753
HLA B*4002	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.635499	1.657009	-2.978490	43201.484162
HLA B*4601	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.398983	1.420375	-2.978608	25060.115038
HLA A*3301	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.533543	1.554677	-2.978865	34161.958859
HLA A*0212	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.399629	1.420375	-2.979254	25097.425207
HLA B*0802	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.401088	1.421817	-2.979272	25181.882830
HLA B*4501	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.631321	1.651959	-2.979362	42787.930594
HLA B*3501	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.041960	1.062587	-2.979373	11014.379052
HLA A*2902	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.408724	1.429220	-2.979504	25628.549383
HLA B*0801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.411962	1.432365	-2.979596	25820.319710
HLA B*5401	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.284697	1.305053	-2.979644	19261.808523
HLA A*6802	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.444283	1.464436	-2.979847	27815.282852
HLA B*0803	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.475283	1.495432	-2.979850	29873.257729
HLA A*3001	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.139764	1.159900	-2.979864	13796.355608
HLA A*1101	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.302837	1.322784	-2.980054	20083.409104
HLA B*4002	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.632188	1.651959	-2.980229	42873.431274
HLA A*0201	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.308427	1.328104	-2.980323	20343.555583
HLA A*0101	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.367023	1.386690	-2.980333	23282.146401
HLA A*3201	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.589599	1.609246	-2.980353	38868.620571
HLA B*3501	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.281232	1.300706	-2.980526	19108.718864
HLA B*0801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.378601	1.398016	-2.980585	23911.194817
HLA A*6901	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.367359	1.386690	-2.980669	23300.164768
HLA A*0216	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.250108	1.269415	-2.980693	17787.214532
HLA A*0212	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.238257	1.257536	-2.980721	17308.408669
HLA A*3001	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.103892	1.123062	-2.980831	12702.594748
HLA A*0101	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.378956	1.398016	-2.980940	23930.735691
HLA B*4601	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.402815	1.421817	-2.980998	25282.212094
HLA A*3301	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.590722	1.609455	-2.981267	38969.262057
HLA B*5101	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.448287	1.466619	-2.981668	28072.882186
HLA B*4403	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-3.389691	0.407915	-2.981777	2452.964670
HLA B*1501	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.119202	1.137355	-2.981847	13158.357672
HLA B*4002	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.643987	1.661630	-2.982357	44054.203775
HLA B*1801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.442171	1.459786	-2.982385	27680.331925
HLA B*4001	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.290460	1.307776	-2.982685	19519.125124
HLA A*0212	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.415136	1.432365	-2.982770	26009.725553
HLA B*4402	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.419950	1.437023	-2.982927	26299.643677
HLA B*1509	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.367975	1.384650	-2.983325	23333.213626
HLA A*3001	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-3.976734	0.993286	-2.983448	9478.369079
HLA B*4501	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.511274	1.527790	-2.983484	32454.456940
HLA A*3101	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.033821	1.050133	-2.983688	10809.893177
HLA B*3801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.431951	1.448126	-2.983825	27036.535134
HLA A*2902	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.146578	1.162617	-2.983961	14014.508990
HLA A*0201	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.253458	1.269415	-2.984043	17924.964686
HLA B*1517	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.416623	1.432365	-2.984258	26098.947495
HLA A*0219	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.404728	1.420375	-2.984352	25393.791599
HLA B*0801	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.406194	1.421817	-2.984377	25479.660075
HLA B*1801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-3.663129	0.678719	-2.984410	4603.933655
HLA B*1501	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.367841	1.383422	-2.984419	23326.019620
HLA A*2301	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.421522	1.437023	-2.984499	26395.000217
HLA A*2501	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.168423	1.183813	-2.984611	14737.485746
HLA A*2301	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.515313	1.530697	-2.984616	32757.678122
HLA A*0206	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.147635	1.162617	-2.985018	14048.668176
HLA A*2601	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.254433	1.269415	-2.985018	17965.253305
HLA A*0219	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.033821	1.048747	-2.985074	10809.893177
HLA B*1501	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.167131	1.181912	-2.985220	14693.700428
HLA A*2301	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.433474	1.448126	-2.985348	27131.480956
HLA B*4402	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.314120	1.328755	-2.985365	20611.977609
HLA A*0201	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.899515	0.914083	-2.985432	7934.424676

HLA B*1502	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.219600	1.234017	-2.985583	16580.586184
HLA A*2402	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.254173	1.268289	-2.985884	17954.468450
HLA B*1503	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.450481	1.464436	-2.986045	28215.088840
HLA B*1502	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.169885	1.183813	-2.986072	14787.160193
HLA A*6901	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.369619	1.383422	-2.986198	23421.742215
HLA B*4402	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.378181	1.391860	-2.986321	23888.051137
HLA A*0216	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.384461	1.398016	-2.986445	24235.997191
HLA B*4801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.423592	1.437023	-2.986569	26521.102023
HLA A*0301	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.325181	1.338560	-2.986621	21143.702399
HLA A*3101	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.407345	1.420375	-2.986969	25547.292323
HLA B*5701	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.309813	1.322784	-2.987029	20408.592586
HLA B*4402	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.407458	1.420375	-2.987082	25553.927170
HLA B*2705	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.292253	1.305053	-2.987200	19599.861618
HLA A*0301	1:235-243	9	IGVAERIPK	0.603044	0.187675	-3.777962	0.790719	-2.987244	5997.392684
HLA A*3301	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.643080	1.655822	-2.987258	43962.305014
HLA B*1509	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.482768	1.495432	-2.987336	30392.613341
HLA B*2705	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.424536	1.437023	-2.987513	26578.842227
HLA A*0216	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.374297	1.386690	-2.987607	23675.383436
HLA A*2501	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.221794	1.234017	-2.987777	16664.577192
HLA B*3501	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.436063	1.448126	-2.987937	27293.713758
HLA A*0216	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.454595	1.466619	-2.987976	28483.632270
HLA B*1502	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.417210	1.429220	-2.987991	26134.269479
HLA B*4501	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.630302	1.642298	-2.988004	42687.587003
HLA B*1501	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.257452	1.269415	-2.988037	18090.577596
HLA B*4001	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.372768	1.384650	-2.988117	23592.149230
HLA B*3801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.417377	1.429220	-2.988157	26144.309635
HLA B*0802	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.374856	1.386690	-2.988166	23705.886394
HLA B*4403	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.633490	1.645215	-2.988275	43002.119064
HLA B*4001	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.293336	1.305053	-2.988283	19648.803872
HLA A*3101	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.230142	1.241782	-2.988360	16987.990896
HLA B*5401	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.516187	1.527790	-2.988397	32823.668633
HLA B*1503	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.101444	1.112802	-2.988642	12631.190341
HLA B*4002	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.630985	1.642298	-2.988688	42754.842046
HLA B*4402	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.316225	1.327486	-2.988738	20712.131778
HLA A*2403	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.453176	1.464436	-2.988740	28390.711816
HLA B*4501	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.598095	1.609246	-2.988849	39636.460530
HLA A*2602	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.631171	1.642298	-2.988873	42773.118569
HLA B*5301	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.546063	1.556999	-2.989065	35161.158096
HLA B*7301	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.582661	1.593495	-2.989166	38252.612299
HLA B*5701	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.411252	1.421817	-2.989435	25778.169261
HLA A*0206	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.810724	0.821048	-2.989676	6467.310384
HLA B*3801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.419637	1.429823	-2.989815	26280.727488
HLA B*4501	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.651708	1.661630	-2.990078	44844.353155
HLA A*3201	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.583714	1.593495	-2.990219	38345.434929
HLA A*2601	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.388528	1.398016	-2.990512	24464.021629
HLA A*6801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.374384	1.383422	-2.990962	23680.122915
HLA A*2602	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.576428	1.585411	-2.991017	37707.515225
HLA A*2501	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.428387	1.437023	-2.991364	26815.559639
HLA B*5401	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.555308	1.563919	-2.991389	35917.689718
HLA A*2402	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.411966	1.420375	-2.991591	25820.599081
HLA B*4501	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.296703	1.305053	-2.991650	19801.720660
HLA A*0301	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.320576	1.328755	-2.991821	20920.692052
HLA B*1509	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.412265	1.420375	-2.991889	25838.345373
HLA A*2601	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.376628	1.384650	-2.991978	23802.781528
HLA B*5401	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.411910	1.419915	-2.991995	25817.246821
HLA B*0801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-3.894459	0.902312	-2.992147	7842.587086
HLA B*5301	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.592512	1.600184	-2.992328	39130.238000
HLA A*6901	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.202529	1.210192	-2.992337	15941.475731
HLA A*2603	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.648379	1.655822	-2.992556	44501.899005
HLA B*5701	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.413087	1.420375	-2.992712	25887.315624
HLA A*8001	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.452525	1.459786	-2.992739	28348.199080
HLA A*0211	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.523456	1.530697	-2.992760	33377.701486
HLA A*2403	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.093559	1.100571	-2.992988	12403.932892
HLA B*1501	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.293021	1.299885	-2.993137	19634.565122
HLA A*2403	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.415251	1.421817	-2.993434	26016.621244

HLA A*0212	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.671014	0.677348	-2.993666	4688.284177
HLA B*4501	1:211-219	9	HVLRGEDLL	1.196256	0.448959	-4.638922	1.645215	-2.993707	43543.352836
HLA B*1517	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.391848	1.398016	-2.993832	24651.745434
HLA B*5101	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.194597	1.200757	-2.993839	15652.966687
HLA B*4403	1:164-172	9	DLAWNDLVR	1.199195	0.462435	-4.655490	1.661630	-2.993860	45236.649908
HLA B*0802	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.453893	1.459786	-2.994106	28437.595619
HLA B*3901	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.416233	1.421817	-2.994416	26075.520075
HLA A*8001	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.302476	1.307776	-2.994700	20066.684123
HLA A*1101	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.381397	1.386690	-2.994707	24065.626107
HLA B*4402	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.414631	1.419915	-2.994716	25979.490548
HLA B*1517	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.054647	1.059725	-2.994922	11340.892593
HLA A*6801	1:324-332	9	ADALNAEHI	1.444411	0.211411	-4.650820	1.655822	-2.994998	44752.742929
HLA A*0301	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.057274	1.062125	-2.995149	11409.693067
HLA A*0201	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.962740	0.967578	-2.995162	9177.831564
HLA B*4501	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.549968	1.554677	-2.995291	35478.725882
HLA A*3002	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.526020	1.530697	-2.995323	33575.285506
HLA A*3101	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.334170	1.338560	-2.995611	21585.900309
HLA A*3001	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-3.830572	0.834835	-2.995737	6769.742561
HLA A*0250	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.425029	1.429220	-2.995810	26609.054990
HLA B*4801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.380500	1.384650	-2.995850	24015.943976
HLA A*6802	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.417871	1.421817	-2.996054	26174.028455
HLA A*2603	1:151-159	9	GRQPVVRLR	1.073513	0.568785	-4.638356	1.642298	-2.996058	43486.618733
HLA B*1801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.462812	1.466619	-2.996193	29027.626031
HLA B*5401	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.553217	1.556999	-2.996219	35745.168838
HLA A*6802	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.428690	1.432365	-2.996325	26834.280098
HLA B*5301	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.589881	1.593495	-2.996386	38893.861755
HLA A*3301	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.598020	1.601532	-2.996488	39629.599400
HLA A*2902	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.297323	1.300814	-2.996509	19830.021895
HLA B*1801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.426434	1.429823	-2.996612	26695.277703
HLA A*8001	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.388563	1.391860	-2.996703	24466.006924
HLA B*5801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.334128	1.337377	-2.996751	21583.798420
HLA A*2403	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.335573	1.338560	-2.997013	21655.729077
HLA A*2501	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.445385	1.448126	-2.997260	27885.946452
HLA B*1517	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.320059	1.322784	-2.997276	20895.807566
HLA A*0219	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.461801	1.464436	-2.997365	28960.178928
HLA A*0216	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.017737	1.020365	-2.997372	10416.860014
HLA A*3101	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.911653	0.914083	-2.997570	8159.299617
HLA A*8001	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.395661	1.398016	-2.997645	24869.146947
HLA B*4501	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.655091	1.657009	-2.998082	45195.065739
HLA A*6901	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.060385	1.062125	-2.998259	11491.710580
HLA B*4403	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.571611	1.573351	-2.998260	37291.638950
HLA B*4002	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.526147	1.527790	-2.998357	33585.095421
HLA B*1503	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.158560	1.159900	-2.998660	14406.558929
HLA A*0101	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.390635	1.391860	-2.998776	24583.025977
HLA B*3501	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.463256	1.464436	-2.998819	29057.321059
HLA A*2902	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.390788	1.391860	-2.998928	24591.671941
HLA B*5101	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.428772	1.429823	-2.998950	26839.361546
HLA B*5301	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.324361	1.325261	-2.999100	21103.819666
HLA A*3101	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.322197	1.322784	-2.999414	20998.931239
HLA B*4002	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.648209	1.648791	-2.999419	44484.568356
HLA A*8001	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.431808	1.432365	-2.999442	27027.614462
HLA B*4403	1:444-452	9	PRKAFSPIR	1.084215	0.567744	-4.651428	1.651959	-2.999469	44815.492691
HLA B*3901	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.241295	1.241782	-2.999513	17429.905195
HLA A*2601	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.391385	1.391860	-2.999525	24625.486876
HLA A*0250	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.563539	1.563919	-2.999619	36604.850744
HLA B*1503	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.162023	1.162401	-2.999623	14521.898632
HLA B*5801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.327197	1.327486	-2.999710	21242.072929
HLA A*3301	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.300692	1.300814	-2.999878	19984.457126
HLA B*4402	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.429733	1.429823	-2.999910	26898.813264
HLA B*4403	1:58-66	9	YLALLDALR	0.982293	0.674716	-4.656952	1.657009	-2.999943	45389.125413
HLA B*4601	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.300706	1.300706	-3.000001	19985.105818
HLA B*5401	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.517284	1.517234	-3.000050	32906.699790
HLA A*2403	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.323095	1.322784	-3.000311	21042.372032
HLA B*4601	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.387229	1.386690	-3.000538	24390.942749
HLA B*2705	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.392553	1.391860	-3.000693	24691.786881

HLA A*2601	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.300937	1.299885	-3.001052	19995.704114
HLA A*3001	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.301085	1.299885	-3.001200	20002.520272
HLA A*6901	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.339020	1.337733	-3.001286	21828.279399
HLA A*3001	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-3.987555	0.986192	-3.001363	9717.517773
HLA A*0203	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.232264	1.230828	-3.001435	17071.182474
HLA B*1501	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.329582	1.328104	-3.001477	21359.034774
HLA B*5701	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.386155	1.384650	-3.001505	24330.715032
HLA A*0211	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.775867	0.774156	-3.001711	5968.521257
HLA B*4002	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.631352	1.629468	-3.001884	42790.939914
HLA A*0201	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.393770	1.391860	-3.001910	24761.078276
HLA B*5401	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.309700	1.307776	-3.001925	20403.293679
HLA A*0219	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.266613	1.264555	-3.002058	18476.217891
HLA B*7301	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.611525	1.609455	-3.002069	40881.283470
HLA B*1509	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.466615	1.464436	-3.002179	29282.984362
HLA B*4001	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.339565	1.337377	-3.002188	21855.693148
HLA B*4002	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.566245	1.563919	-3.002326	36833.691562
HLA B*2705	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.229846	1.227496	-3.002350	16976.415045
HLA B*1503	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.327728	1.325261	-3.002467	21268.060113
HLA B*3801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.496421	1.493912	-3.002509	31363.238620
HLA B*7301	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.566579	1.563919	-3.002660	36861.998232
HLA A*0219	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.424576	1.421817	-3.002759	26581.286745
HLA A*2501	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.469691	1.466619	-3.003072	29491.089112
HLA B*1509	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.424935	1.421817	-3.003119	26603.297531
HLA B*5701	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.308305	1.305053	-3.003252	20337.833456
HLA B*0802	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.423176	1.419915	-3.003261	26495.718886
HLA A*2902	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.389963	1.386690	-3.003273	24545.019834
HLA B*4501	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.652142	1.648791	-3.003352	44889.257173
HLA A*3001	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.271928	1.268289	-3.003639	18703.703548
HLA B*4403	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.612915	1.609246	-3.003669	41012.421975
HLA B*4601	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.273093	1.269415	-3.003678	18753.958684
HLA B*4402	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.308815	1.305053	-3.003762	20361.722993
HLA A*6801	1:54-62	9	SEESYLALL	1.352077	0.257378	-4.613545	1.609455	-3.004090	41071.926973
HLA A*0212	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.387569	1.383422	-3.004148	24410.083339
HLA B*0702	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.425993	1.421817	-3.004176	26668.140829
HLA A*2602	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.127434	1.123062	-3.004372	13410.169978
HLA A*3201	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.568317	1.563919	-3.004398	37009.864311
HLA B*0702	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.333223	1.328755	-3.004468	21538.890310
HLA B*5701	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.343162	1.338560	-3.004602	22037.465536
HLA B*3501	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.071845	1.067176	-3.004669	11799.007238
HLA B*7301	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.604349	1.599646	-3.004704	40211.400100
HLA B*0803	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.426622	1.421817	-3.004806	26706.833683
HLA B*1502	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.469251	1.464436	-3.004815	29461.269559
HLA A*2501	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.434216	1.429220	-3.004996	27177.902568
HLA B*1501	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.397136	1.391860	-3.005277	24953.781332
HLA B*4001	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.397254	1.391860	-3.005394	24960.532105
HLA B*1517	1:323-331	9	KADALNAEH	0.661781	-0.194938	-3.472356	0.466843	-3.005512	2967.259803
HLA B*4601	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.388993	1.383422	-3.005571	24490.240502
HLA A*6801	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.579116	1.573351	-3.005764	37941.607404
HLA A*2603	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.240148	1.234192	-3.005956	17383.950481
HLA B*5101	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.313859	1.307776	-3.006083	20599.603880
HLA B*1517	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.068345	1.062125	-3.006219	11704.280865
HLA A*3002	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.561116	1.554677	-3.006439	36401.252009
HLA A*2301	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.501952	1.495432	-3.006519	31765.199701
HLA B*4801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.398389	1.391860	-3.006529	25025.838672
HLA B*4403	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.173926	1.167129	-3.006796	14925.397007
HLA A*6801	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.606478	1.599646	-3.006832	40408.974426
HLA A*0250	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.169561	1.162617	-3.006943	14776.124741
HLA A*0101	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.335902	1.328755	-3.007147	21672.137002
HLA B*5801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.217387	1.210192	-3.007195	16496.304537
HLA B*1501	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-3.970733	0.963515	-3.007218	9348.308394
HLA A*0101	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.344724	1.337377	-3.007347	22116.889781
HLA A*0101	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.390917	1.383422	-3.007496	24598.990132
HLA B*7301	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.564591	1.556999	-3.007593	36693.674965
HLA B*4501	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.123341	1.115540	-3.007801	13284.385803
HLA A*6901	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-3.856666	0.848752	-3.007914	7188.951177

HLA A*1101	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.429735	1.421817	-3.007919	26898.958784
HLA B*5801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.336217	1.328104	-3.008112	21687.853375
HLA B*5401	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.428685	1.420375	-3.008310	26833.989759
HLA B*1509	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-3.868859	0.860349	-3.008510	7393.658056
HLA A*0201	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.392038	1.383422	-3.008616	24662.550221
HLA B*3801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.473600	1.464436	-3.009164	29757.768062
HLA A*0216	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.071394	1.062125	-3.009269	11786.757987
HLA A*2601	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.392762	1.383422	-3.009340	24703.678348
HLA A*2301	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.429261	1.419915	-3.009346	26869.579722
HLA B*1502	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.594949	1.585411	-3.009538	39350.377710
HLA A*1101	1:425-433	9	APLIEAALK	0.788948	0.145204	-3.944287	0.934152	-3.010135	8796.040652
HLA B*1503	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.310135	1.299885	-3.010250	20423.724119
HLA A*0212	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.396986	1.386690	-3.010296	24945.143007
HLA A*0203	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.443041	1.432365	-3.010675	27735.794000
HLA B*0802	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.395363	1.384650	-3.010712	24852.066320
HLA B*3501	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.432733	1.421817	-3.010917	27085.285163
HLA B*4402	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.443557	1.432365	-3.011192	27768.824117
HLA A*3101	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.409448	1.398016	-3.011432	25671.288444
HLA B*0802	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.409499	1.398016	-3.011483	25674.343960
HLA B*5301	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.448616	1.437023	-3.011593	28094.152205
HLA B*5101	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-3.914134	0.902312	-3.011822	8206.045814
HLA A*6901	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.337189	1.325261	-3.011929	21736.481969
HLA A*2402	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.441227	1.429220	-3.012007	27620.198831
HLA A*8001	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.349439	1.337377	-3.012063	22358.335569
HLA B*0802	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.319859	1.307776	-3.012084	20886.201034
HLA A*2902	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.396901	1.384650	-3.012251	24940.285264
HLA B*5701	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.404450	1.391860	-3.012590	25377.586216
HLA B*3901	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.240207	1.227496	-3.012711	17386.301771
HLA B*4601	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.404807	1.391860	-3.012948	25398.462867
HLA B*1801	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.477397	1.464436	-3.012961	30019.062307
HLA A*3001	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.277724	1.264555	-3.013168	18955.000047
HLA B*3901	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.477698	1.464436	-3.013261	30039.856680
HLA B*0702	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.411567	1.398016	-3.013551	25796.863279
HLA B*0702	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.339438	1.325261	-3.014177	21849.309289
HLA B*5701	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.397637	1.383422	-3.014215	24982.552307
HLA B*5801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.176628	1.162401	-3.014227	15018.542909
HLA B*1517	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.478779	1.464436	-3.014342	30114.705429
HLA B*5801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.352285	1.337733	-3.014551	22505.294292
HLA B*1509	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.339915	1.325261	-3.014654	21873.317545
HLA A*0101	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.342220	1.327486	-3.014733	21989.710036
HLA B*0702	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.406595	1.391860	-3.014736	25503.241986
HLA A*0101	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.337744	1.322784	-3.014960	21764.251394
HLA A*2403	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.399972	1.384650	-3.015322	25117.256084
HLA B*0801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.398915	1.383422	-3.015493	25056.183746
HLA B*3901	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.482268	1.466619	-3.015649	30357.611908
HLA A*3301	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.448031	1.432365	-3.015665	28056.333107
HLA A*0212	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.480137	1.464436	-3.015700	30209.018959
HLA B*7301	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.616104	1.600184	-3.015919	41314.611031
HLA A*0206	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.437186	1.420375	-3.016810	27364.384645
HLA B*4002	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.476638	1.459786	-3.016852	29966.652975
HLA A*2403	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.449234	1.432365	-3.016868	28134.153038
HLA B*1509	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.483541	1.466619	-3.016922	30446.755909
HLA B*0803	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.403722	1.386690	-3.017032	25335.062006
HLA B*5301	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.446358	1.429220	-3.017138	27948.472435
HLA A*2501	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.477099	1.459786	-3.017312	29998.444616
HLA A*6802	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.437895	1.420375	-3.017520	27409.128749
HLA A*2602	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.437470	1.419915	-3.017555	27382.303142
HLA B*2705	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-3.900841	0.883265	-3.017576	7958.670985
HLA A*0202	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.548342	1.530697	-3.017645	35346.154493
HLA B*0803	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.454948	1.437023	-3.017925	28506.755644
HLA A*0211	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.201739	1.183813	-3.017926	15912.524868
HLA B*5801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.346921	1.328755	-3.018166	22229.045875
HLA A*3002	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.582210	1.563919	-3.018291	38212.899988
HLA A*3001	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.252920	1.234017	-3.018903	17902.771832
HLA B*5801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.260697	1.241782	-3.018915	18226.239469

HLA A*1101	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.260791	1.241782	-3.019009	18230.183973
HLA B*1517	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-3.984064	0.965021	-3.019043	9639.710890
HLA A*6901	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.039521	1.020365	-3.019156	10952.701529
HLA B*4403	1:44-52	9	RIEDTDAQR	0.951024	0.697767	-4.668067	1.648791	-3.019277	46565.817110
HLA B*4402	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.403929	1.384650	-3.019279	25347.126147
HLA A*2601	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.346810	1.327486	-3.019324	22223.394530
HLA B*2705	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-3.570113	0.550534	-3.019579	3716.318654
HLA B*4501	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.891457	0.871584	-3.019872	7788.551718
HLA B*4403	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.583864	1.563919	-3.019945	38358.713679
HLA B*5301	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.514037	1.493912	-3.020126	32661.591356
HLA A*3301	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.288686	1.268289	-3.020398	19439.562511
HLA A*6802	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.251280	1.230828	-3.020452	17835.296605
HLA B*1509	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.412359	1.391860	-3.020499	25843.937281
HLA B*1502	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.480435	1.459786	-3.020649	30229.781376
HLA A*0219	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.358591	1.337733	-3.020857	22834.458342
HLA A*0216	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.453768	1.432365	-3.021403	28429.443043
HLA B*4403	1:225-233	9	QLALHQALI	1.319205	0.310263	-4.650876	1.629468	-3.021408	44758.553883
HLA B*1503	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-3.914933	0.893488	-3.021444	8221.153596
HLA A*0219	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.344567	1.322784	-3.021783	22108.874689
HLA A*2501	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.350769	1.328755	-3.022014	22426.901652
HLA B*0803	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.451919	1.429220	-3.022699	28308.659641
HLA A*3002	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.345638	1.322784	-3.022854	22163.482609
HLA B*1801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.330728	1.307776	-3.022952	21415.497678
HLA A*2902	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.345774	1.322784	-3.022991	22170.438016
HLA B*1501	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.345899	1.322784	-3.023115	22176.795727
HLA B*7301	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.577882	1.554677	-3.023205	37833.998849
HLA B*1517	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-3.707079	0.683810	-3.023268	5094.229694
HLA A*6802	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-3.688546	0.665274	-3.023272	4881.415607
HLA A*2403	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.352052	1.328755	-3.023297	22493.244155
HLA B*3501	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.352057	1.328755	-3.023302	22493.487529
HLA B*0802	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.406734	1.383422	-3.023312	25511.383498
HLA B*5701	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.185725	1.162401	-3.023324	15336.455740
HLA A*8001	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.361236	1.337733	-3.023503	22973.979767
HLA B*4002	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.190828	1.167129	-3.023699	15517.726281
HLA B*5401	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.554500	1.530697	-3.023803	35850.908989
HLA B*2705	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.351916	1.328104	-3.023812	22486.187477
HLA A*2403	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.251311	1.227496	-3.023814	17836.550980
HLA B*1503	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-3.991737	0.967687	-3.024050	9811.545607
HLA A*8001	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.352872	1.328755	-3.024117	22535.752671
HLA A*3101	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.361913	1.337733	-3.024180	23009.802231
HLA A*3001	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.084326	1.059725	-3.024601	12142.998235
HLA B*1517	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.011403	0.986777	-3.024626	10266.032065
HLA B*2705	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.408165	1.383422	-3.024743	25595.572485
HLA B*0803	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.422856	1.398016	-3.024840	26476.231965
HLA A*2501	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.446849	1.421817	-3.025033	27980.090718
HLA A*8001	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.353354	1.328104	-3.025250	22560.759299
HLA B*2705	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.410087	1.384650	-3.025437	25709.091290
HLA B*4403	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.582734	1.556999	-3.025735	38259.028051
HLA B*7301	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.611287	1.585411	-3.025876	40858.952087
HLA A*0203	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.188573	1.162617	-3.025955	15437.343983
HLA A*2602	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.455953	1.429823	-3.026131	28572.837589
HLA A*0202	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.490573	1.464436	-3.026137	30943.756445
HLA B*1509	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.463277	1.437023	-3.026254	29058.735865
HLA A*0101	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-3.981470	0.954860	-3.026610	9582.309134
HLA B*1501	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.365219	1.338560	-3.026659	23185.614533
HLA B*4801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.410270	1.383422	-3.026848	25719.942080
HLA A*0212	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.047260	1.020365	-3.026896	11149.630023
HLA A*0201	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.749585	0.722436	-3.027149	5618.047486
HLA A*2501	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.491870	1.464436	-3.027434	31036.300622
HLA A*1101	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.332504	1.305053	-3.027452	21503.263766
HLA B*5801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.352719	1.325261	-3.027459	22527.829529
HLA A*0301	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.355219	1.327486	-3.027733	22657.876389
HLA B*5301	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.333118	1.305053	-3.028065	21533.647413
HLA A*6802	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.912066	0.883995	-3.028072	8167.072117
HLA B*0702	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.460488	1.432365	-3.028122	28872.731932

HLA B*3501	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.460601	1.432365	-3.028235	28880.230423
HLA A*1101	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.458115	1.429823	-3.028292	28715.401886
HLA B*0803	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.488242	1.459786	-3.028456	30778.138173
HLA A*6901	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-3.996126	0.967578	-3.028548	9911.200570
HLA B*3501	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-3.900220	0.871584	-3.028636	7947.312439
HLA B*0702	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-3.790532	0.761813	-3.028719	6173.511057
HLA B*4001	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.286321	1.257536	-3.028784	19333.948413
HLA A*2403	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.366523	1.337733	-3.028789	23255.333686
HLA A*0301	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.366610	1.337733	-3.028876	23259.989077
HLA A*8001	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.412429	1.383422	-3.029008	25848.132006
HLA A*2301	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.367634	1.338560	-3.029074	23314.917439
HLA B*4501	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.079213	1.050133	-3.029080	12000.889931
HLA B*2705	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.298564	1.269415	-3.029149	19886.745771
HLA A*2403	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.337105	1.307776	-3.029329	21732.249071
HLA A*0219	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.461761	1.432365	-3.029396	28957.515638
HLA B*5401	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-3.997108	0.967687	-3.029421	9933.638462
HLA A*0101	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.294013	1.264555	-3.029457	19679.441514
HLA B*3501	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-3.819788	0.790220	-3.029569	6603.710372
HLA B*1801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.461977	1.432365	-3.029612	28971.931664
HLA B*5701	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.299494	1.269415	-3.030079	19929.395134
HLA B*1501	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.097582	1.067176	-3.030405	12519.348421
HLA B*4501	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.567061	1.536595	-3.030465	36902.901870
HLA B*3901	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.079312	1.048747	-3.030565	12003.617027
HLA B*0802	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.463147	1.432365	-3.030782	29050.090902
HLA B*4801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.344597	1.313812	-3.030785	22110.429629
HLA B*2705	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.451167	1.420375	-3.030792	28259.695089
HLA A*0211	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.451219	1.420375	-3.030844	28263.058689
HLA A*2601	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.368759	1.337377	-3.031383	23375.412593
HLA B*1517	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.300862	1.269415	-3.031446	19992.242828
HLA A*2501	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.339264	1.307776	-3.031488	21840.564066
HLA B*5401	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.360280	1.328755	-3.031525	22923.450735
HLA A*0250	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.038398	1.006851	-3.031547	10924.415231
HLA A*2603	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.527103	1.495432	-3.031671	33659.125391
HLA A*0212	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.423613	1.391860	-3.031753	26522.393340
HLA B*0803	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.423697	1.391860	-3.031837	26527.559238
HLA B*5801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.332716	1.300814	-3.031901	21513.736040
HLA B*1503	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.333017	1.300814	-3.032202	21528.638726
HLA A*0219	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.300533	1.268289	-3.032244	19977.106746
HLA A*2902	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.369767	1.337377	-3.032391	23429.726245
HLA A*3201	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.461693	1.429220	-3.032473	28952.972943
HLA A*2603	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.462461	1.429823	-3.032639	29004.237060
HLA B*3801	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.499297	1.466619	-3.032678	31571.605824
HLA B*0702	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.263733	1.230828	-3.032904	18354.079422
HLA B*4403	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.587654	1.554677	-3.032976	38694.902297
HLA A*0211	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.528482	1.495432	-3.033050	33766.183372
HLA A*6802	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.419995	1.386690	-3.033304	26302.347101
HLA B*0803	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.466021	1.432365	-3.033655	29242.932100
HLA B*4002	1:118-126	9	EARHVAAGR	0.989892	0.619354	-4.642902	1.609246	-3.033656	43944.233559
HLA B*5401	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.196129	1.162401	-3.033728	15708.276066
HLA A*2601	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.372469	1.338560	-3.033910	23575.945671
HLA B*7301	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.607425	1.573351	-3.034073	40497.169585
HLA B*3901	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.466761	1.432365	-3.034396	29292.807906
HLA B*4801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.339468	1.305053	-3.034415	21850.845973
HLA B*0802	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.359918	1.325261	-3.034658	22904.360636
HLA A*2501	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.334591	1.299885	-3.034706	21606.813575
HLA B*4801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.373496	1.338560	-3.034936	23631.748008
HLA A*0301	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.340185	1.305053	-3.035132	21886.929984
HLA B*0702	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.418580	1.383422	-3.035158	26216.826182
HLA B*0702	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.343028	1.307776	-3.035252	22030.671030
HLA A*2603	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.472310	1.437023	-3.035288	29669.517742
HLA A*3101	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.269425	1.234017	-3.035409	18596.251404
HLA A*2301	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.372833	1.337377	-3.035457	23595.723166
HLA A*0301	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.343841	1.307776	-3.036065	22071.947135
HLA B*1509	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.374100	1.337733	-3.036366	23664.627059
HLA A*3001	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.920604	0.883995	-3.036610	8329.221644

HLA A*0301	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.359460	1.322784	-3.036676	22880.210916
HLA B*4402	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-3.942535	0.905846	-3.036689	8760.613327
HLA A*3101	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.337084	1.299885	-3.037199	21731.190975
HLA B*5101	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.375063	1.337733	-3.037330	23717.174748
HLA B*3901	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.375035	1.337377	-3.037658	23715.635111
HLA B*4002	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.637846	1.600184	-3.037661	43435.597748
HLA B*0803	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.268765	1.230828	-3.037937	18568.003253
HLA B*0802	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.366760	1.328755	-3.038005	23268.043845
HLA B*3501	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.272304	1.234192	-3.038112	18719.900151
HLA A*0203	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-3.717181	0.678487	-3.038694	5214.123440
HLA B*5801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.352621	1.313812	-3.038809	22522.711442
HLA B*7301	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-3.589543	0.550534	-3.039009	3886.361421
HLA A*0301	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.206222	1.167129	-3.039092	16077.625665
HLA B*4002	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.639406	1.599646	-3.039760	43591.906217
HLA A*0250	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.367923	1.328104	-3.039819	23330.436730
HLA A*0203	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.431704	1.391860	-3.039845	27021.181706
HLA A*2301	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.347847	1.307776	-3.040071	22276.477537
HLA A*2501	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.426850	1.386690	-3.040160	26720.852019
HLA A*0219	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.426895	1.386690	-3.040205	26723.598740
HLA A*6802	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.432301	1.391860	-3.040441	27058.337354
HLA B*3501	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.145121	1.104589	-3.040532	13967.581233
HLA A*2501	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.345607	1.305053	-3.040555	22161.923939
HLA B*4601	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.378498	1.337733	-3.040765	23905.503790
HLA B*3501	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.275135	1.234017	-3.041118	18842.332244
HLA A*0202	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.536621	1.495432	-3.041188	34404.923038
HLA A*0250	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.164321	1.123062	-3.041259	14598.935750
HLA B*3501	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.009081	0.967578	-3.041503	10211.306809
HLA B*1503	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.364298	1.322784	-3.041514	23136.497443
HLA A*8001	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.426406	1.384650	-3.041756	26693.544737
HLA B*0803	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.370792	1.328755	-3.042036	23485.055441
HLA B*3901	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.369770	1.327486	-3.042283	23429.852997
HLA A*0250	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.506871	1.464436	-3.042435	32127.091604
HLA A*2602	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.105133	1.062587	-3.042546	12738.930583
HLA B*7301	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-3.582974	0.540290	-3.042684	3828.018485
HLA A*0101	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.380429	1.337733	-3.042696	24012.046584
HLA B*1517	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.464646	1.421817	-3.042830	29150.530795
HLA B*1503	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.381646	1.338560	-3.043087	24079.430456
HLA B*1503	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.475708	1.432365	-3.043342	29902.523649
HLA A*0203	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.357205	1.313812	-3.043393	22761.690721
HLA B*1801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.435367	1.391860	-3.043507	27250.042568
HLA B*2705	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.285360	1.241782	-3.043578	19291.216548
HLA A*0250	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.575286	1.530697	-3.044589	37608.504612
HLA A*3301	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.608625	1.563919	-3.044706	40609.277008
HLA B*4001	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.314124	1.269415	-3.044709	20612.200627
HLA A*2301	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.474141	1.429220	-3.044921	29794.817940
HLA B*4501	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.644796	1.599646	-3.045150	44136.265065
HLA A*0211	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.509646	1.464436	-3.045210	32333.011250
HLA A*3002	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.350281	1.305053	-3.045228	22401.679818
HLA B*1509	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-3.844072	0.798809	-3.045263	6983.486445
HLA B*3801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.443496	1.398016	-3.045481	27764.918509
HLA A*6901	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-3.739624	0.693953	-3.045671	5490.647834
HLA B*3501	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.373301	1.327486	-3.045814	23621.139243
HLA A*0203	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.227729	1.181912	-3.045817	16893.868077
HLA A*2301	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.512752	1.466619	-3.046133	32565.081735
HLA B*1501	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.314439	1.268289	-3.046150	20627.148347
HLA B*0801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.346049	1.299885	-3.046165	22184.475392
HLA A*3002	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.478666	1.432365	-3.046300	30106.886418
HLA B*1801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.247058	1.200757	-3.046301	17662.749579
HLA B*3801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.506108	1.459786	-3.046321	32070.654931
HLA B*4002	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.640024	1.593495	-3.046529	43653.972962
HLA A*6801	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.506336	1.459786	-3.046549	32087.488720
HLA A*0250	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.277498	1.230828	-3.046670	18945.158336
HLA A*6801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.431409	0.384545	-3.046864	2700.279683
HLA A*0212	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.316493	1.269415	-3.047077	20724.909456
HLA B*1502	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.184494	1.137355	-3.047139	15293.041796

HLA B*4501	1:279-287	9	GLLNYLALL	1.290918	0.282433	-4.620490	1.573351	-3.047139	41734.013943
HLA B*5801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.347024	1.299885	-3.047140	22234.337799
HLA B*3801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.484229	1.437023	-3.047207	30495.055256
HLA A*8001	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.374736	1.327486	-3.047250	23699.346739
HLA A*0211	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.278321	1.230828	-3.047492	18981.064241
HLA A*1101	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.432233	1.384650	-3.047583	27054.092591
HLA A*0101	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.372927	1.325261	-3.047667	23600.829728
HLA A*2501	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.468060	1.420375	-3.047685	29380.573500
HLA A*0202	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.434493	1.386690	-3.047803	27195.257581
HLA A*3301	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.604873	1.556999	-3.047874	40259.940619
HLA A*0203	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.431354	1.383422	-3.047933	26999.409424
HLA A*0101	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.376395	1.328104	-3.048291	23790.036671
HLA B*1501	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.349202	1.300814	-3.048388	22346.122338
HLA A*2601	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.290338	1.241782	-3.048556	19513.634888
HLA A*6801	1:278-286	9	EGLLNYLAL	1.397948	0.156729	-4.603254	1.554677	-3.048577	40110.154499
HLA A*3301	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.634486	1.585411	-3.049075	43100.870238
HLA B*1502	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.116312	1.067176	-3.049135	13071.090474
HLA B*4501	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.649443	1.600184	-3.049258	44611.092654
HLA B*2705	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.387097	1.337733	-3.049364	24383.554540
HLA A*2602	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.354733	1.305053	-3.049680	22632.517235
HLA A*2402	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.387158	1.337377	-3.049781	24386.984502
HLA B*5301	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.545377	1.495432	-3.049945	35105.658297
HLA A*0301	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.350685	1.300706	-3.049979	22422.534303
HLA B*3801	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.545513	1.495432	-3.050081	35116.675253
HLA A*0206	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.005416	0.955018	-3.050398	10125.491854
HLA A*6801	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.544390	1.493912	-3.050479	35025.983406
HLA A*2403	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.442477	1.391860	-3.050617	27699.805951
HLA A*3002	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.173841	1.123062	-3.050779	14922.490479
HLA A*0212	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.373595	1.322784	-3.050811	23637.118114
HLA B*3501	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.373651	1.322784	-3.050867	23640.187293
HLA B*3501	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.449074	1.398016	-3.051058	28123.805162
HLA A*0250	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-3.162534	0.111406	-3.051128	1453.897150
HLA A*3002	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.235271	1.183813	-3.051458	17189.804811
HLA A*0250	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.274329	1.222401	-3.051928	18807.400982
HLA B*4403	1:112-120	9	STPEEVEAR	0.994604	0.605580	-4.652234	1.600184	-3.052050	44898.729162
HLA A*3001	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.219229	1.167129	-3.052099	16566.419776
HLA A*0202	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.072644	1.020365	-3.052279	11820.729859
HLA B*5101	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.516948	1.464436	-3.052512	32881.252546
HLA B*4403	1:15-23	9	PTGTPHVGL	1.448516	0.151130	-4.652159	1.599646	-3.052513	44890.957126
HLA A*0101	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.352506	1.299885	-3.052621	22516.741810
HLA A*0212	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.775073	0.722436	-3.052636	5957.617534
HLA B*3801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.473022	1.420375	-3.052647	29718.191791
HLA A*2601	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.357743	1.305053	-3.052690	22789.906848
HLA B*1509	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.485212	1.432365	-3.052846	30564.092780
HLA A*3001	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-2.974998	-0.077849	-3.052847	944.056077
HLA B*1502	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.519620	1.466619	-3.053001	33084.129889
HLA A*0211	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.519622	1.466619	-3.053003	33084.308871
HLA A*6901	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.107092	1.054023	-3.053070	12796.536553
HLA A*1101	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.451151	1.398016	-3.053135	28258.624937
HLA A*0250	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.451362	1.398016	-3.053347	28272.387129
HLA A*2602	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.237256	1.183813	-3.053443	17268.565418
HLA B*1801	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.490472	1.437023	-3.053449	30936.558983
HLA A*6901	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.121142	1.067176	-3.053966	13217.288263
HLA A*6801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-3.650447	0.596390	-3.054056	4471.431032
HLA A*3001	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.264275	1.210192	-3.054084	18377.030566
HLA B*5101	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.486680	1.432365	-3.054315	30667.610408
HLA B*0802	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.446320	1.391860	-3.054461	27946.053370
HLA A*6801	1:64-72	9	ALRWLGLDW	1.185951	0.415581	-4.656141	1.601532	-3.054609	45304.489623
HLA A*2601	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.392423	1.337733	-3.054690	24684.441083
HLA B*2705	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.382440	1.327486	-3.054954	24123.500999
HLA B*1501	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.217589	1.162617	-3.054972	16503.981236
HLA B*3901	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.377812	1.322784	-3.055028	23867.770373
HLA B*4501	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.172173	1.117129	-3.055044	14865.282814
HLA B*4402	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.368867	1.313812	-3.055056	23381.230403
HLA A*6901	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.369356	1.313812	-3.055544	23407.555103

HLA B*5701	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.384308	1.328755	-3.055553	24227.476276
HLA A*0250	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.320423	1.264555	-3.055868	20913.336734
HLA A*0202	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.003452	0.947523	-3.055929	10079.801023
HLA A*1101	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.072832	1.016861	-3.055972	11825.846874
HLA A*3001	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.046645	0.990658	-3.055987	11133.837833
HLA A*2501	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.440851	1.384650	-3.056201	27596.301621
HLA A*6802	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.439824	1.383422	-3.056403	27531.137667
HLA A*6801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.219027	1.162401	-3.056626	16558.714034
HLA B*4601	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.379511	1.322784	-3.056727	23961.308384
HLA B*4601	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.395306	1.338560	-3.056747	24848.839804
HLA B*5401	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.257633	1.200757	-3.056876	18098.115004
HLA B*4601	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.394352	1.337377	-3.056976	24794.321334
HLA B*3501	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-3.282080	0.225072	-3.057009	1914.609374
HLA A*1101	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.477731	1.420375	-3.057355	30042.131938
HLA B*5401	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.524084	1.466619	-3.057465	33425.948423
HLA B*0802	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.288329	1.230828	-3.057501	19423.583868
HLA B*1801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.505718	1.448126	-3.057592	32041.867077
HLA A*0216	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.449824	1.391860	-3.057964	28172.381853
HLA B*5101	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.479920	1.421817	-3.058104	30193.987376
HLA B*5401	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.495523	1.437023	-3.058501	31298.490978
HLA A*0101	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.363670	1.305053	-3.058617	23103.102276
HLA A*3001	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.292826	1.234192	-3.058634	19625.750773
HLA A*6901	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.359455	1.300814	-3.058641	22879.963358
HLA A*0250	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.396544	1.337733	-3.058811	24919.785219
HLA B*1509	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.366656	1.307776	-3.058881	23262.505892
HLA B*7301	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.552914	1.493912	-3.059003	35720.231856
HLA B*0803	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.328430	1.269415	-3.059015	21302.490248
HLA B*4501	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.218994	1.159900	-3.059094	16557.459951
HLA B*5101	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.221508	1.162401	-3.059107	16653.582092
HLA A*3002	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.523701	1.464436	-3.059264	33396.486015
HLA B*4501	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.652908	1.593495	-3.059414	44968.494790
HLA A*0201	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.023042	0.963515	-3.059527	10544.887848
HLA A*0203	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.387893	1.328104	-3.059789	24428.313850
HLA A*2402	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.555398	1.495432	-3.059966	35925.074284
HLA B*0802	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.397421	1.337377	-3.060044	24970.121340
HLA A*6901	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.388352	1.328104	-3.060247	24454.097569
HLA A*0202	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-3.656330	0.595974	-3.060355	4532.414779
HLA A*2902	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.329798	1.269415	-3.060383	21369.668021
HLA B*1509	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.360296	1.299885	-3.060412	22924.318845
HLA B*4601	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.368541	1.307776	-3.060765	23363.654920
HLA B*4601	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.388314	1.327486	-3.060828	24451.980957
HLA A*2501	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.329140	1.268289	-3.060851	21337.322416
HLA B*1503	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.051588	0.990658	-3.060930	11261.291694
HLA A*1101	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.228091	1.167129	-3.060961	16907.948610
HLA B*0801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.388565	1.327486	-3.061079	24466.139283
HLA B*3801	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.493484	1.432365	-3.061119	31151.864565
HLA A*2601	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.374943	1.313812	-3.061131	23710.631979
HLA B*1509	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.329513	1.268289	-3.061225	21355.684087
HLA A*3101	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-3.954719	0.893488	-3.061231	9009.878640
HLA A*0216	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.283680	1.222401	-3.061279	19216.740889
HLA B*4001	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.361250	1.299885	-3.061366	22974.725499
HLA B*4801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.399145	1.337733	-3.061412	25069.471283
HLA A*2602	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.589327	1.527790	-3.061537	38844.236331
HLA B*5401	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.555644	1.493912	-3.061733	35945.486902
HLA B*1517	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.976273	0.914377	-3.061897	9468.324127
HLA A*0206	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.528818	1.466619	-3.062199	33792.315476
HLA A*0101	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.363045	1.300814	-3.062231	23069.880116
HLA A*0301	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.362303	1.299885	-3.062418	23030.475272
HLA B*4403	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.599115	1.536595	-3.062519	39729.631989
HLA A*2601	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.370303	1.307776	-3.062527	23458.643582
HLA A*0101	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.376473	1.313812	-3.062661	23794.284198
HLA A*0212	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.327740	1.264555	-3.063184	21268.635410
HLA A*6801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.273457	1.210192	-3.063265	18769.691089
HLA B*4601	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.392106	1.328755	-3.063351	24666.419753
HLA B*4402	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.297605	1.234192	-3.063413	19842.899461

HLA A*6801	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.483360	1.419915	-3.063445	30434.075605
HLA A*2603	1:385-393	9	FFNDDQYVI	1.270301	0.266294	-4.600047	1.536595	-3.063452	39815.052049
HLA B*2705	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.371283	1.307776	-3.063507	23511.624231
HLA A*0202	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.328139	1.264555	-3.063584	21288.204770
HLA A*2602	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.594293	1.530697	-3.063596	39291.028661
HLA A*2403	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.273831	1.210192	-3.063639	18785.843205
HLA B*4403	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.559204	1.495432	-3.063772	36241.306076
HLA B*4001	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.391909	1.328104	-3.063805	24655.213121
HLA B*5401	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-3.908683	0.844865	-3.063819	8103.695841
HLA A*0216	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.447397	1.383422	-3.063975	28015.381976
HLA B*0702	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.401859	1.337733	-3.064126	25226.606330
HLA B*0801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.392280	1.328104	-3.064176	24676.296482
HLA A*2601	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.389552	1.325261	-3.064292	24521.793309
HLA A*0211	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.392473	1.328104	-3.064368	24687.245584
HLA A*8001	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.389745	1.325261	-3.064484	24532.673857
HLA B*5701	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.392000	1.327486	-3.064514	24660.415567
HLA A*1101	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.219844	1.155314	-3.064530	16589.917519
HLA B*7301	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.595473	1.530697	-3.064776	39397.878860
HLA A*0219	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.948817	0.883995	-3.064822	8888.265828
HLA A*0101	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.334459	1.269415	-3.065044	21600.268701
HLA B*1517	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.456940	1.391860	-3.065080	28637.833272
HLA A*8001	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.387929	1.322784	-3.065145	24430.296247
HLA B*0802	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.403128	1.337733	-3.065394	25300.409577
HLA A*2301	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.525190	1.459786	-3.065404	33511.228274
HLA A*2902	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.394202	1.328755	-3.065447	24785.738210
HLA A*0101	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.275760	1.210192	-3.065568	18869.466454
HLA A*2501	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.498012	1.432365	-3.065646	31478.316931
HLA B*4402	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.404319	1.338560	-3.065759	25369.899144
HLA A*2601	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.388544	1.322784	-3.065761	24464.948080
HLA A*3201	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.403602	1.337733	-3.065869	25328.072917
HLA A*0219	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.323546	1.257536	-3.066010	21064.240072
HLA B*1517	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-3.478117	0.412011	-3.066105	3006.882868
HLA A*2601	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.367079	1.300706	-3.066374	23285.169489
HLA B*0803	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.451043	1.384650	-3.066393	28251.593514
HLA A*2902	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.057166	0.990658	-3.066508	11406.854062
HLA A*2403	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.243294	1.176703	-3.066591	17510.334263
HLA A*6802	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.324168	1.257536	-3.066632	21094.459858
HLA A*0101	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.334945	1.268289	-3.066657	21624.471247
HLA B*1502	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.594723	1.527790	-3.066933	39329.946423
HLA B*3501	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.056024	0.989026	-3.066998	11376.902483
HLA A*0216	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.030513	0.963515	-3.066998	10727.865684
HLA B*7301	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.594817	1.527790	-3.067027	39338.458169
HLA A*2301	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.204418	1.137355	-3.067062	16010.965005
HLA B*3501	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.250977	1.183813	-3.067164	17822.854127
HLA A*0201	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.331781	1.264555	-3.067225	21467.463876
HLA A*3002	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.324791	1.257536	-3.067255	21124.722998
HLA A*2403	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.450709	1.383422	-3.067288	28229.898854
HLA A*2602	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.951345	0.883995	-3.067350	8940.155665
HLA B*1801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.454081	1.386690	-3.067391	28449.905821
HLA A*8001	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.309249	1.241782	-3.067467	20382.111807
HLA A*6801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-3.981555	0.914083	-3.067471	9584.175528
HLA B*0802	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.395626	1.328104	-3.067521	24867.128938
HLA A*3201	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.532135	1.464436	-3.067699	34051.435399
HLA B*0801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.368435	1.300706	-3.067729	23357.967847
HLA B*5701	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.405496	1.337733	-3.067763	25438.753832
HLA A*0201	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.381672	1.313812	-3.067860	24080.863436
HLA A*3101	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.337643	1.269415	-3.068228	21759.189069
HLA A*0212	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.382419	1.313812	-3.068607	24122.326478
HLA B*5101	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.391596	1.322784	-3.068813	24637.479699
HLA A*2403	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.394291	1.325261	-3.069031	24790.834081
HLA A*3001	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.250973	1.181912	-3.069061	17822.661289
HLA B*2705	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.394322	1.325261	-3.069061	24792.577646
HLA A*0212	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.300042	1.230828	-3.069213	19954.532059
HLA A*2501	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.452648	1.383422	-3.069226	28356.174954
HLA B*0702	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.253099	1.183813	-3.069286	17910.134098

HLA A*2501	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.467694	1.398016	-3.069678	29355.788440
HLA B*4002	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.517808	1.448126	-3.069682	32946.422562
HLA A*6802	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.725010	0.655319	-3.069691	5308.964149
HLA B*4002	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.587135	1.517234	-3.069900	38648.666877
HLA A*3001	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-3.301482	0.231300	-3.070182	2002.083692
HLA A*0216	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.371031	1.300814	-3.070217	23498.018274
HLA A*0203	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.335279	1.264555	-3.070724	21641.089640
HLA A*0219	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.398849	1.328104	-3.070745	25052.388600
HLA A*2501	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.396215	1.325261	-3.070955	24900.918506
HLA A*3301	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.598753	1.527790	-3.070963	39696.546106
HLA B*3501	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.371797	1.300814	-3.070983	23539.496505
HLA B*3801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.378775	1.307776	-3.070999	23920.769145
HLA B*4501	1:55-63	9	EESYLALLD	1.112493	-0.915046	-3.268589	0.197447	-3.071143	1856.049003
HLA A*0203	1:204-212	9	DALMKITHV	0.852595	-0.031547	-3.892260	0.821048	-3.071212	7802.975296
HLA B*5301	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.602401	1.530697	-3.071705	40031.463880
HLA B*5701	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.397035	1.325261	-3.071775	24947.977128
HLA A*1101	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.409161	1.337377	-3.071784	25654.350817
HLA A*0206	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.340319	1.268289	-3.072030	21893.680159
HLA B*0801	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.329847	1.257536	-3.072311	21372.095917
HLA A*1101	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.455815	1.383422	-3.072393	28563.719067
HLA B*4501	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.636316	1.563919	-3.072397	43282.893674
HLA B*4403	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-3.918988	0.846543	-3.072445	8298.277872
HLA A*0201	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.397825	1.325261	-3.072564	24993.366874
HLA A*0206	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.386606	1.313812	-3.072794	24356.000444
HLA B*3501	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.456574	1.383422	-3.073152	28613.674777
HLA B*4801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.398518	1.325261	-3.073257	25033.286066
HLA A*2601	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.401424	1.328104	-3.073320	25201.371428
HLA B*4001	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.387247	1.313812	-3.073436	24391.998391
HLA B*3501	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.465300	1.391860	-3.073440	29194.404696
HLA A*2402	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.342938	1.269415	-3.073523	22026.142523
HLA A*0202	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.041316	0.967687	-3.073629	10998.064426
HLA A*1101	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.381475	1.307776	-3.073699	24069.922839
HLA B*5701	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.381865	1.307776	-3.074089	24091.548340
HLA B*1517	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.026533	0.952354	-3.074179	10630.000864
HLA A*0211	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-3.781369	0.707098	-3.074271	6044.623271
HLA A*3301	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.382062	1.307776	-3.074286	24102.498766
HLA A*2902	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.388121	1.313812	-3.074310	24441.136197
HLA B*1503	1:304-312	9	VAAFDVADV	0.706341	0.208036	-3.988782	0.914377	-3.074405	9744.998459
HLA A*0206	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.538848	1.464436	-3.074412	34581.824501
HLA B*0801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.413165	1.338560	-3.074605	25891.937604
HLA B*4601	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.402803	1.328104	-3.074699	25281.528233
HLA B*0803	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.413324	1.338560	-3.074765	25901.464287
HLA A*2902	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.258721	1.183813	-3.074908	18143.503597
HLA B*1517	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.458446	1.383422	-3.075025	28737.314189
HLA B*0801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.388890	1.313812	-3.075078	24484.411659
HLA B*1509	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.402669	1.327486	-3.075183	25273.733530
HLA B*4001	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.309477	1.234192	-3.075285	20392.810315
HLA B*1801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.459990	1.384650	-3.075340	28839.636879
HLA B*5401	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.523499	1.448126	-3.075373	33380.951898
HLA B*3901	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.309573	1.234192	-3.075381	20397.334054
HLA A*0202	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.495878	1.420375	-3.075503	31324.068950
HLA B*5101	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.403064	1.327486	-3.075578	25296.714292
HLA B*0702	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.403196	1.327486	-3.075709	25304.379188
HLA A*1101	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.404580	1.328755	-3.075824	25385.138285
HLA B*4801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.383613	1.307776	-3.075837	24188.711205
HLA A*3101	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-3.187593	0.111406	-3.076187	1540.257358
HLA B*1801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.413952	1.337377	-3.076575	25938.904442
HLA A*0211	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.509019	1.432365	-3.076653	32286.341856
HLA B*5701	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.318600	1.241782	-3.076818	20825.725029
HLA A*0219	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.468725	1.391860	-3.076865	29425.589569
HLA A*8001	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.346437	1.269415	-3.077022	22204.286799
HLA A*2603	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.405891	1.328755	-3.077135	25461.884642
HLA A*2301	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.542048	1.464436	-3.077612	34837.573745
HLA A*3001	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.178334	1.100571	-3.077762	15077.645419
HLA B*5301	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.078194	1.000328	-3.077866	11972.746191

HLA A*3201	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.498305	1.420375	-3.077930	31499.610906
HLA B*1801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.383028	1.305053	-3.077975	24156.149438
HLA A*2501	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.415744	1.337733	-3.078011	26046.194918
HLA A*6901	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.309061	1.230828	-3.078233	20373.292518
HLA A*6802	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-3.958882	0.880484	-3.078398	9096.665571
HLA B*3501	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.416209	1.337733	-3.078476	26074.109457
HLA A*0219	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.042063	0.963515	-3.078548	11017.001173
HLA A*0206	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.309381	1.230828	-3.078552	20388.287580
HLA A*2403	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.336231	1.257536	-3.078694	21688.557360
HLA B*4001	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.403980	1.325261	-3.078720	25350.143079
HLA A*3201	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.609751	1.530697	-3.079054	40714.645790
HLA B*5701	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.379962	1.300706	-3.079256	23986.209894
HLA B*4601	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.380121	1.300814	-3.079307	23995.035384
HLA A*2902	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.462788	1.383422	-3.079366	29026.055711
HLA B*0702	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.313452	1.234017	-3.079436	20580.333506
HLA B*4403	1:232-240	9	LIRIGVAER	0.803790	0.789705	-4.673128	1.593495	-3.079633	47111.617881
HLA A*2603	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.610380	1.530697	-3.079683	40773.718744
HLA B*0803	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.463340	1.383422	-3.079919	29062.980698
HLA B*5801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.047627	0.967687	-3.079940	11159.043644
HLA A*0250	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.575420	1.495432	-3.079988	37620.103497
HLA B*1503	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.080332	1.000328	-3.080004	12031.833333
HLA B*4601	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.380056	1.299885	-3.080171	23991.400966
HLA B*5301	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.043901	0.963515	-3.080385	11063.707690
HLA B*0702	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.032905	0.952354	-3.080551	10787.109894
HLA B*5701	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.408914	1.328104	-3.080810	25639.782300
HLA A*6801	1:210-218	9	THVLRGEDL	1.116170	0.447749	-4.644927	1.563919	-3.081008	44149.638339
HLA B*0702	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.419616	1.338560	-3.081057	26279.447937
HLA B*4001	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.382060	1.300814	-3.081245	24102.368375
HLA A*0202	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-3.719169	0.637857	-3.081312	5238.041957
HLA A*2603	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.323102	1.241782	-3.081320	21042.713546
HLA A*0219	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.350805	1.269415	-3.081389	22428.721632
HLA A*0101	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.382165	1.300706	-3.081460	24108.236690
HLA B*4801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.409575	1.328104	-3.081470	25678.788996
HLA B*0803	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.408978	1.327486	-3.081491	25643.527700
HLA A*0219	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.464919	1.383422	-3.081497	29168.829868
HLA B*4402	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.404523	1.322784	-3.081740	25381.842561
HLA B*4001	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-3.837498	0.755651	-3.081847	6878.574344
HLA A*1101	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.409382	1.327486	-3.081895	25667.400131
HLA A*0101	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.323720	1.241782	-3.081938	21072.674445
HLA B*4001	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.405235	1.322784	-3.082451	25423.482504
HLA B*1502	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.340760	1.257536	-3.083224	21915.958655
HLA A*0202	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.421132	1.337733	-3.083398	26371.307050
HLA A*0250	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.550027	1.466619	-3.083408	35483.524606
HLA B*2705	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.383669	1.299885	-3.083784	24191.852007
HLA B*4601	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.409086	1.325261	-3.083825	25649.910011
HLA A*2902	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.409126	1.325261	-3.083865	25652.269094
HLA B*4002	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-3.927385	0.843357	-3.084028	8460.285768
HLA B*7301	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.601356	1.517234	-3.084122	39935.208017
HLA A*0101	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.341775	1.257536	-3.084239	21967.237729
HLA B*5301	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.514164	1.429823	-3.084342	32671.134311
HLA A*2603	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-3.968388	0.883995	-3.084394	9297.972235
HLA B*5801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.348953	1.264555	-3.084398	22333.311667
HLA B*3801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.409727	1.325261	-3.084467	25687.820345
HLA A*2603	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.189221	1.104589	-3.084632	15460.411152
HLA B*1801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.483229	1.398016	-3.085213	30424.856883
HLA B*1501	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.410827	1.325261	-3.085566	25752.939892
HLA A*3001	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.286457	1.200757	-3.085699	19340.015847
HLA A*0301	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.355163	1.269415	-3.085748	22654.934742
HLA B*4501	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.313384	1.227496	-3.085888	20577.104977
HLA B*4801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.413458	1.327486	-3.085972	25909.452590
HLA A*8001	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.386803	1.300706	-3.086097	24367.071073
HLA A*6801	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.613949	1.527790	-3.086159	41110.162226
HLA B*0803	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.009664	0.923460	-3.086204	10225.016029
HLA A*6801	1:292-300	9	ADDHDLFGL	1.312172	0.273239	-4.671817	1.585411	-3.086406	46969.615626
HLA A*0203	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.287303	1.200757	-3.086545	19377.718392

HLA B*4402	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.424076	1.337377	-3.086699	26550.674600
HLA B*1501	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.296938	1.210192	-3.086746	19812.436070
HLA B*0702	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.328534	1.241782	-3.086752	21307.561592
HLA B*5101	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.412058	1.325261	-3.086797	25826.047433
HLA A*0203	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-3.752081	0.665274	-3.086806	5650.417766
HLA B*1801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.425476	1.338560	-3.086916	26636.419938
HLA A*2501	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.424715	1.337377	-3.087338	26589.772407
HLA A*0201	1:34-42 9		ARHTGGTFV	0.979623	0.277913	-4.345022	1.257536	-3.087486	22132.090542
HLA A*3001	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-3.931233	0.843615	-3.087618	8535.588884
HLA A*2301	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.401624	1.313812	-3.087812	25212.962706
HLA B*7301	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.583300	1.495432	-3.087868	38308.942064
HLA B*0803	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.356182	1.268289	-3.087894	22708.188572
HLA A*3001	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-3.428895	0.340987	-3.087908	2684.694047
HLA A*0216	1:26-34 9		TALFNWAYA	1.066638	-0.152555	-4.002014	0.914083	-3.087931	10046.483477
HLA B*1501	1:85-93 9		YRQSQRAEI	0.995777	0.235051	-4.318786	1.230828	-3.087957	20834.627455
HLA A*0202	1:43-51 9		FRIEDTDAQ	1.010766	0.051821	-4.150666	1.062587	-3.088079	14147.053321
HLA A*2602	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.547919	1.459786	-3.088133	35311.751866
HLA B*3901	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.480099	1.391860	-3.088239	30206.404233
HLA B*2705	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-3.334262	0.245974	-3.088288	2159.047728
HLA A*0206	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-3.976137	0.887847	-3.088290	9465.353684
HLA A*2301	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.520677	1.432365	-3.088312	33164.769670
HLA A*6801	1:227-235	9	ALHQALIRI	1.220562	0.336437	-4.645486	1.556999	-3.088488	44206.519977
HLA B*0702	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.251210	1.162617	-3.088593	17832.402230
HLA B*1502	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.426601	1.337733	-3.088868	26705.533386
HLA A*0212	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.414227	1.325261	-3.088966	25955.327851
HLA A*3201	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.251583	1.162617	-3.088966	17847.747769
HLA A*2403	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.417185	1.328104	-3.089080	26132.714307
HLA A*3002	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.330968	1.241782	-3.089186	21427.318197
HLA A*6802	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.427001	1.337733	-3.089267	26730.105259
HLA A*2602	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.584811	1.495432	-3.089379	38442.434013
HLA B*1801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-3.977279	0.887847	-3.089432	9490.272794
HLA A*2402	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.556147	1.466619	-3.089528	35987.125675
HLA B*5401	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.803675	0.714055	-3.089621	6363.195249
HLA A*0216	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.090087	1.000328	-3.089759	12305.148781
HLA B*2705	1:37-45 9		TGGTFVFRI	1.297464	0.025320	-4.412756	1.322784	-3.089972	25867.576455
HLA B*1503	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.173292	1.083182	-3.090110	14903.611840
HLA B*4402	1:34-42 9		ARHTGGTFV	0.979623	0.277913	-4.348081	1.257536	-3.090545	22288.532125
HLA B*4403	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.618491	1.527790	-3.090701	41542.319837
HLA A*6802	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.355325	1.264555	-3.090770	22663.393007
HLA B*1509	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.428638	1.337377	-3.091262	26831.086537
HLA B*7301	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.145619	1.054023	-3.091596	13983.609792
HLA A*0201	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.359930	1.268289	-3.091641	22904.980194
HLA B*5801	1:34-42 9		ARHTGGTFV	0.979623	0.277913	-4.349505	1.257536	-3.091969	22361.722597
HLA B*4001	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.259153	1.167129	-3.092024	18161.572987
HLA A*0211	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.513950	1.421817	-3.092134	32655.054273
HLA A*2501	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.430908	1.338560	-3.092348	26971.671558
HLA B*3801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.477014	1.384650	-3.092364	29992.602807
HLA A*0202	1:26-34 9		TALFNWAYA	1.066638	-0.152555	-4.006478	0.914083	-3.092395	10150.281711
HLA A*0201	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.315316	1.222401	-3.092915	20668.813659
HLA B*4402	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.421038	1.328104	-3.092933	26365.601033
HLA B*2705	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.393669	1.300706	-3.092963	24755.318894
HLA B*3501	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-3.339356	0.246392	-3.092964	2184.519503
HLA B*5301	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.552900	1.459786	-3.093114	35719.072419
HLA B*4402	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-3.674909	0.581735	-3.093174	4730.525353
HLA B*0801	1:91-99 9		AEIYRDVLA	1.321993	-0.140081	-4.275527	1.181912	-3.093615	18859.363069
HLA B*5701	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.361922	1.268289	-3.093633	23010.300158
HLA B*1509	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-3.328858	0.235091	-3.093768	2132.349690
HLA B*4801	1:37-45 9		TGGTFVFRI	1.297464	0.025320	-4.416856	1.322784	-3.094072	26112.929288
HLA A*0206	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-3.759420	0.665274	-3.094146	5746.724136
HLA A*0206	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-3.940721	0.846543	-3.094178	8724.101498
HLA A*2501	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.486055	1.391860	-3.094195	30623.510519
HLA A*0201	1:78-86 9		VGGPYGPYR	0.889086	0.411728	-4.395066	1.300814	-3.094252	24835.131780
HLA A*0211	1:13-21 9		PSPTGTPHV	1.188362	-0.065300	-4.217490	1.123062	-3.094428	16500.231705
HLA B*4601	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.408287	1.313812	-3.094475	25602.773897
HLA B*4402	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.419778	1.325261	-3.094518	26289.259422

HLA B*5101	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.481217	1.386690	-3.094527	30284.289201
HLA B*5401	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.516805	1.421817	-3.094988	32870.403416
HLA B*4501	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.590494	1.495432	-3.095062	38948.817941
HLA A*3101	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.352694	1.257536	-3.095157	22526.488965
HLA B*1501	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.353274	1.257536	-3.095738	22556.609940
HLA A*3002	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.326805	1.230828	-3.095976	21222.890413
HLA A*3101	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.364683	1.268289	-3.096394	23157.033757
HLA A*0216	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.051767	0.955018	-3.096748	11265.922744
HLA A*2902	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.401932	1.305053	-3.096879	25230.837352
HLA A*0250	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.419788	1.322784	-3.097004	26289.828316
HLA A*2402	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.556885	1.459786	-3.097099	36048.309144
HLA B*3901	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.252504	1.155314	-3.097190	17885.637230
HLA A*6801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.331426	1.234017	-3.097409	21449.934410
HLA A*0301	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.365759	1.268289	-3.097470	23214.481757
HLA A*0211	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.319902	1.222401	-3.097501	20888.234990
HLA A*3002	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.495601	1.398016	-3.097585	31304.079082
HLA A*6802	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.423159	1.325261	-3.097899	26494.715533
HLA B*4402	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-3.944442	0.846543	-3.097900	8799.181862
HLA A*3101	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.160036	1.062125	-3.097910	14455.587159
HLA B*5701	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.398774	1.300814	-3.097960	25048.051995
HLA B*4501	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.615455	1.517234	-3.098221	41252.969001
HLA B*0801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.282183	1.183813	-3.098370	19150.632064
HLA A*8001	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.398436	1.299885	-3.098551	25028.546559
HLA A*6801	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.528090	1.429220	-3.098870	33735.691040
HLA B*3901	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.482362	1.383422	-3.098940	30364.181872
HLA B*5701	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.399098	1.299885	-3.099214	25066.758969
HLA A*6901	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.333872	1.234192	-3.099680	21571.074682
HLA B*4801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.399615	1.299885	-3.099730	25096.610575
HLA B*4801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.400748	1.300814	-3.099933	25162.137053
HLA A*2501	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.167178	1.067176	-3.100002	14695.290340
HLA A*2601	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.400823	1.300814	-3.100008	25166.493409
HLA B*5401	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.564718	1.464436	-3.100282	36704.396002
HLA A*8001	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.405421	1.305053	-3.100368	25434.350346
HLA B*1502	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.595851	1.495432	-3.100419	39432.209052
HLA B*1517	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.429176	1.328755	-3.100421	26864.347220
HLA A*3001	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.117425	1.016861	-3.100565	13104.651519
HLA B*0801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.263256	1.162617	-3.100638	18333.933898
HLA B*3501	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.438027	1.337377	-3.100650	27417.433707
HLA A*0211	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.266973	0.166266	-3.100707	1849.153622
HLA B*5401	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.529967	1.429220	-3.100747	33881.829226
HLA A*2602	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.529974	1.429220	-3.100754	33882.379121
HLA B*0702	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.428944	1.328104	-3.100840	26849.963091
HLA B*4601	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.284930	1.183813	-3.101117	19272.127507
HLA A*0206	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.533693	1.432365	-3.101328	34173.788901
HLA A*0301	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.218533	1.117129	-3.101404	16539.912747
HLA A*0202	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.332387	1.230828	-3.101559	21497.448039
HLA B*0802	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.424506	1.322784	-3.101722	26576.973041
HLA A*3002	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.597157	1.495432	-3.101725	39550.995689
HLA B*4001	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.335883	1.234017	-3.101866	21671.199072
HLA B*1501	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.069468	0.967578	-3.101890	11734.586448
HLA A*3101	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.269071	1.167129	-3.101941	18581.066455
HLA B*1502	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.550391	1.448126	-3.102265	35513.291184
HLA B*4402	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.410714	1.307776	-3.102938	25746.253373
HLA B*5101	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.403670	1.300706	-3.102964	25332.046868
HLA B*1509	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.486431	1.383422	-3.103009	30650.029162
HLA A*0202	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.569708	1.466619	-3.103089	37128.584123
HLA A*0219	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.215949	1.112802	-3.103147	16441.778026
HLA B*3501	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-3.983754	0.880484	-3.103270	9632.829578
HLA B*0702	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.417288	1.313812	-3.103476	26138.935551
HLA A*2603	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.186745	1.083182	-3.103563	15372.506385
HLA B*4001	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.241055	1.137355	-3.103700	17420.289874
HLA B*4002	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-3.859358	0.755651	-3.103707	7233.659200
HLA A*0301	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.368289	1.264555	-3.103734	23350.134592
HLA B*4801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.334649	1.230828	-3.103821	21609.736035
HLA A*2902	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.368494	1.264555	-3.103938	23361.127162

HLA A*2602	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.552094	1.448126	-3.103969	35652.853852
HLA A*3002	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.404006	1.299885	-3.104122	25351.651680
HLA A*8001	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.326652	1.222401	-3.104251	21215.428848
HLA A*2902	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.372826	1.268289	-3.104537	23595.340218
HLA B*5701	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.418399	1.313812	-3.104587	26205.907537
HLA A*2603	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-3.831033	0.726109	-3.104924	6776.924585
HLA B*4801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.405632	1.300706	-3.104926	25446.737093
HLA A*3001	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.289403	1.184382	-3.105021	19471.664581
HLA A*0219	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.332657	1.227496	-3.105161	21510.826564
HLA A*2402	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.569725	1.464436	-3.105288	37129.990180
HLA B*1801	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.430666	1.325261	-3.105405	26956.646628
HLA B*0802	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.373832	1.268289	-3.105543	23650.036936
HLA B*1501	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.327972	1.222401	-3.105571	21280.029495
HLA A*2403	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.419433	1.313812	-3.105621	26268.361102
HLA A*0219	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.741701	0.635887	-3.105814	5516.968878
HLA B*0801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.283139	1.176703	-3.106436	19192.844858
HLA B*4403	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.211607	1.105060	-3.106547	16278.220702
HLA A*6901	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.364093	1.257536	-3.106557	23125.610573
HLA B*5101	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.490016	1.383422	-3.106595	30904.107525
HLA A*6801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.021346	0.914477	-3.106869	10503.780483
HLA A*2601	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.364488	1.257536	-3.106952	23146.638101
HLA B*0802	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.406868	1.299885	-3.106983	25519.251496
HLA B*4001	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.375293	1.268289	-3.107004	23729.752196
HLA B*3501	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.269637	1.162617	-3.107020	18605.307938
HLA A*2301	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.435292	1.328104	-3.107188	27245.325545
HLA B*1503	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.127867	1.020365	-3.107502	13423.525370
HLA B*5301	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.527488	1.419915	-3.107573	33689.001753
HLA B*1501	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.220507	1.112802	-3.107705	16615.246226
HLA A*1101	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.445649	1.337733	-3.107915	27902.847878
HLA B*4403	1:419-427	9	SVTDWTAPL	1.029427	0.487807	-4.625412	1.517234	-3.108178	42209.706066
HLA A*2902	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.445919	1.337733	-3.108185	27920.212681
HLA B*1517	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.445935	1.337733	-3.108202	27921.270017
HLA A*8001	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.256381	1.148177	-3.108204	18046.004781
HLA A*2301	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.530026	1.421817	-3.108209	33886.411959
HLA B*0802	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.422067	1.313812	-3.108255	26428.149229
HLA A*0301	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.365799	1.257536	-3.108263	23216.616848
HLA B*1502	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.545403	1.437023	-3.108380	35107.747455
HLA A*0216	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.422306	1.313812	-3.108495	26442.736536
HLA B*5801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.342936	1.234017	-3.108919	22026.023364
HLA B*0801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.410075	1.300814	-3.109261	25708.395883
HLA A*2602	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.507323	1.398016	-3.109307	32160.479309
HLA B*4002	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.603236	1.493912	-3.109324	40108.418605
HLA B*0802	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.436915	1.327486	-3.109429	27347.365537
HLA A*6802	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-3.878088	0.768573	-3.109515	7552.454863
HLA A*0211	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.219243	1.109528	-3.109715	16566.957520
HLA A*0206	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.337250	1.227496	-3.109754	21739.539575
HLA A*2603	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.574407	1.464436	-3.109971	37532.488308
HLA B*0702	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.367916	1.257536	-3.110380	23330.058087
HLA A*2501	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.411179	1.300706	-3.110473	25773.846456
HLA B*0803	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.352405	1.241782	-3.110623	22511.504457
HLA B*5301	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.559032	1.448126	-3.110907	36226.996416
HLA B*5701	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.074430	0.963515	-3.110915	11869.431025
HLA A*0212	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.379222	1.268289	-3.110933	23945.369441
HLA B*5101	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.439890	1.328755	-3.111135	27535.308314
HLA A*0203	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-3.954766	0.843615	-3.111151	9010.853542
HLA A*0206	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.503256	1.391860	-3.111396	31860.717671
HLA A*0206	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.494873	1.383422	-3.111451	31251.624084
HLA B*3501	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.013851	0.902312	-3.111539	10324.066179
HLA A*0202	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.544108	1.432365	-3.111743	35003.252383
HLA B*1502	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.417015	1.305053	-3.111963	26122.537282
HLA A*0203	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.235048	1.123062	-3.111986	17180.972562
HLA A*6802	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.425854	1.313812	-3.112042	26659.630158
HLA A*0203	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.339605	1.227496	-3.112108	21857.703267
HLA A*6802	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.353974	1.241782	-3.112192	22593.003838
HLA B*2705	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.296005	1.183813	-3.112192	19769.930048

HLA A*3001	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.067386	0.955018	-3.112368	11678.475259
HLA A*0211	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.067424	0.955018	-3.112405	11679.486171
HLA B*0702	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.179818	1.067176	-3.112642	15129.284870
HLA A*0250	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-3.291628	0.178924	-3.112704	1957.169720
HLA A*6802	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.440928	1.328104	-3.112824	27601.228727
HLA B*3801	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.504693	1.391860	-3.112834	31966.378614
HLA A*0101	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.027313	0.914477	-3.112836	10649.110386
HLA A*0206	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-3.040328	-0.072551	-3.112878	1097.305541
HLA B*4002	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-3.615801	0.502859	-3.112942	4128.583102
HLA A*0211	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.119860	1.006851	-3.113008	13178.304647
HLA B*4002	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.450399	1.337377	-3.113022	28209.746928
HLA A*2902	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.313875	1.200757	-3.113118	20600.383985
HLA A*0301	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.268511	1.155314	-3.113197	18557.157731
HLA A*0203	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.438772	1.325261	-3.113511	27464.493160
HLA A*3001	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.167855	1.054023	-3.113832	14718.204155
HLA B*5101	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.505824	1.391860	-3.113964	32049.668459
HLA A*0101	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.348098	1.234017	-3.114081	22289.376190
HLA B*4601	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.315015	1.200757	-3.114257	20654.506167
HLA A*3101	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.206217	1.091927	-3.114290	16077.451709
HLA A*3001	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.053148	0.938712	-3.114436	11301.816871
HLA A*0201	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.345469	1.230828	-3.114640	22154.851348
HLA B*5801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.345546	1.230828	-3.114718	22158.806925
HLA B*0702	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.415432	1.300706	-3.114726	26027.461024
HLA B*4002	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.645533	1.530697	-3.114836	44211.303283
HLA A*0219	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.428706	1.313812	-3.114895	26835.296311
HLA B*0803	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.440162	1.325261	-3.114902	27552.593441
HLA B*0803	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.428749	1.313812	-3.114937	26837.909605
HLA B*4601	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.346005	1.230828	-3.115176	22182.195214
HLA B*5401	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.545095	1.429823	-3.115273	35082.875567
HLA B*5301	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.346110	1.230828	-3.115282	22187.596016
HLA A*2602	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.263664	1.148177	-3.115487	18351.200135
HLA B*4001	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.380063	1.264555	-3.115507	23991.790341
HLA A*2602	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-3.964540	0.848752	-3.115788	9215.943181
HLA B*1509	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.349919	1.234017	-3.115902	22383.024238
HLA A*2402	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.548478	1.432365	-3.116113	35357.246922
HLA A*2402	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.423946	1.307776	-3.116171	26542.775783
HLA A*0101	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.350466	1.234192	-3.116274	22411.255922
HLA B*4801	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.384656	1.268289	-3.116367	24246.882102
HLA B*7301	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.553532	1.437023	-3.116510	35771.090804
HLA A*3201	1:335-343	9	LDVGDFTVR	0.933685	0.561747	-4.612013	1.495432	-3.116581	40927.311310
HLA B*4402	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.416473	1.299885	-3.116588	26089.912745
HLA A*0216	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.384997	1.268289	-3.116708	24265.909640
HLA B*5801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.351039	1.234192	-3.116847	22440.858604
HLA B*1801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.351082	1.234017	-3.117065	22443.043957
HLA B*1801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.444582	1.327486	-3.117095	27834.400073
HLA B*5101	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.454546	1.337377	-3.117169	28480.396494
HLA B*1509	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.358967	1.241782	-3.117185	22854.232001
HLA B*1501	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.279747	1.162401	-3.117346	19043.496763
HLA B*3501	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.445486	1.328104	-3.117382	27892.434182
HLA A*0201	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.179598	1.062125	-3.117472	15121.593137
HLA B*3901	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.072339	0.954860	-3.117479	11812.419433
HLA A*0219	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.348342	1.230828	-3.117514	22301.920357
HLA A*2403	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.417403	1.299885	-3.117518	26145.865498
HLA B*1517	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.445052	1.327486	-3.117565	27864.532576
HLA B*1509	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.456534	1.338560	-3.117974	28611.043353
HLA A*2402	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.502729	1.384650	-3.118079	31822.131754
HLA A*1101	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.419283	1.300706	-3.118577	26259.267705
HLA A*0211	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.346207	1.227496	-3.118710	22192.517892
HLA B*5401	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.517120	1.398016	-3.119104	32894.240637
HLA A*2602	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.223937	1.104589	-3.119348	16747.000361
HLA A*6901	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.119704	1.000328	-3.119376	13173.600138
HLA A*3201	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.268157	1.148177	-3.119979	18542.004704
HLA A*8001	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.434933	1.313812	-3.121121	27222.783565
HLA A*2301	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.513044	1.391860	-3.121184	32586.934576
HLA A*0216	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.009081	0.887847	-3.121234	10211.306809

HLA A*0212	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.331452	1.210192	-3.121260	21451.210908
HLA B*2705	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.422461	1.300814	-3.121647	26452.179672
HLA A*0301	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.355668	1.234017	-3.121651	22681.300619
HLA B*4601	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.379294	1.257536	-3.121758	23949.385573
HLA B*5801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.349444	1.227496	-3.121948	22358.577482
HLA B*1509	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.391838	1.269415	-3.122423	24651.211987
HLA B*3801	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.544374	1.421817	-3.122557	35024.657025
HLA B*0802	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.427616	1.305053	-3.122563	26768.019131
HLA A*0212	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.306559	1.183813	-3.122746	20256.248643
HLA B*4801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.392200	1.269415	-3.122785	24671.758034
HLA A*8001	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.423866	1.300814	-3.123052	26537.894054
HLA B*0802	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.461719	1.338560	-3.123159	28954.695950
HLA A*0202	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.003696	0.880484	-3.123212	10085.473802
HLA B*0702	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.446093	1.322784	-3.123309	27931.392267
HLA B*1801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.345774	1.222401	-3.123373	22170.438016
HLA B*0801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.228119	1.104589	-3.123530	16909.046287
HLA A*3002	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.590335	1.466619	-3.123716	38934.492378
HLA B*4002	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.553222	1.429220	-3.124002	35745.555595
HLA B*4601	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.392506	1.268289	-3.124217	24689.115429
HLA A*2601	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.388887	1.264555	-3.124332	24484.279201
HLA B*4001	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.366358	1.241782	-3.124576	23246.528739
HLA A*3301	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.234526	1.109528	-3.124998	17160.350679
HLA A*0216	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.737683	0.612666	-3.125017	5466.167236
HLA B*3801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.462668	1.337377	-3.125291	29018.048401
HLA B*1503	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.013301	0.887847	-3.125454	10311.005067
HLA A*6802	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.839585	0.714055	-3.125530	6911.698388
HLA A*0212	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.426503	1.300814	-3.125688	26699.466168
HLA B*0702	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.425727	1.299885	-3.125843	26651.843110
HLA A*2603	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.425788	1.299885	-3.125904	26655.592145
HLA B*4402	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.394345	1.268289	-3.126056	24793.918933
HLA B*3501	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.356908	1.230828	-3.126080	22746.180591
HLA B*0702	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.394425	1.268289	-3.126136	24798.479853
HLA A*2603	1:365-373	9	AAELVQTRI	1.206674	0.321116	-4.653984	1.527790	-3.126195	45080.052692
HLA A*0206	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.390924	1.264555	-3.126369	24599.389369
HLA B*3901	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.395901	1.269415	-3.126485	24882.873745
HLA B*0803	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.434350	1.307776	-3.126574	27186.284539
HLA B*1509	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.047298	0.920689	-3.126609	11150.595157
HLA A*2402	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.454783	1.328104	-3.126679	28495.962401
HLA B*5401	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.559232	1.432365	-3.126867	36243.658889
HLA A*2603	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.556309	1.429220	-3.127089	36000.561542
HLA A*2403	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.391711	1.264555	-3.127156	24644.011581
HLA B*1501	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.050710	0.923460	-3.127249	11238.529774
HLA A*3201	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.082432	0.954860	-3.127572	12090.165531
HLA A*0101	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.358405	1.230828	-3.127577	22824.701408
HLA B*5301	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.594293	1.466619	-3.127674	39291.028661
HLA A*3301	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.557726	1.429823	-3.127903	36118.193009
HLA A*0216	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.453244	1.325261	-3.127984	28395.166292
HLA A*2602	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.514714	1.386690	-3.128024	32712.519349
HLA B*5801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.350450	1.222401	-3.128049	22410.407242
HLA B*3901	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.453409	1.325261	-3.128148	28405.921358
HLA B*1801	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.451001	1.322784	-3.128217	28248.842564
HLA A*3301	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.565334	1.437023	-3.128311	36756.457368
HLA B*4403	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.456174	1.327486	-3.128688	28587.371417
HLA A*0212	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.182854	1.054023	-3.128831	15235.402595
HLA A*2402	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.359674	1.230828	-3.128845	22891.477615
HLA A*0216	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.356394	1.227496	-3.128898	22719.247654
HLA B*5801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.092573	0.963515	-3.129057	12375.781248
HLA A*0219	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.454349	1.325261	-3.129088	28467.457068
HLA B*4601	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.393704	1.264555	-3.129148	24757.327828
HLA A*2403	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.371123	1.241782	-3.129341	23502.976543
HLA B*0801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.356873	1.227496	-3.129377	22744.334852
HLA B*5401	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.512910	1.383422	-3.129488	32576.887498
HLA B*5301	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.063679	0.934152	-3.129526	11579.202730
HLA B*3901	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.183695	1.054023	-3.129672	15264.938206
HLA A*8001	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.387607	1.257536	-3.130071	24412.196324

HLA A*3002	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.278252	1.148177	-3.130075	18978.086596
HLA B*7301	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.596772	1.466619	-3.130153	39515.920744
HLA B*5301	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.551998	1.421817	-3.130181	35644.946731
HLA B*1502	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.455617	1.325261	-3.130357	28550.741786
HLA B*1517	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.431197	1.300814	-3.130383	26989.624922
HLA B*4801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.372248	1.241782	-3.130466	23563.959653
HLA B*4002	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.388051	1.257536	-3.130515	24437.169804
HLA B*4403	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.528762	1.398016	-3.130746	33787.928257
HLA B*4501	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.661500	1.530697	-3.130804	45867.008675
HLA A*0211	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.431686	1.300814	-3.130871	27020.012278
HLA A*2902	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.365172	1.234017	-3.131155	23183.106036
HLA A*3301	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.590943	1.459786	-3.131157	38989.084119
HLA A*2403	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.315231	1.183813	-3.131418	20664.788676
HLA A*2603	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.194037	1.062587	-3.131451	15632.825623
HLA B*0802	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.354066	1.222401	-3.131665	22597.771141
HLA A*3101	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-3.907377	0.775701	-3.131676	8079.357369
HLA B*3901	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.445496	1.313812	-3.131684	27893.037768
HLA B*4403	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.625732	1.493912	-3.131820	42240.773070
HLA A*2602	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.400195	1.268289	-3.131906	25130.168151
HLA B*2705	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.400264	1.268289	-3.131975	25134.111051
HLA A*2301	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.516631	1.384650	-3.131981	32857.246982
HLA B*4001	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.363055	1.230828	-3.132226	23070.379344
HLA A*0250	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.552700	1.420375	-3.132325	35702.651116
HLA B*1509	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.460478	1.328104	-3.132374	28872.107145
HLA B*0803	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.433304	1.300706	-3.132598	27120.914976
HLA B*3501	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.192477	1.059725	-3.132752	15576.770652
HLA A*0301	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.367030	1.234192	-3.132838	23282.524266
HLA B*7301	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.562167	1.429220	-3.132947	36489.384780
HLA B*4501	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.552945	1.419915	-3.133030	35722.744096
HLA B*0702	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.281405	1.148177	-3.133228	19116.370224
HLA B*1503	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.013771	0.880484	-3.133287	10322.167383
HLA B*4402	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.434566	1.300814	-3.133752	27199.818787
HLA B*1501	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.334906	1.200757	-3.134148	21622.482577
HLA B*1503	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.234803	1.100571	-3.134232	17171.308776
HLA B*4403	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.582363	1.448126	-3.134237	38226.339641
HLA A*1101	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.127528	0.993286	-3.134242	13413.072194
HLA B*0803	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.440087	1.305053	-3.135034	27547.824047
HLA B*4402	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.376860	1.241782	-3.135079	23815.533213
HLA A*6901	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.194860	1.059725	-3.135135	15662.453813
HLA B*1517	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.135629	1.000328	-3.135301	13665.618309
HLA A*2402	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.557235	1.421817	-3.135418	36077.378445
HLA A*0101	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.245515	1.109528	-3.135986	17600.082353
HLA B*4002	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.436913	1.300706	-3.136207	27347.217591
HLA A*3002	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.298608	1.162401	-3.136208	19888.789992
HLA A*0301	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.367340	1.230828	-3.136512	23299.156379
HLA A*2603	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.473922	1.337377	-3.136546	29779.831350
HLA B*0803	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.394091	1.257536	-3.136555	24779.436870
HLA A*0301	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.364269	1.227496	-3.136773	23134.995501
HLA A*2501	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-3.733402	0.596390	-3.137012	5412.552888
HLA A*2403	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.437869	1.300814	-3.137055	27407.497714
HLA B*1502	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.557585	1.420375	-3.137210	36106.471186
HLA A*3201	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.464802	1.327486	-3.137315	29160.940929
HLA B*1509	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.168372	1.031013	-3.137359	14735.731831
HLA A*0219	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.104945	0.967578	-3.137367	12733.418480
HLA A*2603	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.604544	1.466619	-3.137925	40229.459909
HLA B*0801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.402608	1.264555	-3.138053	25270.178850
HLA B*1517	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.438955	1.300706	-3.138249	27476.084835
HLA A*0301	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.360943	1.222401	-3.138542	22958.449183
HLA A*2902	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.276051	1.137355	-3.138696	18882.128834
HLA A*2403	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.407051	1.268289	-3.138762	25530.022161
HLA B*2705	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.372960	1.234017	-3.138943	23602.617286
HLA B*0803	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.361506	1.222401	-3.139106	22988.277182
HLA B*0803	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.476977	1.337733	-3.139243	29990.006813
HLA A*8001	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.407585	1.268289	-3.139296	25561.393431
HLA A*0203	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.440355	1.300814	-3.139541	27564.818784

HLA B*0801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.276920	1.137355	-3.139565	18919.962269
HLA A*2301	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.523062	1.383422	-3.139640	33347.379563
HLA B*4402	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.409058	1.269415	-3.139642	25648.244907
HLA A*2402	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.453529	1.313812	-3.139717	28413.759756
HLA B*4601	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.130409	0.990658	-3.139751	13502.330394
HLA A*0216	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.370702	1.230828	-3.139874	23480.227978
HLA B*3901	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.046119	0.905846	-3.140273	11120.353851
HLA B*0803	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.468394	1.328104	-3.140290	29403.152453
HLA B*5401	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.408834	1.268289	-3.140545	25635.066649
HLA A*6802	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.322961	1.181912	-3.141049	21035.884329
HLA B*5101	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.441039	1.299885	-3.141154	27608.247640
HLA A*2501	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.405728	1.264555	-3.141173	25452.381944
HLA A*0216	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-3.895521	0.754283	-3.141238	7861.787794
HLA A*0211	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.024569	0.883265	-3.141304	10582.033458
HLA A*6802	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.442122	1.300814	-3.141308	27677.187405
HLA B*1801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.455192	1.313812	-3.141380	28522.798870
HLA B*3901	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.469496	1.328104	-3.141392	29477.849972
HLA B*1801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.442275	1.300706	-3.141569	27686.921600
HLA A*0203	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.301630	1.159900	-3.141730	20027.641082
HLA B*0702	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.442550	1.300814	-3.141735	27704.451779
HLA A*2902	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.399361	1.257536	-3.141825	25081.951710
HLA A*2902	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.304228	1.162401	-3.141828	20147.832429
HLA A*2601	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.754740	0.612321	-3.142419	5685.127065
HLA A*3001	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.255373	1.112802	-3.142571	18004.171410
HLA A*0212	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.370160	1.227496	-3.142663	23450.903431
HLA B*1517	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.468232	1.325261	-3.142971	29392.178824
HLA B*4402	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.370719	1.227496	-3.143222	23481.117173
HLA B*4801	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.400816	1.257536	-3.143279	25166.084969
HLA A*3002	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.058383	0.915076	-3.143307	11438.864577
HLA B*1502	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.412894	1.269415	-3.143479	25875.834275
HLA A*0219	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.444389	1.300814	-3.143575	27822.055168
HLA B*4403	1:82-90	9	YGPYRQSQR	1.080557	0.450140	-4.674333	1.530697	-3.143636	47242.547087
HLA A*0206	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.471850	1.328104	-3.143746	29638.074690
HLA A*2602	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.608240	1.464436	-3.143804	40573.263550
HLA A*0211	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-3.322397	0.178488	-3.143909	2100.861119
HLA A*0206	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.327850	1.183813	-3.144037	21274.043962
HLA A*2501	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.472148	1.328104	-3.144044	29658.444701
HLA A*2501	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.467038	1.322784	-3.144255	29311.513436
HLA B*1502	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.542309	1.398016	-3.144293	34858.499910
HLA B*1503	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.206447	1.062125	-3.144322	16085.977738
HLA B*4601	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.386740	1.241782	-3.144958	24363.512108
HLA A*3101	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.375921	1.230828	-3.145092	23764.053176
HLA A*2501	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.414584	1.269415	-3.145168	25976.679777
HLA B*2705	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-3.754811	0.609548	-3.145263	5686.049817
HLA B*5301	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.609711	1.464436	-3.145274	40710.901513
HLA A*2501	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.322082	1.176703	-3.145379	20993.365484
HLA B*0802	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.446313	1.300706	-3.145608	27945.599819
HLA B*4601	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.368184	1.222401	-3.145783	23344.450810
HLA B*4001	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.373447	1.227496	-3.145950	23629.063413
HLA B*4601	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.379980	1.234017	-3.145964	23987.248019
HLA B*5401	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.301350	1.155314	-3.146036	20014.751900
HLA A*3201	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-3.823622	0.677348	-3.146274	6662.272268
HLA A*2301	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.411217	1.264555	-3.146661	25776.077491
HLA A*3001	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.302405	1.155314	-3.147091	20063.427631
HLA A*3301	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.475947	1.328755	-3.147192	29919.028675
HLA A*8001	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.411868	1.264555	-3.147312	25814.732912
HLA A*0219	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.270405	1.123062	-3.147343	18638.250485
HLA A*2902	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.378244	1.230828	-3.147416	23891.540648
HLA B*5701	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.412009	1.264555	-3.147453	25823.113562
HLA A*3101	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.369894	1.222401	-3.147493	23436.571865
HLA A*3002	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.461376	1.313812	-3.147564	28931.835292
HLA A*3101	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.922174	0.774156	-3.148018	8359.376289
HLA B*0801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.148476	1.000328	-3.148148	14075.903163
HLA B*5701	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.358438	1.210192	-3.148246	22826.430181
HLA B*0802	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.449267	1.300814	-3.148452	28136.283956

HLA A*3201	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.413012	1.264555	-3.148456	25882.834492
HLA B*4403	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.608294	1.459786	-3.148508	40578.312292
HLA B*1502	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.533179	1.384650	-3.148529	34133.324942
HLA A*2501	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.462607	1.313812	-3.148795	29013.967093
HLA A*3001	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.114085	0.965021	-3.149063	13004.226013
HLA A*0211	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.541254	1.391860	-3.149394	34773.929965
HLA B*4601	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.311862	1.162401	-3.149461	20505.096001
HLA A*2601	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.383688	1.234192	-3.149496	24192.899032
HLA B*1501	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.149858	1.000328	-3.149530	14120.750111
HLA A*6801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.924068	0.774156	-3.149912	8395.905851
HLA A*2603	1:446-454	9	KAFSPIRVA	1.515913	-0.056127	-4.610197	1.459786	-3.150411	40756.517033
HLA B*1503	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.273521	1.123062	-3.150459	18772.432922
HLA A*2501	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.384651	1.234192	-3.150459	24246.619757
HLA B*5101	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.065131	0.914377	-3.150754	11617.980399
HLA A*3002	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.571238	1.420375	-3.150863	37259.575505
HLA A*2602	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.571341	1.420375	-3.150966	37268.445648
HLA B*5801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.351798	1.200757	-3.151041	22480.105910
HLA A*0250	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.573040	1.421817	-3.151223	37414.501028
HLA A*3201	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.013353	0.862113	-3.151239	10312.232331
HLA A*6901	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.373658	1.222401	-3.151257	23640.570969
HLA B*0801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.205353	1.054023	-3.151330	16045.475928
HLA A*3101	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.168367	1.016861	-3.151506	14735.572394
HLA B*4402	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.382389	1.230828	-3.151560	24120.630049
HLA A*0202	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.201861	1.050133	-3.151728	15917.001918
HLA A*3002	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.289109	1.137355	-3.151754	19458.501589
HLA A*0201	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.379283	1.227496	-3.151786	23948.737764
HLA B*7301	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.572737	1.419915	-3.152822	37388.399466
HLA B*5101	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.386860	1.234017	-3.152843	24370.235034
HLA B*1503	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.421362	1.268289	-3.153073	26385.292010
HLA B*0702	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.380688	1.227496	-3.153191	24026.340113
HLA B*0801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.266059	1.112802	-3.153257	18452.643731
HLA A*6801	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.491886	1.338560	-3.153327	31037.475965
HLA A*0101	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.380911	1.227496	-3.153414	24038.691371
HLA B*0803	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.476215	1.322784	-3.153432	29937.486249
HLA A*6901	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.380930	1.227496	-3.153433	24039.731766
HLA A*0101	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.376012	1.222401	-3.153611	23769.067580
HLA A*2402	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.545593	1.391860	-3.153733	35123.135076
HLA A*3001	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.248649	1.094888	-3.153761	17727.557918
HLA A*0301	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.364032	1.210192	-3.153840	23122.358020
HLA A*3201	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.538740	1.384650	-3.154090	34573.219715
HLA B*4403	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.454875	1.300706	-3.154169	28501.975275
HLA B*1502	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.385076	1.230828	-3.154248	24270.373431
HLA B*3801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.483217	1.328755	-3.154462	30424.033919
HLA B*0802	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.412143	1.257536	-3.154606	25831.077700
HLA A*0301	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.339318	1.184382	-3.154936	21843.281801
HLA B*5401	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.214680	1.059725	-3.154955	16393.816091
HLA A*2902	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.069064	0.914083	-3.154980	11723.672483
HLA A*2601	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.355764	1.200757	-3.155007	22686.332014
HLA A*2402	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.538474	1.383422	-3.155053	34552.090961
HLA A*3201	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.621933	1.466619	-3.155314	41872.871137
HLA B*1517	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.483485	1.328104	-3.155380	30442.803040
HLA B*0702	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.377824	1.222401	-3.155423	23868.415992
HLA B*3901	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.455620	1.299885	-3.155735	28550.896242
HLA B*3501	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.469651	1.313812	-3.155839	29488.376997
HLA A*2902	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.366168	1.210192	-3.155976	23236.344318
HLA A*6901	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-3.547929	0.391537	-3.156393	3531.255227
HLA A*6901	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.311723	1.155314	-3.156409	20498.552158
HLA A*2501	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.483933	1.327486	-3.156447	30474.275506
HLA B*0802	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.398238	1.241782	-3.156457	25017.175403
HLA A*3301	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.879075	0.722436	-3.156639	7569.634709
HLA A*6802	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.176031	1.019055	-3.156976	14997.919923
HLA B*5101	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.421625	1.264555	-3.157070	26401.283902
HLA B*1501	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.384679	1.227496	-3.157183	24248.193866
HLA B*7301	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.384740	1.227496	-3.157244	24251.604787
HLA B*1502	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.549127	1.391860	-3.157267	35410.079300

HLA A*2603	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.495932	1.338560	-3.157373	31327.966767
HLA B*4403	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.486255	1.328755	-3.157500	30637.595690
HLA B*0801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.085078	0.927578	-3.157500	12164.037969
HLA A*8001	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.388345	1.230828	-3.157516	24453.700690
HLA A*3002	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.320165	1.162617	-3.157548	20900.895165
HLA B*4801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.045630	0.887847	-3.157783	11107.847634
HLA A*0101	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.225925	1.067986	-3.157938	16823.823133
HLA A*0250	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.267588	1.109528	-3.158060	18517.745521
HLA B*4801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.422654	1.264555	-3.158099	26463.916751
HLA A*2601	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.380535	1.222401	-3.158134	24017.892909
HLA B*1517	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.458127	1.299885	-3.158242	28716.178632
HLA A*3002	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.072668	0.914377	-3.158291	11821.369365
HLA B*4601	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.275605	1.117129	-3.158476	18862.730263
HLA A*0201	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.281652	1.123062	-3.158590	19127.232140
HLA B*1501	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.423204	1.264555	-3.158649	26497.439009
HLA A*0250	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.591286	1.432365	-3.158921	39019.891571
HLA A*0219	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.221343	1.062125	-3.159218	16647.276704
HLA A*3201	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.551180	1.391860	-3.159321	35577.903207
HLA A*0201	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.393556	1.234192	-3.159364	24748.891399
HLA A*0101	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.360167	1.200757	-3.159410	22917.498868
HLA B*7301	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.497180	1.337733	-3.159446	31418.090471
HLA B*4403	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-3.741578	0.581735	-3.159843	5515.417094
HLA B*0801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.344287	1.184382	-3.159905	22094.646089
HLA A*2601	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.344341	1.184382	-3.159959	22097.395440
HLA B*1801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.315374	1.155314	-3.160060	20671.609248
HLA A*2602	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.626686	1.466619	-3.160067	42333.653302
HLA A*6801	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.467882	1.307776	-3.160106	29368.496114
HLA B*1503	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.127918	0.967578	-3.160340	13425.123101
HLA A*6801	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.489377	1.328755	-3.160622	30858.665886
HLA B*4002	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.580847	1.419915	-3.160933	38093.185921
HLA A*3001	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.276744	1.115540	-3.161204	18912.287208
HLA A*6901	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.067146	0.905846	-3.161301	11672.032753
HLA B*5801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.345173	1.183813	-3.161360	22139.754727
HLA B*1509	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.395619	1.234192	-3.161427	24866.725357
HLA A*2403	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.298803	1.137355	-3.161448	19897.722478
HLA B*5701	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.395630	1.234017	-3.161614	24867.397997
HLA A*2601	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.392637	1.230828	-3.161809	24696.596223
HLA B*5301	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.372232	1.210192	-3.162040	23563.067321
HLA B*0803	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.461935	1.299885	-3.162051	28969.110573
HLA A*0250	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.548934	1.386690	-3.162244	35394.374486
HLA B*4501	1:463-471	9	PLFESLELL	1.291656	0.202256	-4.656169	1.493912	-3.162258	45307.430826
HLA B*3501	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.775030	0.612666	-3.162365	5957.037421
HLA A*0211	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.545885	1.383422	-3.162463	35146.704502
HLA A*3101	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.427069	1.264555	-3.162513	26734.299188
HLA A*2501	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.463667	1.300814	-3.162852	29084.843540
HLA B*3801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.490982	1.328104	-3.162878	30972.898157
HLA B*5301	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.595280	1.432365	-3.162915	39380.405408
HLA A*2403	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.311162	1.148177	-3.162984	20472.065405
HLA B*1517	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-3.550175	0.387024	-3.163151	3549.565672
HLA A*0212	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.799160	0.635887	-3.163273	6297.374761
HLA B*4001	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.373571	1.210192	-3.163379	23635.839406
HLA B*1517	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.154162	0.990658	-3.163504	14261.395503
HLA B*1517	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.183921	1.020365	-3.163556	15272.868101
HLA B*1501	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.246819	1.083182	-3.163637	17653.005809
HLA A*1101	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.776027	0.612321	-3.163706	5970.717315
HLA A*6901	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.340450	1.176703	-3.163747	21900.313938
HLA A*2603	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.561936	1.398016	-3.163920	36470.044362
HLA B*1517	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.386505	1.222401	-3.164104	24350.335283
HLA A*0212	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.386815	1.222401	-3.164414	24367.730198
HLA B*5101	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.422118	1.257536	-3.164582	26431.294831
HLA A*0219	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.374854	1.210192	-3.164662	23705.758148
HLA A*3002	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.502694	1.337733	-3.164961	31819.549546
HLA A*3101	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.399321	1.234192	-3.165129	25079.645076
HLA B*5701	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.422673	1.257536	-3.165137	26465.062110
HLA B*5401	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.503707	1.338560	-3.165147	31893.828551

HLA A*3002	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.399319	1.234017	-3.165302	25079.509399
HLA B*5701	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.393055	1.227496	-3.165559	24720.389518
HLA B*0801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.399862	1.234192	-3.165670	25110.870462
HLA A*8001	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.349898	1.183813	-3.166085	22381.934457
HLA B*4001	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.367072	1.200757	-3.166315	23284.791582
HLA A*3301	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.586246	1.419915	-3.166332	38569.713501
HLA A*3201	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.598828	1.432365	-3.166462	39703.418826
HLA B*7301	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.588305	1.421817	-3.166488	38752.931597
HLA B*3901	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.467257	1.300706	-3.166551	29326.264346
HLA A*3002	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.588380	1.421817	-3.166563	38759.640948
HLA A*0202	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.348504	1.181912	-3.166593	22310.246824
HLA A*6901	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.258583	1.091927	-3.166656	18137.713414
HLA A*0212	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.215526	1.048747	-3.166779	16425.775144
HLA A*2403	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.400806	1.234017	-3.166789	25165.540392
HLA B*3801	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.550283	1.383422	-3.166861	35504.454627
HLA A*2301	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.436648	1.269415	-3.167232	27330.504868
HLA A*0301	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.368019	1.200757	-3.167262	23335.612122
HLA B*4801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.401459	1.234192	-3.167267	25203.416561
HLA B*4601	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.401708	1.234192	-3.167516	25217.873560
HLA B*1503	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.344346	1.176703	-3.167642	22097.634530
HLA A*3002	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.559683	1.391860	-3.167823	36281.324690
HLA B*7301	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.632447	1.464436	-3.168010	42898.952323
HLA A*6802	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.402207	1.234192	-3.168015	25246.812443
HLA A*0202	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.481878	1.313812	-3.168066	30330.361748
HLA B*1502	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.589916	1.421817	-3.168100	38897.018055
HLA B*5401	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-2.943693	-0.224761	-3.168454	878.401875
HLA B*3901	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.136146	0.967687	-3.168459	13681.892478
HLA B*3501	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-3.855082	0.686428	-3.168654	7162.786085
HLA A*6901	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.218810	1.050133	-3.168677	16550.474651
HLA A*0201	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.331675	1.162617	-3.169058	21462.238365
HLA B*5801	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.351140	1.181912	-3.169229	22446.079521
HLA A*0216	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.403623	1.234192	-3.169431	25329.306145
HLA B*4402	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.403558	1.234017	-3.169541	25325.469631
HLA B*4501	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.229613	1.059725	-3.169888	16967.325268
HLA B*5401	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.307459	1.137355	-3.170104	20298.262849
HLA B*1517	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.484004	1.313812	-3.170192	30479.221781
HLA B*1502	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.602622	1.432365	-3.170257	40051.826240
HLA B*1517	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.404944	1.234017	-3.170927	25406.433484
HLA A*6802	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.393600	1.222401	-3.171200	24751.435416
HLA A*2601	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.398779	1.227496	-3.171282	25048.323011
HLA B*5401	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.563513	1.391860	-3.171653	36602.672498
HLA B*5301	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.558379	1.386690	-3.171689	36172.553804
HLA A*0202	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.555283	1.383422	-3.171861	35915.552364
HLA A*3101	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.172272	1.000328	-3.171944	14868.660818
HLA A*2301	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.477035	1.305053	-3.171982	29994.063153
HLA B*7301	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.592543	1.420375	-3.172168	39132.990070
HLA B*5301	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.334786	1.162401	-3.172385	21616.517663
HLA A*1101	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.441894	1.269415	-3.172479	27662.667356
HLA A*2602	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.594702	1.421817	-3.172886	39328.031533
HLA B*7301	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.472787	1.299885	-3.172903	29702.118927
HLA B*4801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.373733	1.200757	-3.172976	23644.663895
HLA B*5701	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.403952	1.230828	-3.173124	25348.497435
HLA A*6901	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-3.846492	0.673165	-3.173327	7022.508347
HLA B*4002	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.571541	1.398016	-3.173525	37285.587133
HLA A*2902	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.407735	1.234192	-3.173543	25570.245159
HLA B*3501	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.431112	1.257536	-3.173576	26984.369042
HLA A*0201	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.355640	1.181912	-3.173728	22679.828227
HLA B*1503	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.241213	1.067176	-3.174036	17426.605222
HLA A*2902	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.396537	1.222401	-3.174136	24919.380782
HLA B*3801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.511899	1.337733	-3.174166	32501.193513
HLA A*2902	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.283753	1.109528	-3.174224	19219.963933
HLA B*4601	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.401950	1.227496	-3.174454	25231.929344
HLA A*1101	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.358417	1.183813	-3.174604	22825.318812
HLA A*2501	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.279383	1.104589	-3.174793	19027.534859
HLA B*3901	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.443330	1.268289	-3.175041	27754.255993

HLA B*5801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-3.797750	0.622672	-3.175078	6276.967040
HLA B*5401	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.089222	0.914083	-3.175139	12280.675578
HLA B*4801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.402867	1.227496	-3.175370	25285.221300
HLA A*0301	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.338181	1.162617	-3.175564	21786.162463
HLA B*2705	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.357477	1.181912	-3.175565	22775.979238
HLA A*6802	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.352320	1.176703	-3.175617	22507.120633
HLA B*5701	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.225807	1.050133	-3.175674	16819.272997
HLA A*0216	1:435-443	9	ALIEGLALK	0.478643	0.243793	-3.898125	0.722436	-3.175688	7909.054105
HLA A*6901	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.335791	1.159900	-3.175891	21666.627242
HLA B*2705	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-3.738275	0.562255	-3.176020	5473.624300
HLA A*3301	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.624614	1.448126	-3.176488	42132.138483
HLA B*5101	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.477578	1.300814	-3.176764	30031.569696
HLA B*4801	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.358852	1.181912	-3.176940	22848.174499
HLA B*0802	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.410970	1.234017	-3.176953	25761.439848
HLA B*1509	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.490904	1.313812	-3.177092	30967.369173
HLA A*6901	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.339715	1.162617	-3.177098	21863.261618
HLA B*0802	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.411327	1.234192	-3.177135	25782.632273
HLA A*0212	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.411424	1.234192	-3.177232	25788.351636
HLA A*0206	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.337269	1.159900	-3.177369	21740.480463
HLA A*8001	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.404906	1.227496	-3.177410	25404.234443
HLA A*3301	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.606788	1.429220	-3.177568	40437.840998
HLA B*4402	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.442138	1.264555	-3.177583	27678.235539
HLA A*0301	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.340100	1.162401	-3.177700	21882.667788
HLA B*4002	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.644340	1.466619	-3.177721	44089.967538
HLA B*1509	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.478656	1.300814	-3.177842	30106.234925
HLA A*3101	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.405519	1.227496	-3.178023	25440.130077
HLA B*1801	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.446346	1.268289	-3.178057	27947.716455
HLA B*4002	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.642611	1.464436	-3.178174	43914.764498
HLA B*0801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.326384	1.148177	-3.178207	21202.348747
HLA A*0202	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.133313	0.955018	-3.178294	13592.917912
HLA B*5801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.362749	1.184382	-3.178367	23054.159982
HLA A*3001	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.209422	1.031013	-3.178409	16196.527448
HLA B*4001	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.341031	1.162617	-3.178413	21929.597631
HLA B*0803	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.412432	1.234017	-3.178415	25848.271842
HLA A*3101	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.360475	1.181912	-3.178563	22933.746152
HLA B*5801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-3.645409	0.466843	-3.178566	4419.867404
HLA B*5101	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.492478	1.313812	-3.178667	31079.817965
HLA B*5701	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.413118	1.234192	-3.178926	25889.136306
HLA A*3301	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.448473	1.269415	-3.179057	28084.882573
HLA B*7301	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.570991	1.391860	-3.179131	37238.416647
HLA A*6802	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.380227	1.200757	-3.179470	24000.877567
HLA B*5401	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.566616	1.386690	-3.179926	36865.189079
HLA B*4801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.413977	1.234017	-3.179961	25940.448081
HLA B*1801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.480853	1.300814	-3.180039	30258.905475
HLA B*5101	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.410911	1.230828	-3.180083	25757.955920
HLA A*2603	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.628295	1.448126	-3.180169	42490.823295
HLA A*0101	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.362117	1.181912	-3.180206	23020.634581
HLA A*0219	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.180580	1.000328	-3.180252	15155.826797
HLA B*0702	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.444829	1.264555	-3.180273	27850.215572
HLA A*2601	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.390546	1.210192	-3.180354	24577.972822
HLA B*4403	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.567373	1.386690	-3.180683	36929.463626
HLA B*4801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.403189	1.222401	-3.180788	25303.968510
HLA A*6801	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.578885	1.398016	-3.180870	37921.497266
HLA B*1509	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.503871	1.322784	-3.181088	31905.908783
HLA A*2601	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.285691	1.104589	-3.181102	19305.937393
HLA A*2402	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.509865	1.328755	-3.181110	32349.282718
HLA B*3801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.412093	1.230828	-3.181265	25828.143259
HLA B*0801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.391991	1.210192	-3.181799	24659.881932
HLA A*2402	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.446473	1.264555	-3.181918	27955.882126
HLA A*0212	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.145554	0.963515	-3.182038	13981.491759
HLA A*0101	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.358797	1.176703	-3.182094	22845.331736
HLA A*0211	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.450540	1.268289	-3.182251	28218.905110
HLA A*0206	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.507565	1.325261	-3.182304	32178.404720
HLA B*3901	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.483142	1.300814	-3.182327	30418.767474
HLA A*2603	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.487730	1.305053	-3.182677	30741.861192

HLA B*2705	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.447427	1.264555	-3.182872	28017.352327
HLA B*4501	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.619976	1.437023	-3.182953	41684.598193
HLA B*3901	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.405451	1.222401	-3.183050	25436.139170
HLA B*4501	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.647490	1.464436	-3.183054	44410.988361
HLA A*0301	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.365181	1.181912	-3.183269	23183.607714
HLA A*2301	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.512268	1.328755	-3.183513	32528.810213
HLA B*2705	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.393800	1.210192	-3.183608	24762.819748
HLA A*2603	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.605665	1.421817	-3.183848	40333.406780
HLA A*0212	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.366469	1.181912	-3.184557	23252.440264
HLA A*0216	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.347344	1.162617	-3.184727	22250.702619
HLA A*2601	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.368898	1.183813	-3.185085	23382.874829
HLA A*2301	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.485033	1.299885	-3.185148	30551.528888
HLA B*3801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.412655	1.227496	-3.185158	25861.559704
HLA A*8001	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.419210	1.234017	-3.185193	26254.864223
HLA A*6901	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-3.911305	0.726109	-3.185196	8152.769378
HLA A*0101	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.322655	1.137355	-3.185300	21021.095296
HLA B*4001	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.345227	1.159900	-3.185327	22142.509692
HLA A*3001	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.253338	1.067986	-3.185352	17920.019793
HLA A*3301	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.419391	1.234017	-3.185374	26265.803266
HLA A*6901	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.029090	0.843615	-3.185475	10692.753114
HLA B*0803	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.413404	1.227496	-3.185908	25906.228943
HLA B*3901	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.298745	1.112802	-3.185943	19895.031548
HLA A*2501	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.387085	1.200757	-3.186328	24382.894987
HLA B*1801	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.514662	1.328104	-3.186558	32708.626216
HLA B*5701	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.409112	1.222401	-3.186711	25651.436452
HLA A*0203	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.421073	1.234192	-3.186881	26367.740645
HLA A*0206	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.030391	0.843357	-3.187034	10724.848207
HLA B*5801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.354277	1.167129	-3.187148	22608.776450
HLA B*5801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.349862	1.162617	-3.187245	22380.118274
HLA B*0802	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.451825	1.264555	-3.187270	28302.534436
HLA B*5101	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.515536	1.328104	-3.187432	32774.517912
HLA B*5801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.364312	1.176703	-3.187608	23137.248451
HLA B*2705	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.410073	1.222401	-3.187672	25708.256804
HLA B*4402	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.350537	1.162617	-3.187919	22414.893490
HLA B*0702	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.348244	1.159900	-3.188344	22296.853594
HLA B*5401	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.515997	1.327486	-3.188510	32809.288419
HLA A*1101	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.446323	1.257536	-3.188787	27946.204555
HLA A*3001	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.293968	1.105060	-3.188908	19677.418810
HLA A*3301	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.526295	1.337377	-3.188918	33596.543946
HLA A*1101	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.419776	1.230828	-3.188948	26289.117200
HLA B*3501	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-3.855533	0.666384	-3.189149	7170.229927
HLA A*3301	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.573827	1.384650	-3.189177	37482.369290
HLA A*0219	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.423387	1.234192	-3.189195	26508.622528
HLA B*5401	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.527096	1.337733	-3.189362	33658.579119
HLA A*2602	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.621853	1.432365	-3.189487	41865.169908
HLA B*0803	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.373310	1.183813	-3.189497	23621.650400
HLA B*1517	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.447202	1.257536	-3.189665	28002.805311
HLA B*4002	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.574335	1.384650	-3.189685	37526.194391
HLA A*1101	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.489661	1.299885	-3.189777	30878.872476
HLA A*2301	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.527775	1.337733	-3.190041	33711.244051
HLA A*0206	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.157757	0.967687	-3.190069	14379.928814
HLA B*1501	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.424292	1.234192	-3.190100	26563.892420
HLA A*3001	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.050503	0.860349	-3.190153	11233.180718
HLA B*4501	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.657013	1.466619	-3.190394	45395.510166
HLA B*1517	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.113859	0.923460	-3.190399	12997.474030
HLA B*1509	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.253017	1.062587	-3.190430	17906.743204
HLA A*3101	1:235-243	9	IGVAERIPK	0.603044	0.187675	-3.981160	0.790719	-3.190442	9575.468798
HLA A*2902	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.258500	1.067986	-3.190514	18134.279434
HLA A*0206	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.424748	1.234192	-3.190555	26591.786351
HLA A*2902	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.345974	1.155314	-3.190660	22180.635227
HLA A*0219	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.244704	1.054023	-3.190681	17567.263989
HLA B*3801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.491402	1.300706	-3.190697	31002.905915
HLA B*7301	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.575359	1.384650	-3.190709	37614.812334
HLA A*2301	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.424921	1.234017	-3.190905	26602.434020
HLA B*5401	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.528339	1.337377	-3.190962	33755.042261

HLA A*3001	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.198008	1.006851	-3.191157	15776.407419
HLA B*0803	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.492044	1.300814	-3.191229	31048.727927
HLA A*0206	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.492234	1.300814	-3.191420	31062.336493
HLA A*0211	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.192125	1.000328	-3.191797	15564.135489
HLA A*2403	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.414278	1.222401	-3.191877	25958.417175
HLA B*1501	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.368618	1.176703	-3.191915	23367.826321
HLA B*4501	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.576863	1.384650	-3.192213	37745.272910
HLA A*3001	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.054393	0.862113	-3.192280	11334.268407
HLA A*6901	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.376759	1.184382	-3.192377	23809.993764
HLA B*1801	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.450054	1.257536	-3.192518	28187.321940
HLA A*3001	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.297185	1.104589	-3.192595	19823.693490
HLA A*3002	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.461007	1.268289	-3.192718	28907.272395
HLA B*3501	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.457466	1.264555	-3.192911	28672.558069
HLA A*6802	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.147856	0.954860	-3.192996	14055.814156
HLA A*3001	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.108098	0.915076	-3.193022	12826.200399
HLA B*3801	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.493848	1.300814	-3.193034	31177.997380
HLA B*1801	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.375077	1.181912	-3.193165	23717.944605
HLA B*7301	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.623117	1.429823	-3.193294	41987.196832
HLA B*4001	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.377361	1.183813	-3.193548	23842.991822
HLA A*8001	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.428086	1.234192	-3.193894	26796.997208
HLA B*0801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.311086	1.117129	-3.193958	20468.521661
HLA A*3201	1:465-473	9	FESLELLGR	0.858673	0.563144	-4.615979	1.421817	-3.194163	41302.766833
HLA A*2402	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.499217	1.305053	-3.194164	31565.799196
HLA A*2403	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.395149	1.200757	-3.194391	24839.834661
HLA B*1517	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.162164	0.967687	-3.194477	14526.613109
HLA B*4403	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.631570	1.437023	-3.194548	42812.474295
HLA B*4403	1:467-475	9	SLELLGRDR	0.924235	0.540201	-4.659057	1.464436	-3.194621	45609.672428
HLA A*6801	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.624470	1.429823	-3.194648	42118.237035
HLA A*2301	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.519996	1.325261	-3.194735	33112.779323
HLA B*5801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.354768	1.159900	-3.194868	22634.353900
HLA A*2602	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.494819	1.299885	-3.194934	31247.735766
HLA B*1517	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.422600	1.227496	-3.195104	26460.624118
HLA B*5401	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-3.441582	0.246392	-3.195190	2764.279919
HLA A*6901	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.214314	1.019055	-3.195258	16379.986486
HLA B*4402	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.355320	1.159900	-3.195420	22663.147796
HLA B*4002	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.616050	1.420375	-3.195674	41309.470679
HLA B*0702	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.405942	1.210192	-3.195750	25464.915234
HLA A*6801	1:445-453	9	RKAFSPIRV	1.241076	0.207050	-4.643978	1.448126	-3.195852	44053.250472
HLA A*3101	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.358640	1.162401	-3.196239	22837.052659
HLA B*7301	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.628631	1.432365	-3.196266	42523.707515
HLA A*0101	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.380805	1.184382	-3.196423	24032.839984
HLA B*2705	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.373306	1.176703	-3.196602	23621.394820
HLA B*5801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.352125	1.155314	-3.196811	22497.016736
HLA B*7301	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.497523	1.300706	-3.196817	31442.915658
HLA A*3201	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.419238	1.222401	-3.196837	26256.568709
HLA B*3501	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.971076	0.774156	-3.196920	9355.695014
HLA A*2402	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.522185	1.325261	-3.196925	33280.156112
HLA B*3501	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.040503	0.843357	-3.197146	10977.497266
HLA A*0211	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.247380	1.050133	-3.197247	17675.845263
HLA A*3301	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.617657	1.420375	-3.197281	41462.613932
HLA A*0219	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-3.922724	0.725139	-3.197585	8369.965241
HLA B*0702	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.217993	1.020365	-3.197628	16519.345353
HLA B*3501	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.111716	0.914083	-3.197633	12933.504784
HLA A*0202	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.292591	1.094888	-3.197703	19615.136330
HLA B*1503	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-3.973477	0.775701	-3.197776	9407.565039
HLA A*2501	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.428725	1.230828	-3.197897	26836.457744
HLA B*4002	1:1-9	9	VTATETVRV	1.280980	0.156043	-4.635358	1.437023	-3.198335	43187.463523
HLA B*1503	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.314545	1.115540	-3.199005	20632.170535
HLA A*0202	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.591056	1.391860	-3.199196	38999.209911
HLA A*3301	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.524497	1.325261	-3.199237	33457.789778
HLA A*2402	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.537095	1.337733	-3.199362	34442.541206
HLA A*2602	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.591227	1.391860	-3.199367	39014.614595
HLA A*2601	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.347560	1.148177	-3.199382	22261.779769
HLA A*0101	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.362049	1.162401	-3.199648	23017.023231
HLA A*0301	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.249889	1.050133	-3.199756	17778.267685

HLA A*1101	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.468199	1.268289	-3.199910	29389.952790
HLA B*7301	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.583382	1.383422	-3.199961	38316.196400
HLA B*0702	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-3.926083	0.726109	-3.199975	8434.967586
HLA A*2602	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.584651	1.384650	-3.200001	38428.294701
HLA A*0212	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-3.906639	0.706599	-3.200040	8065.644573
HLA B*5701	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.383904	1.183813	-3.200091	24204.943072
HLA A*0216	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.248846	1.048747	-3.200099	17735.615695
HLA A*2902	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.427788	1.227496	-3.200291	26778.592496
HLA A*3301	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.262490	1.062125	-3.200364	18301.628231
HLA B*7301	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.539151	1.338560	-3.200591	34605.966739
HLA A*6901	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.187374	0.986777	-3.200598	15394.810383
HLA A*3002	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.310144	1.109528	-3.200616	20424.166084
HLA B*4501	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.155478	0.954860	-3.200618	14304.666454
HLA B*1517	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.114775	0.914083	-3.200692	13024.925788
HLA A*0301	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.217617	1.016861	-3.200756	16505.052688
HLA A*0202	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.126574	0.925719	-3.200855	13383.643851
HLA B*1501	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-3.676126	0.475212	-3.200914	4743.800403
HLA B*0803	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.435109	1.234192	-3.200917	27233.831224
HLA B*1801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.293002	1.091927	-3.201076	19633.715373
HLA B*4402	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.293049	1.091927	-3.201123	19635.839813
HLA B*4501	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.435172	1.234017	-3.201155	27237.809479
HLA B*4403	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.630504	1.429220	-3.201284	42707.452044
HLA B*4403	1:471-479	9	LGRDRSMQR	0.894548	0.572071	-4.667957	1.466619	-3.201338	46553.978567
HLA B*4801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.378397	1.176703	-3.201694	23899.943414
HLA B*0801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.268939	1.067176	-3.201763	18575.438103
HLA A*0211	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.364749	1.162617	-3.202132	23160.541778
HLA A*3101	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.402930	1.200757	-3.202173	25288.914907
HLA B*1517	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.433011	1.230828	-3.202182	27102.581033
HLA A*0201	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.252368	1.050133	-3.202235	17880.026071
HLA B*3801	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.525033	1.322784	-3.202249	33499.083909
HLA A*6901	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.386066	1.183813	-3.202253	24325.713740
HLA A*0301	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.136564	0.934152	-3.202412	13695.073942
HLA B*3801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.529979	1.327486	-3.202492	33882.745723
HLA B*4002	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.632320	1.429823	-3.202497	42886.421910
HLA B*3801	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.436601	1.234017	-3.202584	27327.547928
HLA A*3001	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.285841	1.083182	-3.202660	19312.622901
HLA A*2603	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.472099	1.269415	-3.202684	29655.075466
HLA A*2402	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.379482	1.176703	-3.202779	23959.752898
HLA A*0201	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.074505	0.871584	-3.202921	11871.485997
HLA A*0206	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.086271	0.883265	-3.203006	12197.513444
HLA B*4601	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.265685	1.062587	-3.203098	18436.778101
HLA B*2705	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.230544	1.027215	-3.203329	17003.713606
HLA A*2301	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.404265	1.200757	-3.203507	25366.742629
HLA A*2403	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.363529	1.159900	-3.203629	23095.604379
HLA B*0801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.366469	1.162401	-3.204068	23252.440264
HLA A*3101	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.414274	1.210192	-3.204082	25958.136312
HLA B*1503	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-3.800113	0.595974	-3.204139	6311.221611
HLA B*1801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.445959	1.241782	-3.204177	27922.780568
HLA A*6901	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.386277	1.181912	-3.204365	24337.560571
HLA A*3002	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.308960	1.104589	-3.204371	20368.553728
HLA A*0211	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.518238	1.313812	-3.204426	32979.055991
HLA A*0216	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.388424	1.183813	-3.204612	24458.199025
HLA A*0201	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.191420	0.986777	-3.204644	15538.895901
HLA A*1101	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.367108	1.162401	-3.204707	23286.681181
HLA A*2902	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.287902	1.083182	-3.204720	19404.468823
HLA B*5301	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.469303	1.264555	-3.204748	29464.776176
HLA B*1509	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.427200	1.222401	-3.204800	26742.399672
HLA A*6802	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-3.959108	0.754283	-3.204824	9101.391146
HLA B*4402	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.342241	1.137355	-3.204886	21990.780719
HLA B*4801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.388845	1.183813	-3.205032	24481.895087
HLA A*3001	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.102379	0.897326	-3.205053	12658.416310
HLA A*0101	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.365019	1.159900	-3.205119	23174.955297
HLA B*5101	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-3.967016	0.761813	-3.205203	9268.642807
HLA B*4501	1:456-464	9	TGTTVSPPL	1.086640	0.342580	-4.634455	1.429220	-3.205236	43097.839122
HLA A*0219	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-3.912447	0.707098	-3.205349	8174.232893

HLA A*2902	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.387341	1.181912	-3.205430	24397.277282
HLA B*3801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.447279	1.241782	-3.205497	28007.804996
HLA B*1502	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.589024	1.383422	-3.205602	38817.137340
HLA B*3901	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.322787	1.117129	-3.205658	21027.464681
HLA B*3801	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.463624	1.257536	-3.206088	29082.011454
HLA B*0802	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.382847	1.176703	-3.206143	24146.089013
HLA B*5401	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.195179	0.989026	-3.206153	15673.981624
HLA A*2601	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.383014	1.176703	-3.206310	24155.365358
HLA B*3501	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.161253	0.954860	-3.206393	14496.153190
HLA A*2601	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-3.802862	0.596390	-3.206472	6351.295623
HLA B*4601	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-3.996709	0.790220	-3.206489	9924.506881
HLA A*2603	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.383404	1.176703	-3.206700	24177.067625
HLA A*2301	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.507715	1.300814	-3.206901	32189.547871
HLA A*0101	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.390725	1.183813	-3.206912	24588.080172
HLA B*3801	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.520738	1.313812	-3.206926	33169.434859
HLA A*0212	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.121114	0.914083	-3.207031	13216.430242
HLA B*4801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.417302	1.210192	-3.207110	26139.784017
HLA A*0211	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.532382	1.325261	-3.207121	34070.783415
HLA A*0250	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.599011	1.391860	-3.207151	39720.176067
HLA B*5701	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.408045	1.200757	-3.207288	25588.511530
HLA B*1501	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.267161	1.059725	-3.207436	18499.521925
HLA A*0101	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.374816	1.167129	-3.207687	23703.706309
HLA A*2501	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.430433	1.222401	-3.208032	26942.213079
HLA B*5101	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.320980	1.112802	-3.208178	20940.167835
HLA A*0301	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.368181	1.159900	-3.208281	23344.324520
HLA B*0801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.303413	1.094888	-3.208525	20110.045761
HLA B*1517	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.821198	0.612666	-3.208532	6625.180403
HLA B*1509	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.313356	1.104589	-3.208767	20575.769182
HLA B*0801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.375986	1.167129	-3.208857	23767.653153
HLA B*5801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.326097	1.117129	-3.208968	21188.359676
HLA B*7301	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.391077	1.181912	-3.209165	24608.041088
HLA A*2501	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.466893	1.257536	-3.209356	29301.683618
HLA B*4403	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.601248	1.391860	-3.209388	39925.271181
HLA A*2601	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.332469	1.123062	-3.209407	21501.518883
HLA A*0101	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.372065	1.162617	-3.209448	23554.018435
HLA B*1509	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.419722	1.210192	-3.209530	26285.846316
HLA A*6801	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.594286	1.384650	-3.209636	39290.390986
HLA A*3002	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.534945	1.325261	-3.209685	34272.470231
HLA B*5401	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.157268	0.947523	-3.209745	14363.756800
HLA B*2705	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.376900	1.167129	-3.209771	23817.723584
HLA A*2601	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.391693	1.181912	-3.209781	24642.945033
HLA B*1509	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.515236	1.305053	-3.210183	32751.830535
HLA A*2603	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.642801	1.432365	-3.210435	43934.012210
HLA A*1101	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.432940	1.222401	-3.210539	27098.182731
HLA A*6801	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.538209	1.327486	-3.210722	34530.975119
HLA A*3001	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.302849	1.091927	-3.210922	20083.952356
HLA A*0301	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.348328	1.137355	-3.210973	22301.196463
HLA A*0201	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.394886	1.183813	-3.211073	24824.788576
HLA B*1502	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.539245	1.328104	-3.211141	34613.456127
HLA A*2602	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.594564	1.383422	-3.211142	39315.480679
HLA A*0203	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.326906	1.115540	-3.211365	21227.827967
HLA A*2603	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.468941	1.257536	-3.211405	29440.238618
HLA A*0216	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.218416	1.006851	-3.211564	16535.439397
HLA A*6802	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.212086	1.000328	-3.211758	16296.195546
HLA B*0801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.164138	0.952354	-3.211784	14592.776717
HLA B*5101	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.446039	1.234192	-3.211847	27927.917051
HLA A*8001	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.329065	1.117129	-3.211936	21333.628894
HLA B*4402	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.422344	1.210192	-3.212152	26445.025472
HLA B*5101	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.422516	1.210192	-3.212324	26455.471254
HLA B*1509	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.413087	1.200757	-3.212330	25887.315624
HLA A*2603	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.480689	1.268289	-3.212400	30247.448832
HLA A*2602	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.541216	1.328755	-3.212461	34770.920125
HLA B*0702	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.394496	1.181912	-3.212584	24802.504890
HLA A*0216	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.322185	1.109528	-3.212657	20998.363237
HLA B*4001	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.389390	1.176703	-3.212687	24512.641464

HLA B*4002	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.645061	1.432365	-3.212696	44163.254583
HLA B*2705	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.243748	1.031013	-3.212735	17528.626502
HLA A*0201	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.397193	1.184382	-3.212811	24957.021475
HLA A*0301	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.206438	0.993286	-3.213152	16085.629648
HLA B*0803	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.477738	1.264555	-3.213182	30042.619516
HLA B*4601	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.397585	1.184382	-3.213203	24979.579121
HLA A*3001	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.177304	0.963515	-3.213789	15041.960759
HLA A*6802	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.441344	1.227496	-3.213848	27627.670952
HLA A*8001	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.424054	1.210192	-3.213863	26549.381905
HLA A*2501	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.424064	1.210192	-3.213872	26549.956428
HLA B*1501	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.337062	1.123062	-3.214001	21730.132931
HLA A*2403	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.376639	1.162401	-3.214239	23803.425389
HLA A*0219	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.376858	1.162617	-3.214241	23815.404374
HLA B*1503	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-3.988411	0.774156	-3.214255	9736.672359
HLA B*1801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.331724	1.117129	-3.214595	21464.676779
HLA A*3002	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.598020	1.383422	-3.214598	39629.599400
HLA A*2601	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.331926	1.117129	-3.214797	21474.665553
HLA B*4601	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.377415	1.162617	-3.214798	23845.958729
HLA A*0250	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.598259	1.383422	-3.214838	39651.473392
HLA B*4002	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.606800	1.391860	-3.214940	40438.934834
HLA B*1503	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.075600	0.860349	-3.215251	11901.451869
HLA A*0206	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.162949	0.947523	-3.215426	14552.885018
HLA B*4501	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.645322	1.429823	-3.215499	44189.782480
HLA B*5801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.265687	1.050133	-3.215554	18436.877842
HLA B*0801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.087235	0.871584	-3.215650	12224.598221
HLA A*2601	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.378051	1.162401	-3.215651	23880.944451
HLA A*0201	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.392548	1.176703	-3.215844	24691.519723
HLA B*1503	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.168245	0.952354	-3.215891	14731.427651
HLA A*3101	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.076709	0.860662	-3.216047	11931.880674
HLA A*0101	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.371691	1.155314	-3.216377	23533.766630
HLA B*5401	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.530204	1.313812	-3.216392	33900.347276
HLA A*0201	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.276298	1.059725	-3.216573	18892.857654
HLA A*6901	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.233474	1.016861	-3.216613	17118.810692
HLA B*4001	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.401067	1.184382	-3.216685	25180.656779
HLA A*0201	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.376618	1.159900	-3.216718	23802.266452
HLA B*4501	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.608635	1.391860	-3.216775	40610.155784
HLA B*4002	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.458679	1.241782	-3.216897	28752.709414
HLA B*4801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.270934	1.054023	-3.216911	18660.951244
HLA B*0801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.206029	0.989026	-3.217003	16070.495036
HLA A*0212	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.284995	1.067986	-3.217009	19275.047010
HLA A*0202	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.439526	1.222401	-3.217125	27512.228732
HLA B*0802	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.354538	1.137355	-3.217183	22622.357045
HLA A*2301	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.485496	1.268289	-3.217207	30584.106481
HLA B*4403	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.637672	1.420375	-3.217297	43418.212577
HLA A*0203	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.318259	1.100571	-3.217688	20809.395029
HLA B*3501	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.445235	1.227496	-3.217739	27876.293091
HLA A*6901	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.385048	1.167129	-3.217919	24268.797882
HLA A*2602	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.556598	1.338560	-3.218039	36024.524876
HLA A*2501	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.459917	1.241782	-3.218135	28834.800688
HLA A*0219	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.440538	1.222401	-3.218138	27576.452802
HLA A*0212	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.280783	1.062587	-3.218196	19088.984236
HLA A*3001	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.048877	0.830606	-3.218271	11191.206314
HLA A*6802	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.301752	1.083182	-3.218570	20033.275935
HLA A*8001	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.419513	1.200757	-3.218755	26273.193250
HLA B*5401	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.286100	1.067176	-3.218923	19324.119028
HLA A*6802	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.205846	0.986777	-3.219069	16063.715178
HLA A*0216	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.379001	1.159900	-3.219101	23933.195608
HLA B*0801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.379078	1.159900	-3.219178	23937.468695
HLA B*5101	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.374619	1.155314	-3.219305	23692.937064
HLA A*3301	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.520118	1.300706	-3.219412	33122.095729
HLA A*0206	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.092408	0.872828	-3.219580	12371.095523
HLA B*1517	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.484265	1.264555	-3.219709	30497.529980
HLA A*1101	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.453787	1.234017	-3.219770	28430.673470
HLA B*4403	1:347-355	9	HLDTHGHHI	1.366138	0.063685	-4.649685	1.429823	-3.219862	44635.957710
HLA A*3001	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.154195	0.934152	-3.220043	14262.475680

HLA B*0702	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.329586	1.109528	-3.220058	21359.265876
HLA B*5301	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.612006	1.391860	-3.220146	40926.647079
HLA B*4601	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.368353	1.148177	-3.220175	23353.545526
HLA A*6901	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.368383	1.148177	-3.220206	23355.188005
HLA A*2902	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.187825	0.967578	-3.220247	15410.809260
HLA A*0250	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.207025	0.986777	-3.220249	16107.399735
HLA A*2403	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.454443	1.234192	-3.220251	28473.617966
HLA A*2402	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.520177	1.299885	-3.220292	33126.575704
HLA A*1101	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.485101	1.264555	-3.220546	30556.322395
HLA B*5101	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.443083	1.222401	-3.220682	27738.494987
HLA A*0101	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.337812	1.117129	-3.220683	21767.666186
HLA B*1501	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.387832	1.167129	-3.220703	24424.878075
HLA B*0801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.421752	1.200757	-3.220995	26408.997742
HLA A*3301	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.619280	1.398016	-3.221264	41617.900929
HLA A*0101	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.369518	1.148177	-3.221341	23416.294361
HLA B*3901	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.381414	1.159900	-3.221514	24066.537471
HLA B*5701	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.403515	1.181912	-3.221604	25323.003607
HLA A*2402	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.145121	0.923460	-3.221661	13967.581233
HLA B*4601	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.403743	1.181912	-3.221831	25336.295575
HLA A*0212	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.344943	1.123062	-3.221881	22128.020023
HLA B*5401	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.544677	1.322784	-3.221893	35049.108413
HLA A*3002	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.186956	0.965021	-3.221935	15379.992927
HLA A*3201	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.605489	1.383422	-3.222067	40317.045155
HLA A*3101	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.189898	0.967578	-3.222319	15484.517990
HLA A*1101	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.432820	1.210192	-3.222629	27090.707256
HLA B*4501	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.655006	1.432365	-3.222641	45186.264585
HLA A*0101	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.345861	1.123062	-3.222799	22174.876226
HLA A*2402	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.464604	1.241782	-3.222822	29147.692313
HLA B*1509	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.290000	1.067176	-3.222823	19498.439217
HLA B*5101	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.043877	0.821048	-3.222829	11063.109172
HLA A*0203	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.371092	1.148177	-3.222915	23501.323670
HLA A*0212	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.385551	1.162617	-3.222934	24296.910534
HLA A*0202	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-3.888454	0.665274	-3.223180	7734.888653
HLA A*6801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.371499	1.148177	-3.223321	23523.329110
HLA A*2902	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.328212	1.104589	-3.223623	21291.775241
HLA A*2601	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.290867	1.067176	-3.223690	19537.401835
HLA B*4801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.361391	1.137355	-3.224036	22982.184152
HLA B*3901	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.097027	0.872828	-3.224199	12503.374744
HLA A*2403	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.341651	1.117129	-3.224522	21960.940094
HLA B*1801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.073467	0.848752	-3.224715	11843.133156
HLA A*2501	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.218045	0.993286	-3.224758	16521.311563
HLA B*4403	1:337-345	9	VGDFTVRLR	1.013882	0.418483	-4.657144	1.432365	-3.224779	45409.264991
HLA B*0702	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.459019	1.234192	-3.224827	28775.272864
HLA B*5301	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.608325	1.383422	-3.224903	40581.166206
HLA A*2501	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.409347	1.184382	-3.224965	25665.317349
HLA B*4801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.409354	1.184382	-3.224972	25665.733892
HLA A*0212	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.334501	1.109528	-3.224973	21602.372194
HLA A*0201	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.279166	1.054023	-3.225143	19018.067025
HLA B*7301	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.538998	1.313812	-3.225186	34593.799940
HLA B*2705	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.409739	1.184382	-3.225357	25688.515195
HLA A*2301	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.326062	1.100571	-3.225491	21186.640346
HLA B*4601	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.330134	1.104589	-3.225545	21386.206295
HLA B*1501	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.180439	0.954860	-3.225579	15150.908115
HLA B*1517	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.335885	1.109528	-3.226357	21671.316311
HLA B*2705	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.363842	1.137355	-3.226487	23112.227999
HLA A*3101	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.381813	1.155314	-3.226499	24088.681193
HLA B*4601	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.403226	1.176703	-3.226523	25306.158871
HLA A*2902	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.374727	1.148177	-3.226550	23698.833902
HLA A*1101	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.454205	1.227496	-3.226709	28458.064265
HLA B*4403	1:452-460	9	RVAATGTTV	1.107071	0.312844	-4.646710	1.419915	-3.226796	44331.294122
HLA B*3801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.531886	1.305053	-3.226834	34031.914261
HLA A*0201	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.227179	1.000328	-3.226851	16872.495423
HLA A*6901	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.336395	1.109528	-3.226867	21696.772204
HLA B*3501	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.408877	1.181912	-3.226965	25637.563062
HLA B*1501	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.411367	1.184382	-3.226985	25785.003562

HLA A*3002	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.277160	1.050133	-3.227027	18930.405349
HLA A*2902	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.339926	1.112802	-3.227124	21873.909214
HLA B*4001	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.389604	1.162401	-3.227203	24524.712006
HLA A*2601	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.394629	1.167129	-3.227500	24810.154261
HLA A*2902	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.195348	0.967687	-3.227661	15680.088017
HLA A*2301	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.469454	1.241782	-3.227672	29474.979617
HLA A*2403	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-3.103200	-0.124662	-3.227861	1268.235165
HLA B*1517	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.191646	0.963515	-3.228130	15546.968113
HLA B*4501	1:233-241	9	IRIGVAERI	1.016372	0.381644	-4.626188	1.398016	-3.228172	42285.128815
HLA A*3201	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.404998	1.176703	-3.228294	25409.594938
HLA B*4002	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.320388	1.091927	-3.228461	20911.639721
HLA A*0201	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.395623	1.167129	-3.228494	24866.994410
HLA B*1501	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.388406	1.159900	-3.228506	24457.140519
HLA A*2602	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.566020	1.337377	-3.228643	36814.566974
HLA A*2403	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.143726	0.915076	-3.228649	13922.768812
HLA B*5801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.341541	1.112802	-3.228739	21955.356910
HLA B*1509	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.282857	1.054023	-3.228835	19180.389162
HLA B*7301	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.566238	1.337377	-3.228861	36833.093768
HLA A*2603	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.649377	1.420375	-3.229002	44604.335616
HLA B*0802	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.439364	1.210192	-3.229172	27501.960820
HLA A*0219	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.413026	1.183813	-3.229213	25883.674645
HLA A*2601	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.366708	1.137355	-3.229353	23265.274704
HLA B*3801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.493937	1.264555	-3.229382	31184.407481
HLA A*6901	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-3.943451	0.714055	-3.229396	8779.116479
HLA A*2601	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.384924	1.155314	-3.229609	24261.840429
HLA A*2902	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.352759	1.123062	-3.229697	22529.901466
HLA B*1801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.076465	0.846543	-3.229922	11925.169347
HLA B*1801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.460765	1.230828	-3.229937	28891.169213
HLA A*0203	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.406978	1.176703	-3.230275	25525.740968
HLA A*0206	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.073913	0.843615	-3.230298	11855.312721
HLA A*0101	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.343105	1.112802	-3.230303	22034.604436
HLA B*5301	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.568144	1.337733	-3.230410	36995.051051
HLA A*2902	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.325437	1.094888	-3.230549	21156.174050
HLA B*1503	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.322531	1.091927	-3.230604	21015.068905
HLA A*2601	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.390595	1.159900	-3.230695	24580.765227
HLA B*1501	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.325663	1.094888	-3.230775	21167.164349
HLA B*1503	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.495483	1.264555	-3.230928	31295.612647
HLA B*5301	1:229-237	9	HQALIRIGV	1.172366	0.156389	-4.560233	1.328755	-3.231478	36327.282812
HLA B*4403	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.536679	1.305053	-3.231626	34409.576523
HLA A*0216	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.413578	1.181912	-3.231666	25916.602107
HLA A*2602	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.557052	1.325261	-3.231791	36062.158036
HLA A*0219	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.391819	1.159900	-3.231920	24650.145127
HLA A*3301	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.618688	1.386690	-3.231998	41561.202232
HLA A*2603	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.294180	1.062125	-3.232054	19687.001881
HLA B*0702	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.433177	1.200757	-3.232420	27112.993192
HLA B*4501	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.652864	1.420375	-3.232488	44963.872811
HLA B*4403	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.571205	1.338560	-3.232645	37256.753629
HLA B*1801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.502130	1.269415	-3.232715	31778.262698
HLA B*5401	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.533463	1.300706	-3.232757	34155.675815
HLA A*6801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-3.681098	0.448098	-3.233000	4798.416236
HLA B*5101	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.474881	1.241782	-3.233099	29845.635025
HLA B*1517	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.434049	1.200757	-3.233292	27167.465483
HLA B*0702	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.400487	1.167129	-3.233357	25147.031783
HLA B*3901	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.497943	1.264555	-3.233388	31473.378787
HLA B*4002	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.556196	1.322784	-3.233413	35991.214321
HLA B*0801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.388941	1.155314	-3.233627	24487.325907
HLA B*1517	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-3.856384	0.622672	-3.233712	7184.285720
HLA A*2603	1:265-273	9	SNLFAHRDR	0.804463	0.587397	-4.625793	1.391860	-3.233933	42246.714954
HLA A*1101	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.284302	1.050133	-3.234169	19244.310162
HLA B*1801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.498888	1.264555	-3.234332	31541.900801
HLA B*5801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.357472	1.123062	-3.234411	22775.732808
HLA A*0203	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.255025	1.020365	-3.234660	17989.761895
HLA B*5401	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.534638	1.299885	-3.234753	34248.190091
HLA B*1503	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.026646	0.791821	-3.234825	10632.761564
HLA A*1101	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.397512	1.162617	-3.234895	24975.390233

HLA A*0201	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.390290	1.155314	-3.234976	24563.484006
HLA B*4402	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.397696	1.162401	-3.235295	24985.931356
HLA B*5301	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.436182	1.200757	-3.235425	27301.245252
HLA A*8001	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.397909	1.162401	-3.235509	24998.234956
HLA B*4501	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.558407	1.322784	-3.235624	36174.902154
HLA B*5701	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.398393	1.162617	-3.235776	25026.109448
HLA A*1101	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.436549	1.200757	-3.235792	27324.295664
HLA A*8001	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.417781	1.181912	-3.235870	26168.648262
HLA A*0203	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.330855	1.094888	-3.235967	21421.754788
HLA A*3301	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.120015	0.883995	-3.236020	13183.010837
HLA A*2602	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.563595	1.327486	-3.236109	36609.603729
HLA A*0101	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.340817	1.104589	-3.236228	21918.804349
HLA B*4801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.403377	1.167129	-3.236247	25314.922213
HLA A*2501	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.026604	0.790220	-3.236384	10631.726217
HLA B*5701	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.413167	1.176703	-3.236464	25892.077677
HLA B*5401	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.564697	1.328104	-3.236593	36702.608945
HLA A*2603	1:437-445	9	IEGLALKPR	0.838298	0.545124	-4.620145	1.383422	-3.236723	41700.838008
HLA A*0250	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.537584	1.300814	-3.236770	34481.319728
HLA A*2402	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.537650	1.300814	-3.236835	34486.543247
HLA B*2705	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.104832	0.867880	-3.236952	12730.112363
HLA B*5101	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.464487	1.227496	-3.236990	29139.809090
HLA A*2601	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.399667	1.162617	-3.237050	25099.597690
HLA A*6802	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.385452	1.148177	-3.237275	24291.390530
HLA B*4501	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.264515	1.027215	-3.237300	18387.173970
HLA B*4001	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.392816	1.155314	-3.237501	24706.752355
HLA A*8001	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.414281	1.176703	-3.237577	25958.557608
HLA B*4601	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.397717	1.159900	-3.237817	24987.147926
HLA A*0212	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.398236	1.159900	-3.238336	25017.040064
HLA B*4001	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.342936	1.104589	-3.238347	22026.023364
HLA A*0219	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.059482	0.821048	-3.238434	11467.862510
HLA B*1503	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.287279	1.048747	-3.238532	19376.670107
HLA B*3501	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.306533	1.067986	-3.238547	20255.043254
HLA B*1801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.401189	1.162617	-3.238572	25187.741453
HLA A*3101	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.361739	1.123062	-3.238677	23000.592519
HLA B*5301	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.566292	1.327486	-3.238806	36837.677101
HLA B*5801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.354423	1.115540	-3.238883	22616.361002
HLA B*5801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.298637	1.059725	-3.238912	19890.081188
HLA B*1502	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.561767	1.322784	-3.238984	36455.841607
HLA A*2602	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.356293	1.117129	-3.239164	22713.963199
HLA A*3001	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.301987	1.062587	-3.239400	20044.116647
HLA A*3002	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.440536	1.200757	-3.239779	27576.303617
HLA B*1509	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.402528	1.162617	-3.239911	25265.531176
HLA A*3001	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.226991	0.986777	-3.240215	16865.194736
HLA A*2403	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.422422	1.181912	-3.240510	26449.747027
HLA A*6801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.204027	0.963515	-3.240512	15996.592947
HLA B*2705	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.474944	1.234192	-3.240752	29849.994806
HLA A*0206	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-3.622478	0.381582	-3.240896	4192.550158
HLA B*3501	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.463392	1.222401	-3.240991	29066.439909
HLA B*3801	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.509486	1.268289	-3.241197	32321.119014
HLA B*5401	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.475381	1.234017	-3.241364	29880.046163
HLA B*3501	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.119780	0.878392	-3.241388	13175.880903
HLA A*3001	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.230426	0.989026	-3.241400	16999.114817
HLA A*6802	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.425786	1.184382	-3.241404	26655.447942
HLA B*0802	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.389613	1.148177	-3.241436	24525.242716
HLA A*3301	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.397056	1.155314	-3.241742	24949.191850
HLA A*0250	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.510081	1.268289	-3.241792	32365.387280
HLA B*2705	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.359101	1.117129	-3.241972	22861.280503
HLA A*0301	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.365183	1.123062	-3.242122	23183.733135
HLA A*0212	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.337476	1.094888	-3.242588	21750.832923
HLA B*3901	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.233276	0.990658	-3.242618	17111.033146
HLA A*0203	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.269855	1.027215	-3.242641	18614.670990
HLA A*0301	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.334748	1.091927	-3.242821	21614.646656
HLA B*5401	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.424769	1.181912	-3.242857	26593.081110
HLA A*3301	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.405259	1.162401	-3.242858	25424.857924
HLA B*5701	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.427318	1.184382	-3.242936	26749.634322

HLA B*4801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.406079	1.162617	-3.243461	25472.906705
HLA A*0201	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.391857	1.148177	-3.243680	24652.278892
HLA A*2403	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.311700	1.067986	-3.243713	20497.443239
HLA B*5801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.311728	1.067986	-3.243741	20498.773949
HLA B*5801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.348434	1.104589	-3.243845	22306.626239
HLA B*4001	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.367007	1.123062	-3.243945	23281.264741
HLA A*2602	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.294079	1.050133	-3.243945	19682.422721
HLA A*3001	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-3.547755	0.303652	-3.244103	3529.841836
HLA A*3101	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.361495	1.117129	-3.244366	22987.655371
HLA B*1509	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.132232	0.887847	-3.244385	13559.133324
HLA A*0219	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.426329	1.181912	-3.244417	26688.779662
HLA A*0219	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.199629	0.955018	-3.244611	15835.408014
HLA A*3001	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.199756	0.954860	-3.244896	15840.034751
HLA B*4402	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.421785	1.176703	-3.245081	26410.997994
HLA B*4801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.400513	1.155314	-3.245198	25148.528297
HLA A*2501	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.472846	1.227496	-3.245350	29706.136328
HLA B*0702	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.382748	1.137355	-3.245393	24140.603274
HLA A*6801	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.568193	1.322784	-3.245409	36999.254211
HLA A*2402	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.346178	1.100571	-3.245607	22191.077230
HLA B*5301	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.546679	1.300706	-3.245973	35211.030540
HLA A*3301	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.584637	1.338560	-3.246077	38427.047365
HLA B*0801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.346808	1.100571	-3.246237	22223.274304
HLA A*3001	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.294997	1.048747	-3.246250	19724.100357
HLA A*8001	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.413503	1.167129	-3.246373	25912.115905
HLA B*4601	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.214158	0.967687	-3.246471	16374.139012
HLA A*0202	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.547327	1.300814	-3.246513	35263.644435
HLA B*4001	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.394820	1.148177	-3.246642	24821.028479
HLA A*3002	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.022351	0.775701	-3.246650	10528.129457
HLA A*2603	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.584524	1.337733	-3.246791	38417.070129
HLA A*0206	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.395193	1.148177	-3.247016	24842.388027
HLA B*4501	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.633741	1.386690	-3.247051	43027.018396
HLA A*2603	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.631782	1.384650	-3.247132	42833.324337
HLA A*3101	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.314954	1.067176	-3.247777	20651.601168
HLA A*2902	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.632407	0.384545	-3.247863	4289.505121
HLA B*1502	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.586754	1.338560	-3.248194	38614.809945
HLA B*3801	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.517745	1.269415	-3.248330	32941.610528
HLA B*5801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.357891	1.109528	-3.248362	22797.675497
HLA B*0802	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.432877	1.183813	-3.249064	27094.224870
HLA A*0203	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.433518	1.184382	-3.249136	27134.269887
HLA B*4402	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.366292	1.117129	-3.249163	23243.007694
HLA B*5801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.354371	1.105060	-3.249311	22613.669418
HLA A*8001	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.409274	1.159900	-3.249374	25661.013468
HLA A*2501	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.366551	1.117129	-3.249422	23256.843441
HLA A*1101	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.483644	1.234192	-3.249452	30454.004169
HLA A*3101	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.317468	1.067986	-3.249481	20771.491304
HLA B*3901	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.459783	1.210192	-3.249591	28825.910453
HLA A*3301	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.426371	1.176703	-3.249668	26691.378689
HLA B*4402	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.365552	1.115540	-3.250012	23203.432664
HLA B*1517	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.484213	1.234192	-3.250021	30493.900454
HLA A*0212	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.417154	1.167129	-3.250024	26130.876495
HLA A*0201	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.270403	1.020365	-3.250038	18638.149655
HLA A*2501	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.432007	1.181912	-3.250096	27040.045713
HLA B*4601	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.405423	1.155314	-3.250109	25434.487944
HLA A*6901	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.350779	1.100571	-3.250207	22427.386965
HLA A*2602	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.573021	1.322784	-3.250238	37412.881797
HLA B*5701	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.410197	1.159900	-3.250297	25715.629038
HLA B*4601	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.417633	1.167129	-3.250504	26159.730904
HLA B*5801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.250921	1.000328	-3.250593	17820.540205
HLA A*3301	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.388248	1.137355	-3.250893	24448.277327
HLA B*0801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-3.916375	0.665274	-3.251101	8248.506975
HLA A*2402	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.485165	1.234017	-3.251148	30560.785992
HLA A*0216	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.427875	1.176703	-3.251171	26783.953194
HLA B*5401	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.551998	1.300814	-3.251184	35644.946731
HLA B*5301	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.551098	1.299885	-3.251213	35571.167307
HLA A*0203	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.313871	1.062587	-3.251284	20600.161095

HLA B*4801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.399514	1.148177	-3.251337	25090.773149
HLA B*0801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.313495	1.062125	-3.251369	20582.337676
HLA A*0301	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.364215	1.112802	-3.251413	23132.117052
HLA B*4402	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.436011	1.184382	-3.251629	27290.465520
HLA A*3001	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.270941	1.019055	-3.251885	18661.254108
HLA A*2902	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.428603	1.176703	-3.251900	26828.909328
HLA A*0301	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.356580	1.104589	-3.251990	22728.959510
HLA A*0301	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.367589	1.115540	-3.252049	23312.521071
HLA B*0802	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.434061	1.181912	-3.252149	27168.200358
HLA A*2601	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.364979	1.112802	-3.252177	23172.824038
HLA B*3801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.486393	1.234192	-3.252201	30647.376265
HLA A*0211	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.136264	0.883995	-3.252269	13685.593854
HLA B*1517	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.428998	1.176703	-3.252294	26853.304171
HLA A*2602	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.590175	1.337733	-3.252441	38920.172085
HLA B*0802	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.419760	1.167129	-3.252630	26288.121671
HLA A*3001	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.028450	0.775701	-3.252750	10677.030407
HLA B*2705	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.306839	1.054023	-3.252816	20269.293344
HLA A*3101	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.167380	0.914477	-3.252903	14702.128922
HLA B*1503	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.487375	1.234192	-3.253183	30716.758627
HLA A*3101	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.413174	1.159900	-3.253274	25892.497900
HLA A*2601	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.315468	1.062125	-3.253343	20676.082977
HLA B*5701	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.420549	1.167129	-3.253419	26335.949643
HLA B*4501	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-3.384457	0.131008	-3.253449	2423.575985
HLA A*0212	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.401666	1.148177	-3.253489	25215.418014
HLA B*3801	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.553464	1.299885	-3.253579	35765.479233
HLA B*1509	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.354258	1.100571	-3.253687	22607.797983
HLA A*0250	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.313429	1.059725	-3.253704	20579.220163
HLA B*0702	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.358377	1.104589	-3.253788	22823.219707
HLA B*4601	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.303984	1.050133	-3.253851	20136.499874
HLA B*3501	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-3.994547	0.740545	-3.254002	9875.234357
HLA A*3001	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-3.937972	0.683810	-3.254162	8669.056075
HLA A*2403	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.377398	1.123062	-3.254337	23845.055718
HLA A*0301	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.322110	1.067176	-3.254934	20994.728389
HLA B*0803	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.422156	1.167129	-3.255027	26433.582776
HLA B*5801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.355612	1.100571	-3.255040	22678.355931
HLA A*6801	1:462-470	9	PPLFESLEL	1.313352	0.107023	-4.675508	1.420375	-3.255133	47370.508544
HLA B*1502	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.556077	1.300814	-3.255262	35981.285558
HLA A*2402	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.482994	1.227496	-3.255497	30408.401824
HLA A*6802	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.439650	1.183813	-3.255837	27520.118283
HLA B*0801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.365501	1.109528	-3.255972	23200.671212
HLA B*1503	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-3.796326	0.540290	-3.256036	6256.422372
HLA B*4002	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.306204	1.050133	-3.256071	20239.708206
HLA A*3002	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.483649	1.227496	-3.256153	30454.333677
HLA B*1509	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.411489	1.155314	-3.256175	25792.258271
HLA A*2902	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.356772	1.100571	-3.256201	22739.044561
HLA A*3301	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.247030	0.990658	-3.256372	17661.602974
HLA B*5801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.351371	1.094888	-3.256483	22457.982895
HLA B*1801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.440299	1.183813	-3.256486	27561.240073
HLA A*0212	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.211607	0.955018	-3.256589	16278.220702
HLA A*2501	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.319253	1.062587	-3.256667	20857.069425
HLA B*0802	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.419299	1.162617	-3.256682	26260.262142
HLA A*2603	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.247359	0.990658	-3.256701	17674.984665
HLA B*1509	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.440578	1.183813	-3.256765	27578.989073
HLA B*3901	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.324885	1.067986	-3.256899	21129.294789
HLA A*2603	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.579687	1.322784	-3.256903	37991.518357
HLA B*4402	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.440849	1.183813	-3.257036	27596.152328
HLA B*5301	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.498820	1.241782	-3.257038	31536.952682
HLA A*0212	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.433934	1.176703	-3.257231	27160.264761
HLA B*4801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.417323	1.159900	-3.257423	26141.056768
HLA A*0203	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.012394	0.754283	-3.258111	10289.495914
HLA B*3901	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.362714	1.104589	-3.258125	23052.289252
HLA B*4801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.370930	1.112802	-3.258128	23492.552678
HLA B*7301	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.565973	1.307776	-3.258197	36810.583935
HLA B*2705	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.458980	1.200757	-3.258222	28772.626578
HLA A*2403	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.442639	1.184382	-3.258257	27710.147729

HLA A*2501	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.406440	1.148177	-3.258263	25494.137611
HLA B*5801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.350295	1.091927	-3.258368	22402.406974
HLA A*3001	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.278960	1.020365	-3.258595	19009.015244
HLA A*3301	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.421338	1.162617	-3.258721	26383.864633
HLA B*4001	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.368365	1.109528	-3.258836	23354.177235
HLA A*6802	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.418794	1.159900	-3.258894	26229.735900
HLA A*8001	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.396380	1.137355	-3.259025	24910.350076
HLA A*0202	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-3.707173	0.448098	-3.259074	5095.332182
HLA B*0702	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.414485	1.155314	-3.259171	25970.778147
HLA A*0202	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-3.623832	0.364577	-3.259254	4205.634924
HLA B*1501	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.414633	1.155314	-3.259319	25979.631095
HLA A*0211	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.246119	0.986777	-3.259342	17624.569497
HLA B*0802	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.486847	1.227496	-3.259350	30679.392165
HLA B*4001	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.376731	1.117129	-3.259602	23808.448101
HLA B*7301	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.493649	1.234017	-3.259632	31163.663768
HLA B*4801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.309832	1.050133	-3.259699	20409.475871
HLA A*0212	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.444267	1.184382	-3.259885	27814.229529
HLA B*0802	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.460826	1.200757	-3.260069	28895.233247
HLA B*0702	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.444713	1.184382	-3.260332	27842.833888
HLA B*2705	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.423054	1.162617	-3.260436	26488.266311
HLA A*0206	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.437190	1.176703	-3.260487	27364.680724
HLA A*2602	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.518076	1.257536	-3.260540	32966.747789
HLA B*0802	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.416024	1.155314	-3.260710	26062.968253
HLA A*0206	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.370322	1.109528	-3.260793	23459.658873
HLA B*4403	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.518377	1.257536	-3.260841	32989.584041
HLA A*0250	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.586199	1.325261	-3.260939	38565.540569
HLA A*0201	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.310001	1.048747	-3.261254	20417.427155
HLA B*0803	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.371280	1.109528	-3.261752	23511.497036
HLA B*4403	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.495953	1.234192	-3.261761	31329.492132
HLA A*0212	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.377638	1.115540	-3.262098	23858.217258
HLA A*6802	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.282611	1.020365	-3.262246	19169.497059
HLA B*4402	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.417612	1.155314	-3.262298	26158.457244
HLA A*1101	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.399843	1.137355	-3.262488	25109.783709
HLA A*0203	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.372077	1.109528	-3.262549	23554.655566
HLA B*4501	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.600336	1.337377	-3.262960	39841.554453
HLA A*0203	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.249206	0.986192	-3.263013	17750.301773
HLA B*4801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.425452	1.162401	-3.263052	26634.978976
HLA A*6901	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.325743	1.062587	-3.263156	21171.058116
HLA A*0219	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.358079	1.094888	-3.263190	22807.544264
HLA A*0301	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.358095	1.094888	-3.263207	22808.407985
HLA A*2902	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.177793	0.914477	-3.263316	15058.896356
HLA A*0101	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.358732	1.094888	-3.263844	22841.871458
HLA A*0212	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.326316	1.062125	-3.264191	21199.022639
HLA A*2602	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.565103	1.300706	-3.264398	36736.975393
HLA B*1801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.431556	1.167129	-3.264427	27011.973834
HLA B*7301	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.041890	0.777400	-3.264489	11012.591600
HLA A*0301	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.369622	1.105060	-3.264561	23421.868925
HLA A*0301	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.365155	1.100571	-3.264584	23182.228127
HLA B*5301	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.578573	1.313812	-3.264761	37894.221984
HLA A*2402	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.133590	0.868794	-3.264796	13601.597951
HLA B*3901	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.465650	1.200757	-3.264892	29217.947018
HLA A*0216	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.359784	1.094888	-3.264896	22897.298852
HLA A*0202	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.590428	1.325261	-3.265168	38942.918541
HLA B*5101	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.388244	1.123062	-3.265182	24448.012804
HLA B*1503	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.333174	1.067986	-3.265188	21536.443466
HLA B*4801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.374809	1.109528	-3.265281	23703.321609
HLA A*2501	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.149308	0.883995	-3.265313	14102.885765
HLA A*2403	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.378153	1.112802	-3.265351	23886.500407
HLA A*2902	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.432604	1.167129	-3.265475	27077.227300
HLA B*4501	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.573256	1.307776	-3.265480	37433.127227
HLA B*5301	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.602857	1.337377	-3.265481	40073.499696
HLA A*3001	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.055018	0.789406	-3.265613	11350.590506
HLA A*2403	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.370301	1.104589	-3.265711	23458.516673
HLA B*3901	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.428382	1.162617	-3.265765	26815.269502
HLA A*2501	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.378575	1.112802	-3.265774	23909.771933

HLA A*6801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.233368	0.967578	-3.265790	17114.643710
HLA B*1501	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.375472	1.109528	-3.265944	23739.510727
HLA A*3201	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.534363	1.268289	-3.266074	34226.519318
HLA A*6901	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.921422	0.655319	-3.266103	8344.917352
HLA B*5301	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.594289	1.328104	-3.266185	39290.603543
HLA A*2403	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.433596	1.167129	-3.266466	27139.114502
HLA B*4002	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.594021	1.327486	-3.266534	39266.379424
HLA A*3001	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.036058	0.769461	-3.266597	10865.710056
HLA B*1509	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.531167	1.264555	-3.266612	33975.623548
HLA A*0206	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.371687	1.105060	-3.266627	23533.512001
HLA B*0803	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.443492	1.176703	-3.266788	27764.618100
HLA B*4001	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.382417	1.115540	-3.266877	24122.195979
HLA B*4501	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.605594	1.338560	-3.267035	40326.861334
HLA B*3501	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.368036	1.100571	-3.267464	23336.495840
HLA B*5301	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-3.953911	0.686428	-3.267482	8993.126832
HLA B*7301	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.536980	1.269415	-3.267565	34433.412230
HLA B*3801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.377297	1.109528	-3.267769	23839.509402
HLA B*1509	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.383676	1.115540	-3.268136	24192.244636
HLA A*1101	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.452699	1.184382	-3.268317	28359.550037
HLA A*0203	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.435680	1.167129	-3.268550	27269.656445
HLA A*2403	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.318741	1.050133	-3.268608	20832.486018
HLA A*3101	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.373212	1.104589	-3.268622	23616.283808
HLA B*1801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.152743	0.883995	-3.268748	14214.871404
HLA B*7301	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.596859	1.328104	-3.268755	39523.831276
HLA B*3501	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.203285	0.934152	-3.269133	15969.269733
HLA B*0801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.255331	0.986192	-3.269139	18002.418285
HLA A*0201	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.364049	1.094888	-3.269160	23123.233662
HLA B*5701	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.424517	1.155314	-3.269203	26577.691943
HLA B*0801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.232766	0.963515	-3.269251	17090.957504
HLA B*1801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.406898	1.137355	-3.269543	25521.046291
HLA B*4403	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.583542	1.313812	-3.269730	38330.294466
HLA B*4403	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.470671	1.200757	-3.269913	29557.693860
HLA A*0250	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.583815	1.313812	-3.270003	38354.356082
HLA A*3001	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.227771	0.957710	-3.270061	16895.513248
HLA B*2705	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.432654	1.162401	-3.270253	27080.303656
HLA B*1509	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.446999	1.176703	-3.270296	27989.780023
HLA A*3201	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.501258	1.230828	-3.270430	31714.545500
HLA B*5801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.353948	1.083182	-3.270767	22591.659396
HLA A*0201	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.380427	1.109528	-3.270899	24011.916682
HLA A*3201	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.596175	1.325261	-3.270915	39461.658739
HLA B*4001	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.298256	1.027215	-3.271041	19872.657117
HLA A*0202	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.271472	1.000328	-3.271144	18684.083962
HLA A*8001	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.426510	1.155314	-3.271195	26699.899495
HLA A*0206	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.386745	1.115540	-3.271205	24363.775717
HLA B*0702	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.433650	1.162401	-3.271249	27142.491563
HLA A*0219	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.426667	1.155314	-3.271353	26709.578963
HLA B*4002	1:420-428	9	VTDWTAPLI	1.142761	0.195799	-4.609964	1.338560	-3.271405	40734.694541
HLA B*1502	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.585255	1.313812	-3.271443	38481.760314
HLA B*4403	1:148-156	9	LAEGRQPVV	1.309716	0.074934	-4.656137	1.384650	-3.271487	45303.999441
HLA B*3501	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.185965	0.914377	-3.271588	15344.920865
HLA B*2705	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.292187	1.020365	-3.271822	19596.892917
HLA A*0211	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.431810	1.159900	-3.271910	27027.760678
HLA B*1517	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.454010	1.181912	-3.272099	28445.288871
HLA B*5401	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.434803	1.162617	-3.272186	27214.684796
HLA A*0101	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.387734	1.115540	-3.272194	24419.328998
HLA B*3901	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.456080	1.183813	-3.272267	28581.185906
HLA A*0203	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.321039	1.048747	-3.272292	20943.000126
HLA A*0219	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.340413	1.067986	-3.272426	21898.418367
HLA B*4002	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.580483	1.307776	-3.272707	38061.256923
HLA A*2902	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.236293	0.963515	-3.272778	17230.305246
HLA A*1101	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.454760	1.181912	-3.272848	28494.420843
HLA B*4402	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.421092	1.148177	-3.272914	26368.881842
HLA B*4001	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.340918	1.067986	-3.272931	21923.903809
HLA A*6901	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.388718	1.115540	-3.273178	24474.744137
HLA B*1509	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.440477	1.167129	-3.273348	27572.574251

HLA B*1503	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.886199	0.612666	-3.273533	7694.821692
HLA B*4601	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.383082	1.109528	-3.273554	24159.155313
HLA B*0802	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.458080	1.184382	-3.273698	28713.071774
HLA A*3201	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.378350	1.104589	-3.273761	23897.357633
HLA B*0802	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.383347	1.109528	-3.273819	24173.928742
HLA A*2601	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.383533	1.109528	-3.274005	24184.262434
HLA A*2902	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.333743	1.059725	-3.274018	21564.657295
HLA A*0219	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.389599	1.115540	-3.274059	24524.446656
HLA A*0201	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.389672	1.115540	-3.274132	24528.559911
HLA A*2603	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.602456	1.328104	-3.274351	40036.445203
HLA A*2602	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.602735	1.328104	-3.274631	40062.228036
HLA A*2501	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.412070	1.137355	-3.274715	25826.746022
HLA A*8001	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.437399	1.162617	-3.274782	27377.859446
HLA A*0203	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.430128	1.155314	-3.274813	26923.271670
HLA B*4601	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.397928	1.123062	-3.274866	24999.316881
HLA A*2403	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.430281	1.155314	-3.274966	26932.740709
HLA A*0202	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.398135	1.123062	-3.275073	25011.221146
HLA A*0206	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.198544	0.923460	-3.275084	15795.878909
HLA A*1101	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.388053	1.112802	-3.275251	24437.302007
HLA A*2902	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.337387	1.062125	-3.275261	21746.361938
HLA A*0203	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.214238	0.938712	-3.275526	16377.151086
HLA A*6802	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.430924	1.155314	-3.275610	26972.692973
HLA A*2902	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.460074	1.184382	-3.275692	28845.254118
HLA B*3501	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.436361	1.159900	-3.276461	27312.472509
HLA A*0212	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.431836	1.155314	-3.276522	27029.369115
HLA B*7301	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.581836	1.305053	-3.276784	38180.044439
HLA A*2402	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.511295	1.234192	-3.277103	32456.037154
HLA A*2501	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.327401	1.050133	-3.277268	21252.073083
HLA B*3501	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.369401	1.091927	-3.277474	23409.961240
HLA A*2601	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.382734	1.105060	-3.277674	24139.819699
HLA A*3002	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.454447	1.176703	-3.277744	28473.926046
HLA B*3901	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.459872	1.181912	-3.277961	28831.836972
HLA A*2902	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.340603	1.062587	-3.278016	21908.016379
HLA A*3001	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.192562	0.914477	-3.278085	15579.804617
HLA B*0702	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.454859	1.176703	-3.278155	28500.895948
HLA A*0219	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.426597	1.148177	-3.278419	26705.244439
HLA B*4501	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.579177	1.300706	-3.278471	37946.944537
HLA B*7301	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.601368	1.322784	-3.278584	39936.288257
HLA A*2601	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.361828	1.083182	-3.278647	23005.321370
HLA B*1503	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.140930	0.862113	-3.278816	13833.425150
HLA B*1801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.391632	1.112802	-3.278830	24639.479071
HLA A*2603	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.463256	1.184382	-3.278874	29057.321059
HLA B*1801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.506411	1.227496	-3.278914	32093.044073
HLA A*3101	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.272395	0.993286	-3.279109	18723.850198
HLA B*4001	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.362547	1.083182	-3.279366	23043.436519
HLA B*5301	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.247002	0.967578	-3.279424	17660.456444
HLA B*3501	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.266308	0.986777	-3.279531	18463.228402
HLA B*5401	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.265819	0.986192	-3.279627	18442.464210
HLA A*8001	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.402773	1.123062	-3.279711	25279.750282
HLA A*3002	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.489908	1.210192	-3.279716	30896.417843
HLA B*1503	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.464191	1.184382	-3.279809	29119.952823
HLA B*5401	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.213966	0.934152	-3.279813	16366.876876
HLA A*3201	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.507370	1.227496	-3.279873	32163.959190
HLA B*0801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.402937	1.123062	-3.279875	25289.325341
HLA A*6801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-3.532827	0.252948	-3.279879	3410.567257
HLA B*0802	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.203445	0.923460	-3.279985	15975.145468
HLA A*0201	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.385241	1.105060	-3.280181	24279.566173
HLA B*3801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.502729	1.222401	-3.280328	31822.131754
HLA B*3501	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.329123	1.048747	-3.280376	21336.514403
HLA B*5701	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.342520	1.062125	-3.280395	22004.942432
HLA A*0201	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.287265	1.006851	-3.280414	19376.041163
HLA A*3301	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.585469	1.305053	-3.280416	38500.709545
HLA A*3301	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.607913	1.327486	-3.280427	40542.764955
HLA A*3101	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.396255	1.115540	-3.280715	24903.208701
HLA A*2601	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.396276	1.115540	-3.280736	24904.421243

HLA B*5401	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.538392	1.257536	-3.280856	34545.549276
HLA A*0219	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.340760	1.059725	-3.281036	21915.958655
HLA A*3101	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.364288	1.083182	-3.281107	23135.996785
HLA B*3501	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.375998	1.094888	-3.281110	23768.296064
HLA B*5801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.343256	1.062125	-3.281130	22042.234862
HLA A*6802	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.448268	1.167129	-3.281139	28071.667243
HLA A*0219	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.457880	1.176703	-3.281177	28699.871373
HLA B*4002	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.936628	0.655319	-3.281309	8642.271520
HLA A*0219	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.465762	1.184382	-3.281381	29225.535164
HLA A*3101	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.394726	1.112802	-3.281924	24815.657899
HLA A*8001	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.466432	1.184382	-3.282050	29270.630388
HLA B*3801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.465873	1.183813	-3.282060	29232.967134
HLA B*3501	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.458773	1.176703	-3.282069	28758.932046
HLA B*3501	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-3.663698	0.381582	-3.282116	4609.965041
HLA A*3201	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.596020	1.313812	-3.282208	39447.571363
HLA A*0101	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.365402	1.083182	-3.282220	23195.400262
HLA B*3901	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.430407	1.148177	-3.282230	26940.609828
HLA A*2301	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.539908	1.257536	-3.282371	34666.302327
HLA A*6801	1:152-160	9	RQPVVRLRM	1.135383	0.251307	-4.669240	1.386690	-3.282549	46691.692975
HLA A*0219	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.392202	1.109528	-3.282674	24671.891506
HLA B*4403	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.605503	1.322784	-3.282719	40318.353841
HLA B*1503	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.449861	1.167129	-3.282732	28174.820510
HLA B*7301	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.610239	1.327486	-3.282753	40760.486014
HLA A*0250	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-3.961706	0.678487	-3.283219	9156.011081
HLA B*0801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.366454	1.083182	-3.283273	23251.685518
HLA A*0201	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.383866	1.100571	-3.283295	24202.848025
HLA A*3001	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.250996	0.967687	-3.283309	17823.625501
HLA A*2902	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.443334	1.159900	-3.283434	27754.556289
HLA A*0216	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.664031	0.380458	-3.283573	4613.507796
HLA A*6901	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.366863	1.083182	-3.283682	23273.583116
HLA A*2602	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.597580	1.313812	-3.283769	39589.528417
HLA A*3301	1:37-45	9	TGGTFVFRI	1.297464	0.025320	-4.606584	1.322784	-3.283800	40418.812987
HLA A*8001	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.393448	1.109528	-3.283919	24742.733282
HLA A*0211	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.270264	0.986192	-3.284072	18632.201615
HLA B*3901	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.010237	0.726109	-3.284128	10238.522095
HLA A*0101	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-3.896795	0.612666	-3.284129	7884.873642
HLA A*0202	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.511627	1.227496	-3.284130	32480.803881
HLA B*0801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.274930	0.990658	-3.284272	18833.465992
HLA A*0301	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.367794	1.083182	-3.284612	23323.495933
HLA B*1501	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-3.880621	0.595974	-3.284646	7596.628408
HLA A*0203	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.208125	0.923460	-3.284665	16148.232572
HLA B*0803	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.469134	1.184382	-3.284752	29453.301527
HLA B*3501	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.469212	1.184382	-3.284830	29458.560186
HLA B*1509	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.394434	1.109528	-3.284906	24799.016487
HLA B*4001	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.397714	1.112802	-3.284912	24987.012749
HLA A*0250	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.285273	1.000328	-3.284945	19287.355490
HLA A*0202	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.168301	0.883265	-3.285036	14733.340465
HLA B*5701	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.402204	1.117129	-3.285075	25246.675861
HLA B*7301	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.610399	1.325261	-3.285138	40775.483433
HLA B*4501	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.610582	1.325261	-3.285322	40792.693149
HLA B*4601	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.386009	1.100571	-3.285438	24322.555559
HLA A*6901	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.390534	1.105060	-3.285474	24577.308010
HLA B*1801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.447958	1.162401	-3.285557	28051.628270
HLA A*6801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.220042	0.934152	-3.285889	16597.458199
HLA B*0702	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.399108	1.112802	-3.286306	25067.301408
HLA A*6901	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.381200	1.094888	-3.286312	24054.692432
HLA A*3101	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.898759	0.612321	-3.286438	7920.615065
HLA A*0250	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.513948	1.227496	-3.286452	32654.877613
HLA A*2603	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.587186	1.300706	-3.286480	38653.267021
HLA A*3101	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.387254	1.100571	-3.286683	24392.394268
HLA B*4001	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.340920	1.054023	-3.286897	21924.022416
HLA A*3201	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-3.990149	0.703210	-3.286940	9775.729481
HLA B*4501	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.528778	1.241782	-3.286996	33789.207803
HLA B*4501	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.600921	1.313812	-3.287109	39895.259677
HLA B*4801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.404368	1.117129	-3.287239	25372.781523

HLA B*5101	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.404596	1.117129	-3.287467	25386.099619
HLA A*0301	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.202571	0.915076	-3.287494	15943.028156
HLA A*0216	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.435715	1.148177	-3.287538	27271.869422
HLA B*1517	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.471946	1.184382	-3.287564	29644.649305
HLA A*0216	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.454800	1.167129	-3.287670	28497.041541
HLA A*0203	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.370998	1.083182	-3.287817	23496.238638
HLA B*4001	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.318896	1.031013	-3.287884	20839.925641
HLA B*1501	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.388467	1.100571	-3.287895	24460.580832
HLA A*2603	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.595701	1.307776	-3.287925	39418.558687
HLA A*2601	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.379889	1.091927	-3.287962	23982.187587
HLA B*0803	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.488827	1.200757	-3.288070	30819.626183
HLA A*0301	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.347886	1.059725	-3.288162	22278.526357
HLA B*5801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.355398	1.067176	-3.288221	22667.194126
HLA A*3301	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.203299	0.915076	-3.288223	15969.788093
HLA A*2301	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.515745	1.227496	-3.288249	32790.301991
HLA B*4402	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.338453	1.050133	-3.288320	21799.838598
HLA B*4002	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.168813	0.880484	-3.288329	14750.726566
HLA A*2603	1:361-369	9	AFAAAAELV	0.982214	0.345272	-4.615850	1.327486	-3.288363	41290.479275
HLA B*0803	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.498604	1.210192	-3.288412	31521.260337
HLA A*6901	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.256172	0.967687	-3.288485	18037.318079
HLA A*3002	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.510920	1.222401	-3.288519	32427.955938
HLA B*1501	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.404093	1.115540	-3.288553	25356.726724
HLA B*2705	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.401483	1.112802	-3.288681	25204.780074
HLA B*4601	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.404295	1.115540	-3.288755	25368.526698
HLA A*0219	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.455892	1.167129	-3.288763	28568.818899
HLA B*1801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.393889	1.105060	-3.288829	24767.910907
HLA A*3301	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.202928	0.914083	-3.288845	15956.143550
HLA B*5801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.351620	1.062587	-3.289033	22470.865079
HLA B*4001	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.137819	0.848752	-3.289067	13734.694580
HLA A*0216	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.275863	0.986777	-3.289086	18873.958584
HLA B*1501	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.394207	1.105060	-3.289147	24786.006387
HLA A*2301	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.523630	1.234192	-3.289438	33391.066316
HLA A*2601	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.352350	1.062587	-3.289764	22508.703582
HLA A*2603	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.603830	1.313812	-3.290018	40163.352661
HLA A*0203	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.163043	0.872828	-3.290215	14556.034538
HLA B*1801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.257838	0.967578	-3.290260	18106.635074
HLA A*2403	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.405895	1.115540	-3.290355	25462.160136
HLA A*3001	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-3.913274	0.622672	-3.290602	8189.813759
HLA A*2601	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.080835	0.790220	-3.290615	12045.770849
HLA B*4402	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.413752	1.123062	-3.290690	25926.979424
HLA B*3501	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.400240	1.109528	-3.290712	25132.751361
HLA B*4601	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.373966	1.083182	-3.290784	23657.330873
HLA B*1501	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.353431	1.062587	-3.290845	22564.787349
HLA B*5401	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.555541	1.264555	-3.290986	35936.931632
HLA B*5301	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.592108	1.300814	-3.291294	39093.844212
HLA B*3901	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.214812	0.923460	-3.291351	16398.783412
HLA B*3901	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.458846	1.167129	-3.291716	28763.755512
HLA B*0702	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.292194	1.000328	-3.291866	19597.210970
HLA A*2902	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.359249	1.067176	-3.292072	22869.073481
HLA B*2705	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.447509	1.155314	-3.292195	28022.657806
HLA A*2501	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.447585	1.155314	-3.292270	28027.509409
HLA A*2402	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.550245	1.257536	-3.292709	35501.381558
HLA B*4402	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.346735	1.054023	-3.292712	22219.547628
HLA B*1502	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.375921	1.083182	-3.292739	23764.053176
HLA A*0203	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.397860	1.105060	-3.292800	24995.395127
HLA A*0101	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.384773	1.091927	-3.292846	24253.441636
HLA A*2301	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.216597	0.923460	-3.293137	16466.346066
HLA B*1517	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.186702	0.893488	-3.293214	15371.009514
HLA A*0301	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.361210	1.067986	-3.293224	22972.612654
HLA A*3001	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.149529	0.856154	-3.293375	14110.059323
HLA B*3901	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.470257	1.176703	-3.293554	29529.564177
HLA A*0201	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.376755	1.083182	-3.293573	23809.736146
HLA B*4801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.385570	1.091927	-3.293643	24297.962106
HLA B*2705	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.409497	1.115540	-3.293957	25674.205065
HLA B*5101	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.475905	1.181912	-3.293994	29916.115361

HLA A*6801	1:384-392	9	KFFNDDQYV	0.976488	0.324218	-4.594770	1.300706	-3.294064	39334.202066
HLA A*8001	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.362108	1.067986	-3.294121	23020.136431
HLA B*4601	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.361485	1.067176	-3.294309	22987.157933
HLA A*3001	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.242080	0.947523	-3.294557	17461.427813
HLA A*0101	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.395193	1.100571	-3.294622	24842.388027
HLA A*2902	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.178742	0.883995	-3.294748	15091.845001
HLA A*2902	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.315170	1.020365	-3.294805	20661.882231
HLA A*3001	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.049258	0.754283	-3.294974	11201.018609
HLA B*3801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.326041	1.031013	-3.295028	21185.608815
HLA B*0801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.363041	1.067986	-3.295054	23069.630507
HLA A*0101	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.362559	1.067176	-3.295383	23044.059839
HLA B*1503	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.450806	1.155314	-3.295491	28236.161094
HLA B*4001	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.390741	1.094888	-3.295853	24589.011321
HLA A*3301	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-3.991582	0.695627	-3.295955	9808.042994
HLA A*2301	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.458679	1.162617	-3.296062	28752.709414
HLA B*2705	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.363515	1.067176	-3.296339	23094.854724
HLA B*4002	1:263-271	9	PQSNLFAHR	0.907950	0.405862	-4.610246	1.313812	-3.296435	40761.147549
HLA B*4501	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.244079	0.947523	-3.296556	17542.002340
HLA A*0101	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.358715	1.062125	-3.296590	22841.006471
HLA A*0206	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.202585	0.905846	-3.296739	15943.545664
HLA B*2705	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.364899	1.067986	-3.296913	23168.562108
HLA A*2603	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.519777	1.222401	-3.297376	33096.123822
HLA A*0212	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.347621	1.050133	-3.297488	22264.911267
HLA B*5401	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.414720	1.117129	-3.297591	25984.831851
HLA A*3301	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.635461	1.337733	-3.297728	43197.744880
HLA B*1502	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.566053	1.268289	-3.297764	36817.355358
HLA A*0201	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.389712	1.091927	-3.297785	24530.815860
HLA A*2501	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.465072	1.167129	-3.297942	29179.088681
HLA A*2603	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.623354	1.325261	-3.298094	42010.144855
HLA A*2402	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.421310	1.123062	-3.298248	26382.151883
HLA A*3002	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.562864	1.264555	-3.298309	36548.060753
HLA A*0216	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.413968	1.115540	-3.298428	25939.886747
HLA A*0101	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.358306	1.059725	-3.298581	22819.515875
HLA B*1509	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.480592	1.181912	-3.298681	30240.740527
HLA A*0101	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.403757	1.105060	-3.298697	25337.117988
HLA B*2705	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.408416	1.109528	-3.298888	25610.392980
HLA B*1503	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.358687	1.059725	-3.298962	22839.523711
HLA A*1101	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.366981	1.067986	-3.298994	23279.879342
HLA B*4002	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.568456	1.269415	-3.299041	37021.679133
HLA B*1801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.509254	1.210192	-3.299062	32303.813135
HLA A*0211	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.533273	1.234192	-3.299081	34140.712042
HLA B*7301	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.521560	1.222401	-3.299160	33232.299394
HLA A*2601	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.394134	1.094888	-3.299246	24781.849960
HLA B*4402	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.412060	1.112802	-3.299258	25826.187149
HLA A*6802	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.361852	1.062587	-3.299265	23006.565966
HLA A*2301	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.509512	1.210192	-3.299320	32323.042461
HLA A*2902	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.353384	1.054023	-3.299361	22562.346021
HLA B*5801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.348180	1.048747	-3.299433	22293.596997
HLA A*8001	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.404199	1.104589	-3.299610	25362.900444
HLA B*7301	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.600475	1.300814	-3.299661	39854.273248
HLA A*6802	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.400311	1.100571	-3.299739	25136.830654
HLA A*0216	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.359516	1.059725	-3.299791	22883.181815
HLA A*0216	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.484338	1.184382	-3.299956	30502.645044
HLA A*2501	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.462682	1.162617	-3.300065	29018.990323
HLA B*1509	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.383307	1.083182	-3.300126	24171.705614
HLA A*0101	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.350283	1.050133	-3.300150	22401.801009
HLA B*1509	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.484699	1.184382	-3.300317	30528.068086
HLA B*4402	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.401091	1.100571	-3.300519	25182.019062
HLA A*2501	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.463075	1.162401	-3.300674	29045.219420
HLA B*4801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.423789	1.123062	-3.300727	26533.156764
HLA B*3501	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.062664	0.761813	-3.300850	11552.172896
HLA B*1517	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.413966	1.112802	-3.301164	25939.746416
HLA A*0212	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.401739	1.100571	-3.301168	25219.647160
HLA B*4001	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.363771	1.062587	-3.301185	23108.477266
HLA B*0803	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.321701	1.020365	-3.301337	20974.974915

HLA A*2501	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.424677	1.123062	-3.301615	26587.470943
HLA B*5401	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.364284	1.062587	-3.301697	23135.746460
HLA A*0206	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.056123	0.754283	-3.301839	11379.487784
HLA B*0803	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.464776	1.162617	-3.302158	29159.205648
HLA A*2601	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.370517	1.067986	-3.302530	23470.195113
HLA B*4601	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.394505	1.091927	-3.302578	24803.041611
HLA A*0212	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.407686	1.105060	-3.302625	25567.340348
HLA B*3501	1:411-419	9	DAALAALTS	1.231227	-1.062772	-3.471139	0.168455	-3.302683	2958.956224
HLA A*2902	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.309707	1.006851	-3.302856	20403.624821
HLA A*3101	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.397785	1.094888	-3.302897	24991.068387
HLA B*0801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-3.853531	0.550534	-3.302997	7137.256769
HLA B*1801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.487483	1.184382	-3.303102	30724.403595
HLA A*0250	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-3.899252	0.595974	-3.303278	7929.618604
HLA B*4801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.386503	1.083182	-3.303321	24350.203550
HLA B*4403	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.603268	1.299885	-3.303384	40111.456469
HLA B*0803	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.365625	1.062125	-3.303500	23207.324358
HLA B*0801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.146888	0.843357	-3.303531	14024.520401
HLA B*1517	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.463455	1.159900	-3.303555	29070.685867
HLA B*2705	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.395520	1.091927	-3.303593	24861.075897
HLA B*4501	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.631751	1.328104	-3.303647	42830.312037
HLA A*2602	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.209521	0.905846	-3.303675	16200.207966
HLA A*6801	1:412-420	9	AALAALTSV	1.136579	0.168474	-4.608750	1.305053	-3.303697	40620.922337
HLA A*2602	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.488153	1.184382	-3.303771	30771.811583
HLA A*3002	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.371821	1.067986	-3.303834	23540.770001
HLA B*5701	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.217955	0.914083	-3.303872	16517.915530
HLA B*4601	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.398774	1.094888	-3.303886	25048.051995
HLA B*1801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.408534	1.104589	-3.303945	25617.321386
HLA B*0702	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.419649	1.115540	-3.304109	26281.438377
HLA B*0802	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.466707	1.162401	-3.304306	29289.163304
HLA A*2301	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.526718	1.222401	-3.304317	33629.275524
HLA B*5701	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.414020	1.109528	-3.304492	25942.974233
HLA B*4002	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.535646	1.230828	-3.304817	34327.767052
HLA B*5701	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.409539	1.104589	-3.304950	25676.705289
HLA A*0211	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.365031	1.059725	-3.305306	23175.582176
HLA B*1501	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.219821	0.914377	-3.305444	16589.020047
HLA B*5701	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.428634	1.123062	-3.305572	26830.796233
HLA B*1502	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.527993	1.222401	-3.305592	33728.209109
HLA A*6802	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.355764	1.050133	-3.305631	22686.332014
HLA A*3001	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.226348	0.920689	-3.305658	16840.213815
HLA A*2602	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.613564	1.307776	-3.305788	41073.704568
HLA A*0101	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.368395	1.062587	-3.305808	23355.819758
HLA A*0301	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.368414	1.062587	-3.305827	23356.830599
HLA B*5801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.360219	1.054023	-3.306196	22920.226615
HLA A*2601	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.406835	1.100571	-3.306264	25517.318780
HLA B*4402	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.389569	1.083182	-3.306387	24522.721947
HLA B*4801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.411128	1.104589	-3.306538	25770.779098
HLA B*4501	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.220808	0.914083	-3.306724	16626.755700
HLA A*2601	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.366734	1.059725	-3.307009	23266.659233
HLA B*3901	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.469458	1.162401	-3.307058	29475.298532
HLA A*0211	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.369805	1.062587	-3.307218	23431.754368
HLA B*7301	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-3.869560	0.562255	-3.307304	7405.587332
HLA A*2402	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.469926	1.162617	-3.307309	29507.047780
HLA B*5701	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.422985	1.115540	-3.307445	26484.110978
HLA B*1501	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.399415	1.091927	-3.307488	25085.072788
HLA A*0216	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.412605	1.105060	-3.307545	25858.621799
HLA A*2602	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.572218	1.264555	-3.307662	37343.725149
HLA A*2402	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.445082	1.137355	-3.307727	27866.492317
HLA B*4002	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-3.889488	0.581735	-3.307753	7753.322335
HLA B*5301	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.541902	1.234017	-3.307885	34825.890724
HLA B*3901	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.492368	1.184382	-3.307986	31071.916466
HLA B*1801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.467945	1.159900	-3.308045	29372.786196
HLA B*0801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.423709	1.115540	-3.308169	26528.276804
HLA B*5101	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.376184	1.067986	-3.308197	23778.456359
HLA B*4801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.423742	1.115540	-3.308202	26530.286091
HLA B*3501	1:323-331	9	KADALNAEH	0.661781	-0.194938	-3.775068	0.466843	-3.308224	5957.553074

HLA B*5701	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.421061	1.112802	-3.308259	26367.027421
HLA B*3501	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.431401	1.123062	-3.308339	27002.330858
HLA A*8001	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.421275	1.112802	-3.308473	26380.011102
HLA B*4601	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.370665	1.062125	-3.308539	23478.195659
HLA B*0801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.222650	0.914083	-3.308566	16697.425403
HLA B*7301	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.518849	1.210192	-3.308657	33025.476020
HLA B*0802	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.413289	1.104589	-3.308700	25899.362512
HLA B*2705	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.368435	1.059725	-3.308710	23357.967847
HLA B*5701	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.403649	1.094888	-3.308761	25330.813506
HLA B*5301	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.297901	0.989026	-3.308875	19856.429906
HLA B*7301	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.577201	1.268289	-3.308912	37774.688841
HLA A*0212	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.368813	1.059725	-3.309088	23378.321317
HLA B*4801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.371694	1.062587	-3.309107	23533.893945
HLA B*5101	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.485858	1.176703	-3.309154	30609.597418
HLA B*4001	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.409746	1.100571	-3.309175	25688.932115
HLA B*3801	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.519476	1.210192	-3.309285	33073.213821
HLA B*4002	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.469254	1.159900	-3.309354	29461.428942
HLA A*0202	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.543587	1.234192	-3.309395	34961.238872
HLA A*3301	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.302765	0.993286	-3.309479	20080.041267
HLA A*1101	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.469404	1.159900	-3.309504	29471.631224
HLA B*1509	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.017643	0.707963	-3.309679	10414.606095
HLA B*4601	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.414992	1.105060	-3.309932	26001.143676
HLA A*2602	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.540829	1.230828	-3.310000	34739.896348
HLA A*3001	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.178869	0.868794	-3.310075	15096.254486
HLA A*3201	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.567730	1.257536	-3.310194	36959.843329
HLA B*0803	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.472931	1.162401	-3.310530	29711.922340
HLA B*1801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.377817	1.067176	-3.310640	23868.028618
HLA A*3101	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.301357	0.990658	-3.310699	20015.076735
HLA A*6802	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.426256	1.115540	-3.310716	26684.304154
HLA A*3002	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.265779	0.955018	-3.310761	18440.768170
HLA A*6802	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.297116	0.986192	-3.310924	19820.583659
HLA B*4002	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.639030	1.328104	-3.310926	43554.190162
HLA B*1503	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.101792	0.790719	-3.311074	12641.307725
HLA B*0801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.360106	1.048747	-3.311359	22914.275585
HLA B*1501	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.379400	1.067986	-3.311414	23955.216641
HLA A*0212	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.394629	1.083182	-3.311448	24810.154261
HLA A*3002	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.378904	1.067176	-3.311728	23927.887683
HLA B*1501	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.338951	1.027215	-3.311737	21824.855099
HLA A*0211	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.764899	0.452989	-3.311910	5819.683265
HLA B*5101	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.366074	1.054023	-3.312051	23231.316620
HLA B*1501	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.366104	1.054023	-3.312081	23232.950503
HLA B*1801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.332523	1.020365	-3.312158	21504.194429
HLA B*7301	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.360907	1.048747	-3.312160	22956.586219
HLA B*3501	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.319223	1.006851	-3.312371	20855.602629
HLA A*0301	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.366447	1.054023	-3.312424	23251.308154
HLA A*8001	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.428105	1.115540	-3.312565	26798.156984
HLA A*3101	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.372345	1.059725	-3.312620	23569.186847
HLA A*6801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.374767	1.062125	-3.312642	23701.013539
HLA B*1501	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.299487	0.986777	-3.312710	19929.071689
HLA B*5101	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.497116	1.184382	-3.312734	31413.501660
HLA B*1502	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.513523	1.200757	-3.312765	32622.917936
HLA B*1503	1:322-330	9	KKADALNAE	1.083044	-0.624509	-3.771337	0.458535	-3.312802	5906.591524
HLA A*0201	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.375397	1.062587	-3.312810	23735.401383
HLA B*0802	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.472790	1.159900	-3.312890	29702.279612
HLA B*3501	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.480125	1.167129	-3.312995	30208.201833
HLA A*0203	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.260561	0.947523	-3.313038	18220.521454
HLA A*0219	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.363360	1.050133	-3.313227	23086.610116
HLA B*4402	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.340455	1.027215	-3.313240	21900.550895
HLA A*0211	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.495183	1.181912	-3.313271	31273.949007
HLA B*0803	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.495211	1.181912	-3.313299	31275.979336
HLA B*5701	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.418533	1.105060	-3.313473	26213.989733
HLA B*5801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.300262	0.986777	-3.313486	19964.682109
HLA B*4402	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.376097	1.062587	-3.313510	23773.697199
HLA B*0702	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.281241	0.967687	-3.313554	19109.132373
HLA B*4501	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.234289	0.920689	-3.313599	17150.976845

HLA A*0250	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.227715	0.914083	-3.313632	16893.319722
HLA A*2301	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.490350	1.176703	-3.313646	30927.857313
HLA B*4002	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.476265	1.162617	-3.313647	29940.887571
HLA B*4402	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.373590	1.059725	-3.313865	23636.862367
HLA A*3001	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.104198	0.790220	-3.313978	12711.531442
HLA B*1509	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.462212	1.148177	-3.314035	28987.609399
HLA A*3201	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.583505	1.269415	-3.314089	38326.976808
HLA A*0206	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.341343	1.027215	-3.314129	21945.381989
HLA B*1509	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.474091	1.159900	-3.314191	29791.433212
HLA A*0201	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.269242	0.955018	-3.314224	18588.405974
HLA A*0206	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.088391	0.774156	-3.314235	12257.179353
HLA B*1517	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.481401	1.167129	-3.314271	30297.071000
HLA B*0801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.281896	0.967578	-3.314318	19137.996693
HLA B*5701	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.414941	1.100571	-3.314369	25998.049267
HLA A*8001	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.397564	1.083182	-3.314382	24978.362920
HLA B*5701	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.374222	1.059725	-3.314497	23671.285192
HLA B*5401	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.545708	1.230828	-3.314880	35132.446912
HLA B*5401	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.542457	1.227496	-3.314960	34870.382514
HLA A*2902	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.105265	0.790220	-3.315045	12742.790475
HLA B*4002	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.615164	1.299885	-3.315279	41225.304707
HLA A*8001	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.420380	1.105060	-3.315320	26325.693472
HLA A*0219	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.398619	1.083182	-3.315437	25039.110117
HLA A*6801	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.653021	1.337377	-3.315644	44980.173486
HLA B*2705	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.399030	1.083182	-3.315848	25062.826634
HLA B*0702	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.439115	1.123062	-3.316053	27486.194389
HLA B*1509	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.336482	1.020365	-3.316117	21701.115592
HLA A*6802	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.408052	1.091927	-3.316125	25588.926826
HLA A*3001	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-3.601497	0.285370	-3.316128	3994.821384
HLA B*1517	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.439230	1.123062	-3.316168	27493.481521
HLA A*0212	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.041382	0.725139	-3.316243	10999.730505
HLA A*0101	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.343484	1.027215	-3.316269	22053.804764
HLA B*0801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.421562	1.105060	-3.316502	26397.427828
HLA A*2402	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.538928	1.222401	-3.316527	34588.185937
HLA A*6802	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.284274	0.967687	-3.316587	19243.060888
HLA B*5101	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.500429	1.183813	-3.316616	31654.038315
HLA B*4402	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.421291	1.104589	-3.316702	26381.010112
HLA B*3901	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.426258	1.109528	-3.316730	26684.448513
HLA B*4403	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.642068	1.325261	-3.316807	43859.919179
HLA B*1517	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.479512	1.162617	-3.316894	30165.578523
HLA A*6802	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.204812	0.887847	-3.316965	16025.523367
HLA B*0803	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.472515	1.155314	-3.317201	29683.485294
HLA A*2601	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.371325	1.054023	-3.317302	23513.913858
HLA A*0301	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.366149	1.048747	-3.317402	23235.338691
HLA A*3002	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.434752	1.117129	-3.317623	27211.445964
HLA B*4002	1:315-323	9	SPARFDQKK	1.201453	0.123808	-4.643038	1.325261	-3.317778	43958.024261
HLA A*0206	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.401060	1.083182	-3.317878	25180.248109
HLA B*5801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.349103	1.031013	-3.318091	22341.045533
HLA B*3801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.480755	1.162617	-3.318137	30252.030969
HLA B*3501	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.368477	1.050133	-3.318344	23360.242511
HLA A*6901	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.242223	0.923460	-3.318763	17467.191091
HLA B*3801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.519556	1.200757	-3.318799	33079.297742
HLA A*3201	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.500829	1.181912	-3.318917	31683.163329
HLA B*1801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-3.900718	0.581735	-3.318983	7956.432413
HLA B*5101	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.481791	1.162617	-3.319173	30324.291251
HLA A*0203	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.287011	0.967687	-3.319324	19364.723669
HLA A*6802	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.772366	0.452989	-3.319377	5920.603973
HLA B*4403	1:479-487	9	RLRAARQLV	1.087444	0.249933	-4.656794	1.337377	-3.319418	45372.676535
HLA B*5801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.346684	1.027215	-3.319469	22216.903269
HLA A*0216	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.474853	1.155314	-3.319538	29843.697549
HLA A*2403	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.382165	1.062587	-3.319579	24108.236690
HLA B*5101	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.479657	1.159900	-3.319757	30175.698151
HLA A*0206	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.340258	1.020365	-3.319893	21890.600874
HLA B*1801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.310891	0.990658	-3.320234	20459.332932
HLA B*4001	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.370432	1.050133	-3.320299	23465.624597
HLA B*3801	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.504715	1.184382	-3.320333	31967.935063

HLA A*0202	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.480292	1.159900	-3.320392	30219.807096
HLA A*0101	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.320731	1.000328	-3.320403	20928.163175
HLA B*4402	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.415540	1.094888	-3.320652	26033.938891
HLA A*0101	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.369429	1.048747	-3.320682	23411.481033
HLA B*5801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.327594	1.006851	-3.320743	21261.502826
HLA B*1801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.244211	0.923460	-3.320750	17547.317561
HLA A*3101	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.348004	1.027215	-3.320789	22284.553390
HLA B*5101	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.369582	1.048747	-3.320834	23419.714959
HLA A*6802	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.430370	1.109528	-3.320842	26938.277997
HLA A*8001	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.383491	1.062587	-3.320904	24181.907533
HLA B*3901	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.436678	1.115540	-3.321138	27332.427051
HLA A*0212	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.413146	1.091927	-3.321219	25890.817048
HLA A*0219	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.426310	1.105060	-3.321250	26687.624620
HLA B*3501	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.209145	0.887847	-3.321298	16186.191420
HLA A*0202	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.194211	0.872828	-3.321383	15639.085193
HLA B*5401	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.555802	1.234192	-3.321610	35958.518157
HLA A*2602	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.404843	1.083182	-3.321661	25400.523994
HLA A*0216	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.774706	0.452989	-3.321717	5952.591767
HLA B*4601	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.389797	1.067986	-3.321810	24535.593850
HLA B*0802	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.444885	1.123062	-3.321823	27853.831805
HLA A*3001	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.249535	0.927578	-3.321957	17763.750668
HLA B*3801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.470386	1.148177	-3.322209	29538.351826
HLA A*3201	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.098066	0.775701	-3.322365	12533.308225
HLA B*3901	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.372584	1.050133	-3.322451	23582.196119
HLA A*3101	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.376642	1.054023	-3.322619	23803.554163
HLA A*3002	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.556993	1.234192	-3.322801	36057.281059
HLA B*4402	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.389996	1.067176	-3.322820	24546.878906
HLA B*3801	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.478194	1.155314	-3.322879	30074.166352
HLA B*1509	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.371736	1.048747	-3.322989	23536.185741
HLA A*0212	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.207011	0.883995	-3.323017	16106.876908
HLA A*3201	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.624054	1.300814	-3.323240	42077.926004
HLA B*0702	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.415237	1.091927	-3.323310	26015.776776
HLA B*4501	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.111317	0.787998	-3.323319	12921.615551
HLA B*4801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.424026	1.100571	-3.323455	26547.658411
HLA B*0801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.383234	1.059725	-3.323510	24167.652200
HLA A*8001	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.418423	1.094888	-3.323535	26207.325285
HLA A*0202	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.166924	0.843357	-3.323568	14686.706860
HLA A*6901	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.211452	0.887847	-3.323605	16272.409557
HLA B*4501	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.591895	1.268289	-3.323606	39074.603053
HLA B*5301	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.291433	0.967687	-3.323746	19562.890986
HLA A*3101	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.257995	0.934152	-3.323843	18113.199241
HLA A*2403	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.407025	1.083182	-3.323844	25528.502946
HLA B*5401	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.204347	0.880484	-3.323863	16008.366689
HLA B*4801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.428937	1.105060	-3.323877	26849.527328
HLA B*0803	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.407291	1.083182	-3.324109	25544.113737
HLA A*2601	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.372923	1.048747	-3.324175	23600.574374
HLA A*2602	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.625074	1.300814	-3.324260	42176.836495
HLA B*5401	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.202839	0.878392	-3.324447	15952.863690
HLA B*5801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.344818	1.020365	-3.324453	22121.676296
HLA B*3801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.501202	1.176703	-3.324499	31710.428035
HLA B*5701	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.407686	1.083182	-3.324504	25567.340348
HLA B*0702	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.065211	0.740545	-3.324665	11620.117563
HLA B*5401	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.566638	1.241782	-3.324856	36866.984052
HLA B*0801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-3.613748	0.288865	-3.324882	4109.108235
HLA B*0801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.416886	1.091927	-3.324959	26114.765837
HLA A*2602	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.047397	0.722436	-3.324960	11153.129032
HLA A*3002	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.937540	0.612321	-3.325219	8660.431020
HLA B*4501	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.277597	0.952354	-3.325243	18949.463456
HLA B*1801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.379412	1.054023	-3.325389	23955.864625
HLA A*0206	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.205874	0.880484	-3.325390	16064.758047
HLA B*1503	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-3.887693	0.562255	-3.325437	7721.342784
HLA B*4001	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.393091	1.067176	-3.325914	24722.395618
HLA A*3101	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.431234	1.105060	-3.326174	26991.961197
HLA A*2902	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.326567	1.000328	-3.326239	21211.297418
HLA B*5301	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.583791	1.257536	-3.326255	38352.281210

HLA B*5101	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.289802	0.963515	-3.326287	19489.580541
HLA A*2603	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.590849	1.264555	-3.326294	38980.647967
HLA A*2501	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.409490	1.083182	-3.326308	25673.788384
HLA A*6801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.114493	0.787998	-3.326496	13016.472924
HLA A*6801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.291614	0.965021	-3.326593	19571.041830
HLA B*3501	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.388946	1.062125	-3.326821	24487.590856
HLA A*6802	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.380901	1.054023	-3.326879	24038.171190
HLA A*0206	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.427475	1.100571	-3.326904	26759.331820
HLA B*4601	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.380953	1.054023	-3.326930	24041.032324
HLA B*4801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.394947	1.067986	-3.326960	24828.280605
HLA A*2403	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.394192	1.067176	-3.327016	24785.201863
HLA A*2603	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.627882	1.300814	-3.327067	42450.385316
HLA A*0202	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.313281	0.986192	-3.327089	20572.207487
HLA A*2403	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.436751	1.109528	-3.327223	27337.011263
HLA B*4601	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.327580	1.000328	-3.327252	21260.812703
HLA B*1509	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.395391	1.067986	-3.327404	24853.679736
HLA B*0803	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.487601	1.159900	-3.327701	30732.715499
HLA A*6802	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.422797	1.094888	-3.327909	26472.651370
HLA B*0801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.355236	1.027215	-3.328021	22658.734441
HLA B*0803	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.465485	1.137355	-3.328130	29206.884503
HLA B*2705	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.432750	1.104589	-3.328161	27086.310881
HLA A*3201	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.118473	0.790220	-3.328254	13136.308736
HLA A*2501	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.428883	1.100571	-3.328311	26846.186718
HLA B*2705	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.451454	1.123062	-3.328392	28278.352827
HLA B*4601	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.388211	1.059725	-3.328486	24446.161219
HLA B*4403	1:129-137	9	KLGYDNFDR	0.762819	0.565285	-4.656590	1.328104	-3.328486	45351.326440
HLA B*0803	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.420678	1.091927	-3.328751	26343.786911
HLA A*0202	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.249455	0.920689	-3.328765	17760.483571
HLA B*1503	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.081713	0.752921	-3.328792	12070.167712
HLA A*1101	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.391131	1.062125	-3.329006	24611.103194
HLA B*3901	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.421007	1.091927	-3.329080	26363.746844
HLA A*2601	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.335937	1.006851	-3.329086	21673.895732
HLA A*2601	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.379327	1.050133	-3.329194	23951.199531
HLA A*0301	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.356450	1.027215	-3.329236	22722.197652
HLA A*2403	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.253207	0.923460	-3.329747	17914.591677
HLA B*4001	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.389559	1.059725	-3.329834	24522.191292
HLA B*1503	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.316831	0.986777	-3.330054	20741.060949
HLA B*5401	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.297868	0.967578	-3.330290	19854.926068
HLA B*0801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.337147	1.006851	-3.330296	21734.365417
HLA B*4403	1:334-342	9	MLDVGDFTV	1.162214	0.145562	-4.638083	1.307776	-3.330307	43459.337391
HLA B*3501	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.295340	0.965021	-3.330319	19739.685470
HLA A*0211	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.430957	1.100571	-3.330386	26974.735920
HLA B*1517	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.485764	1.155314	-3.330449	30602.974354
HLA B*0803	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.447601	1.117129	-3.330472	28028.570810
HLA A*2902	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.052956	0.722436	-3.330519	11296.804373
HLA A*3001	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.244944	0.914377	-3.330567	17576.960433
HLA A*2403	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.106322	0.775701	-3.330621	12773.849954
HLA A*0101	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.337532	1.006851	-3.330681	21753.657177
HLA A*0202	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.179536	0.848752	-3.330785	15119.466327
HLA A*2603	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.422866	1.091927	-3.330939	26476.804905
HLA A*8001	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.431688	1.100571	-3.331116	27020.158454
HLA A*0206	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.008503	0.677348	-3.331155	10197.726307
HLA A*2402	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.426277	1.094888	-3.331389	26685.603417
HLA B*1503	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.426326	1.094888	-3.331438	26688.635279
HLA B*1517	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.414743	1.083182	-3.331562	25986.237640
HLA B*4001	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.423568	1.091927	-3.331641	26519.667299
HLA B*1801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.350903	1.019055	-3.331848	22433.818360
HLA A*0206	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-3.969868	0.637857	-3.332012	9329.715928
HLA A*0203	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.226348	0.893488	-3.332859	16840.213815
HLA B*1517	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.400914	1.067986	-3.332928	25171.803739
HLA A*0301	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.364079	1.031013	-3.333066	23124.859943
HLA B*5801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.352153	1.019055	-3.333098	22498.477260
HLA A*2301	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.201951	0.868794	-3.333156	15920.274404
HLA A*3201	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.387609	1.054023	-3.333586	24412.328391
HLA B*5301	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.446445	1.112802	-3.333643	27954.067327

HLA A*2403	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.301496	0.967578	-3.333918	20021.466237
HLA B*5701	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.425849	1.091927	-3.333922	26659.341708
HLA B*1503	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.261529	0.927578	-3.333951	18261.177998
HLA B*1801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.396173	1.062125	-3.334048	24898.493822
HLA A*0250	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.164716	0.830606	-3.334110	14612.210190
HLA B*4501	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-3.972044	0.637857	-3.334187	9376.570939
HLA A*0212	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.714813	0.380458	-3.334355	5185.767333
HLA A*0219	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.397139	1.062587	-3.334552	24953.916330
HLA A*0201	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.218566	0.883995	-3.334571	16541.165502
HLA A*3301	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.544825	1.210192	-3.334633	35061.055991
HLA A*0206	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.353793	1.019055	-3.334738	22583.594423
HLA B*5401	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.557242	1.222401	-3.334841	36077.963973
HLA A*3101	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.341818	1.006851	-3.334966	21969.376958
HLA A*0202	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.013672	0.678487	-3.335185	10319.822295
HLA A*2902	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.290131	0.954860	-3.335271	19504.347238
HLA B*5701	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-3.958051	0.622672	-3.335379	9079.261211
HLA A*2501	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.947717	0.612321	-3.335397	8865.790730
HLA A*2501	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.495380	1.159900	-3.335480	31288.164079
HLA B*0801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.122120	0.786321	-3.335799	13247.067451
HLA A*0216	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.419034	1.083182	-3.335852	26244.213691
HLA B*5301	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.076671	0.740545	-3.336126	11930.847916
HLA B*2705	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.229705	0.893488	-3.336217	16970.905508
HLA A*0211	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.512968	1.176703	-3.336265	32581.293730
HLA B*4402	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.092328	0.755651	-3.336677	12368.820239
HLA A*2902	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.452274	1.115540	-3.336734	28331.794243
HLA B*0702	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.399498	1.062587	-3.336911	25089.822999
HLA B*5701	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.405256	1.067986	-3.337270	25424.720379
HLA B*2705	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.399406	1.062125	-3.337281	25084.529964
HLA B*4801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.260967	0.923460	-3.337507	18237.582219
HLA A*0219	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.324368	0.986777	-3.337592	21104.162177
HLA A*2403	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.368661	1.031013	-3.337648	23370.101944
HLA B*4403	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.638539	1.300814	-3.337725	43504.972713
HLA A*6901	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.364988	1.027215	-3.337774	23173.325493
HLA B*1501	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.368950	1.031013	-3.337937	23385.657967
HLA A*6801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.400604	1.062587	-3.338017	25153.834836
HLA B*1502	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.572222	1.234192	-3.338030	37344.129202
HLA A*2501	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.064238	0.726109	-3.338129	11594.121177
HLA A*2902	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.327166	0.989026	-3.338140	21240.579057
HLA A*6901	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.327218	0.989026	-3.338192	21243.107209
HLA B*1501	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.387151	1.048747	-3.338404	24386.588712
HLA B*4501	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.639241	1.300814	-3.338427	43575.401426
HLA A*2301	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.522312	1.183813	-3.338499	33289.879798
HLA B*3901	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.359004	1.020365	-3.338639	22856.210308
HLA B*0801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.306380	0.967687	-3.338693	20247.921966
HLA A*0301	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.359089	1.020365	-3.338724	22860.662126
HLA B*0801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.401434	1.062587	-3.338847	25201.916781
HLA A*8001	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.387605	1.048747	-3.338857	24412.064257
HLA B*3501	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.454518	1.115540	-3.338978	28478.547645
HLA B*5101	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.487387	1.148177	-3.339210	30717.589510
HLA B*0802	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.387962	1.048747	-3.339214	24432.146630
HLA A*0202	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.487622	1.148177	-3.339445	30734.211881
HLA A*3002	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.423061	1.083182	-3.339879	26488.696211
HLA B*5101	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.507022	1.167129	-3.339892	32138.216986
HLA A*2501	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.431923	1.091927	-3.339996	27034.780015
HLA B*2705	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.115912	0.775701	-3.340212	13059.074764
HLA A*3101	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.388967	1.048747	-3.340220	24488.783161
HLA B*5701	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.360585	1.020365	-3.340220	22939.578138
HLA B*5801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.331015	0.990658	-3.340357	21429.636711
HLA A*6901	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.102196	0.761813	-3.340383	12653.075948
HLA A*0250	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.506649	0.166266	-3.340383	3211.061744
HLA B*4801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.331165	0.990658	-3.340507	21437.057641
HLA A*1101	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.331207	0.990658	-3.340550	21439.145240
HLA B*5401	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.390793	1.050133	-3.340660	24591.938019
HLA A*0101	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.394733	1.054023	-3.340710	24816.060652
HLA A*6802	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.288268	0.947523	-3.340745	19420.851995

HLA A*2902	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.295843	0.955018	-3.340825	19762.551659
HLA A*0203	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.432785	1.091927	-3.340858	27088.508979
HLA A*6802	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.976945	0.635887	-3.341058	9482.985126
HLA B*4801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.435987	1.094888	-3.341099	27288.989176
HLA B*4801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.372417	1.031013	-3.341405	23573.139886
HLA A*0211	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.436443	1.094888	-3.341555	27317.644510
HLA B*1503	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.368834	1.027215	-3.341620	23379.459612
HLA B*1502	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.458886	1.117129	-3.341757	28766.400982
HLA B*0801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.289309	0.947523	-3.341786	19467.451455
HLA B*4002	1:78-86	9	VGGPYGPYR	0.889086	0.411728	-4.642695	1.300814	-3.341881	43923.317996
HLA A*0212	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.342342	1.000328	-3.342014	21995.896925
HLA B*3801	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.523955	1.181912	-3.342043	33416.004215
HLA B*4001	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-3.997442	0.655319	-3.342123	9941.272457
HLA A*0216	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.404742	1.062587	-3.342155	25394.615878
HLA A*0250	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.437108	1.094888	-3.342220	27359.499818
HLA A*2403	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.361438	1.019055	-3.342383	22984.670908
HLA B*4601	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.349360	1.006851	-3.342508	22354.223439
HLA A*6802	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.447829	1.105060	-3.342769	28043.282921
HLA B*5301	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.577015	1.234192	-3.342823	37758.548097
HLA B*0702	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.370127	1.027215	-3.342912	23449.127363
HLA A*0301	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.298007	0.954860	-3.343147	19861.264443
HLA B*5101	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.405482	1.062125	-3.343356	25437.928120
HLA B*4501	1:296-304	9	DLFGLDEMV	1.254497	0.045388	-4.643313	1.299885	-3.343428	43985.856609
HLA B*0802	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.458980	1.115540	-3.343439	28772.626578
HLA B*4402	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.453275	1.109528	-3.343747	28397.163354
HLA A*2501	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.453461	1.109528	-3.343932	28409.302363
HLA A*2601	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.298954	0.955018	-3.343935	19904.612917
HLA A*1101	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.435889	1.091927	-3.343962	27282.789404
HLA A*2603	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.527944	1.183813	-3.344131	33724.377544
HLA B*0803	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.412182	1.067986	-3.344196	25833.453445
HLA A*2902	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.363278	1.019055	-3.344223	23082.239170
HLA A*2301	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.526219	1.181912	-3.344308	33590.728335
HLA B*3801	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.481741	1.137355	-3.344386	30320.846375
HLA B*1509	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.134610	0.790220	-3.344390	13633.570552
HLA A*0202	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.427590	1.083182	-3.344409	26766.426246
HLA B*5801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.361579	1.016861	-3.344719	22992.132791
HLA B*4002	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.229209	0.884477	-3.344732	16951.544499
HLA B*4002	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.578820	1.234017	-3.344803	37915.753471
HLA A*0202	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.445409	1.100571	-3.344837	27887.455092
HLA A*3002	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.529222	1.184382	-3.344840	33823.773891
HLA B*5101	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.449441	1.104589	-3.344851	28147.550060
HLA B*4601	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.365315	1.020365	-3.344950	23190.757799
HLA B*5701	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.412204	1.067176	-3.345027	25834.711281
HLA A*6802	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.188765	0.843615	-3.345150	15444.193676
HLA B*4601	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.259529	0.914377	-3.345153	18177.300128
HLA B*2705	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.445799	1.100571	-3.345227	27912.510435
HLA A*2403	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.450383	1.105060	-3.345323	28208.678667
HLA A*2301	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.529713	1.184382	-3.345331	33862.038939
HLA A*1101	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.428521	1.083182	-3.345339	26823.829859
HLA B*0802	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.437432	1.091927	-3.345505	27379.933081
HLA A*2403	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.399622	1.054023	-3.345599	25097.017888
HLA B*0802	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.462772	1.117129	-3.345643	29024.956538
HLA A*6901	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.376712	1.031013	-3.345700	23807.417714
HLA B*1503	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.251626	0.905846	-3.345780	17849.485832
HLA A*2402	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.546557	1.200757	-3.345799	35201.126569
HLA B*1509	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.218684	0.872828	-3.345855	16545.640400
HLA B*2705	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.284641	0.938712	-3.345928	19259.307783
HLA B*5301	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.573435	1.227496	-3.345938	37448.521080
HLA A*2403	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.352818	1.006851	-3.345967	22532.948779
HLA B*1801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.241436	0.895455	-3.345981	17435.563744
HLA A*3101	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.365096	1.019055	-3.346041	23179.093007
HLA B*4403	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.614539	1.268289	-3.346250	41166.022900
HLA B*1503	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.451417	1.105060	-3.346356	28275.905209
HLA A*6801	1:366-374	9	AELVQTRIV	1.123749	0.213984	-4.684220	1.337733	-3.346487	48330.349695
HLA A*0219	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.438417	1.091927	-3.346490	27442.066762

HLA A*2501	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.462215	1.115540	-3.346675	28987.766219
HLA A*1101	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.260890	0.914083	-3.346806	18234.326621
HLA B*4601	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.395745	1.048747	-3.346998	24873.990834
HLA A*2402	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.557383	1.210192	-3.347191	36089.676541
HLA B*5301	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.261637	0.914377	-3.347260	18265.722948
HLA A*0301	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.338080	0.990658	-3.347422	21781.095042
HLA B*4001	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.367845	1.020365	-3.347480	23326.272004
HLA A*3101	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.333726	0.986192	-3.347534	21563.840674
HLA A*0301	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.354472	1.006851	-3.347621	22618.930540
HLA A*0301	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.366833	1.019055	-3.347777	23271.946376
HLA B*1517	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.452612	1.104589	-3.348023	28353.873991
HLA B*1801	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.524930	1.176703	-3.348226	33491.110899
HLA B*5101	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.431429	1.083182	-3.348248	27004.083870
HLA A*0101	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.315959	0.967687	-3.348272	20699.473959
HLA A*3301	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.590191	1.241782	-3.348409	38921.645989
HLA B*1502	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.271970	0.923460	-3.348510	18705.524966
HLA A*2902	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.217462	0.868794	-3.348668	16499.160566
HLA B*1502	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.349066	1.000328	-3.348738	22339.111815
HLA A*0211	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.496935	1.148177	-3.348758	31400.418731
HLA B*4801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.397557	1.048747	-3.348810	24977.957533
HLA A*6901	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.335155	0.986192	-3.348962	21634.885507
HLA A*2501	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.417076	1.067986	-3.349090	26126.211862
HLA B*4002	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.269947	0.920689	-3.349258	18618.598833
HLA A*3001	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-3.728398	0.379131	-3.349267	5350.541661
HLA B*5401	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.403297	1.054023	-3.349274	25310.266310
HLA B*4001	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.411478	1.062125	-3.349352	25791.560614
HLA B*1502	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.411541	1.062125	-3.349416	25795.328185
HLA B*4801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.409330	1.059725	-3.349605	25664.345442
HLA B*1801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.444601	1.094888	-3.349713	27835.604748
HLA A*6901	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-3.946110	0.596390	-3.349720	8833.044699
HLA B*1501	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.356878	1.006851	-3.350027	22744.580942
HLA B*1801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.350391	1.000328	-3.350063	22407.376501
HLA B*5101	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.455343	1.105060	-3.350282	28532.676111
HLA B*4801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.377535	1.027215	-3.350320	23852.538840
HLA B*4801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.370761	1.020365	-3.350396	23483.403829
HLA A*0203	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.124667	0.774156	-3.350511	13324.980722
HLA B*0803	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.499003	1.148177	-3.350826	31550.263180
HLA B*7301	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.256731	0.905846	-3.350885	18060.557051
HLA B*0801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-3.957106	0.606197	-3.350909	9059.537312
HLA A*8001	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.418129	1.067176	-3.350953	26189.608936
HLA B*4402	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.381977	1.031013	-3.350965	24097.805117
HLA A*2402	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.266277	0.915076	-3.351201	18461.929955
HLA B*5401	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.499414	1.148177	-3.351237	31580.146924
HLA B*0702	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.434517	1.083182	-3.351335	27196.728854
HLA B*1502	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.615974	1.264555	-3.351419	41302.319949
HLA A*0201	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.378669	1.027215	-3.351455	23914.946462
HLA B*0702	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.306775	0.955018	-3.351757	20266.332885
HLA A*3002	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.511662	1.159900	-3.351762	32483.439751
HLA A*3001	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.236366	0.884477	-3.351889	17233.195123
HLA A*3301	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.582898	1.230828	-3.352070	38273.519192
HLA A*0301	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.352430	1.000328	-3.352102	22512.844129
HLA B*0702	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.457173	1.105060	-3.352113	28653.175203
HLA B*5401	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.447042	1.094888	-3.352154	27992.505745
HLA A*2402	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.536026	1.183813	-3.352213	34357.865164
HLA A*2402	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.514634	1.162401	-3.352233	32706.502885
HLA A*1101	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.411990	1.059725	-3.352265	25821.995985
HLA A*0250	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.586460	1.234192	-3.352268	38588.706042
HLA A*0101	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.383303	1.031013	-3.352290	24171.444083
HLA B*3901	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.475353	1.123062	-3.352291	29878.106453
HLA B*0801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.059144	0.706599	-3.352546	11458.932248
HLA B*1501	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.266630	0.914083	-3.352546	18476.917584
HLA A*0101	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.338808	0.986192	-3.352616	21817.654015
HLA A*0203	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.273351	0.920689	-3.352662	18765.122258
HLA B*1501	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.128665	0.775701	-3.352965	13448.238818
HLA B*0702	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.407143	1.054023	-3.353120	25535.409198

HLA A*0212	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.236488	0.883265	-3.353223	17238.043748
HLA A*2403	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.413261	1.059725	-3.353536	25897.681214
HLA B*1801	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.501811	1.148177	-3.353633	31754.890602
HLA A*3201	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.321361	0.967578	-3.353783	20958.527885
HLA A*8001	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.445872	1.091927	-3.353945	27917.191939
HLA B*1501	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.520370	0.166266	-3.354104	3314.130831
HLA B*3501	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.142198	0.787998	-3.354201	13873.896377
HLA A*0250	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.321918	0.967687	-3.354230	20985.416964
HLA B*1801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.144586	0.790220	-3.354366	13950.363474
HLA B*5401	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.514315	1.159900	-3.354415	32682.448091
HLA B*1509	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.459550	1.105060	-3.354490	28810.476034
HLA B*4801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.421750	1.067176	-3.354573	26408.854873
HLA B*5401	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.280301	0.925719	-3.354582	19067.825767
HLA A*0216	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.446624	1.091927	-3.354697	27965.563048
HLA A*2602	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.531510	1.176703	-3.354807	34002.469585
HLA A*2403	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.416954	1.062125	-3.354829	26118.863220
HLA A*0202	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-3.880574	0.525631	-3.354943	7595.806514
HLA A*6901	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.227917	0.872828	-3.355089	16901.181176
HLA A*2403	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.276178	0.920689	-3.355488	18887.645752
HLA B*3901	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.422856	1.067176	-3.355680	26476.231965
HLA A*2301	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.518170	1.162401	-3.355769	32973.882419
HLA B*0702	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.450667	1.094888	-3.355779	28227.150016
HLA A*3201	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-3.803905	0.448098	-3.355807	6366.569714
HLA A*8001	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.323410	0.967578	-3.355831	21057.631707
HLA B*0702	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.456513	1.100571	-3.355941	28609.650344
HLA B*3801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.376482	1.020365	-3.356117	23794.799102
HLA B*4002	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.473281	1.117129	-3.356152	29735.881988
HLA B*7301	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.620850	1.264555	-3.356294	41768.572031
HLA B*0702	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.416047	1.059725	-3.356322	26064.378268
HLA A*8001	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.418613	1.062125	-3.356488	26218.811879
HLA B*1503	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.466312	1.109528	-3.356784	29262.555608
HLA A*0211	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.472792	1.115540	-3.357252	29702.440299
HLA A*0216	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.458124	1.100571	-3.357553	28716.023281
HLA A*2601	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.241608	0.883995	-3.357613	17442.450790
HLA B*1517	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.364486	1.006851	-3.357634	23146.512881
HLA A*3301	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.541656	1.183813	-3.357843	34806.113900
HLA B*1503	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.321391	0.963515	-3.357876	20960.001920
HLA B*0802	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.426009	1.067986	-3.358023	26669.150750
HLA B*5701	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.412124	1.054023	-3.358101	25829.959779
HLA A*0101	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.375079	1.016861	-3.358219	23718.072916
HLA B*4801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.375286	1.016861	-3.358426	23729.367073
HLA B*4402	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.426491	1.067986	-3.358504	26698.743972
HLA B*5101	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.347605	0.989026	-3.358579	22264.068128
HLA A*0212	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.246480	0.887847	-3.358633	17639.259048
HLA A*0206	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.543028	1.184382	-3.358646	34916.253370
HLA B*1517	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.474188	1.115540	-3.358648	29798.041847
HLA B*5701	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.421235	1.062587	-3.358648	26377.585094
HLA B*4501	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.559650	1.200757	-3.358893	36278.576902
HLA B*0802	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.464083	1.105060	-3.359023	29112.707081
HLA B*5701	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.390107	1.031013	-3.359094	24553.121106
HLA B*1801	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.468871	1.109528	-3.359343	29435.460953
HLA B*3501	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.413371	1.054023	-3.359348	25904.266920
HLA A*1101	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.482449	1.123062	-3.359387	30370.260354
HLA B*4501	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.569589	1.210192	-3.359397	37118.341598
HLA A*2601	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.378496	1.019055	-3.359440	23905.374465
HLA B*1517	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.024719	0.665274	-3.359445	10585.697941
HLA A*2902	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.408292	1.048747	-3.359545	25603.050915
HLA A*0202	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.243586	0.883995	-3.359591	17522.084596
HLA B*3501	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-3.724982	0.365377	-3.359605	5308.619509
HLA A*2902	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.451593	1.091927	-3.359666	28287.380250
HLA A*0206	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.515052	1.155314	-3.359738	32738.013117
HLA A*0211	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-3.982612	0.622672	-3.359940	9607.536148
HLA B*3901	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.033243	0.673165	-3.360078	10795.516586
HLA B*5701	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.346397	0.986192	-3.360205	22202.244807
HLA B*1801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.203675	0.843357	-3.360318	15983.617243

HLA A*0211	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.129751	0.769405	-3.360346	13481.892966
HLA B*1502	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.587853	1.227496	-3.360357	38712.699875
HLA A*1101	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.455378	1.094888	-3.360490	28534.991584
HLA A*0219	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.461089	1.100571	-3.360518	28912.746393
HLA B*7301	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.602390	1.241782	-3.360608	40030.381066
HLA B*1503	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-3.996573	0.635887	-3.360686	9921.393322
HLA A*2902	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.465753	1.105060	-3.360693	29224.902744
HLA A*3002	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.315661	0.954860	-3.360801	20685.257148
HLA A*2602	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.588464	1.227496	-3.360968	38767.190356
HLA A*2403	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.452920	1.091927	-3.360993	28373.975375
HLA B*0803	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.466157	1.105060	-3.361097	29252.109199
HLA B*5701	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.409896	1.048747	-3.361149	25697.828008
HLA B*0702	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.316183	0.954860	-3.361323	20710.114970
HLA A*0101	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.380521	1.019055	-3.361465	24017.113316
HLA A*0203	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.287281	0.925719	-3.361562	19376.774933
HLA A*2602	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.499104	1.137355	-3.361749	31557.603421
HLA A*1101	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.316612	0.954860	-3.361752	20730.628338
HLA A*2902	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.355052	0.993286	-3.361766	22649.175122
HLA B*5401	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.538571	1.176703	-3.361867	34559.755653
HLA B*1517	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.462497	1.100571	-3.361925	29006.590801
HLA B*3501	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.268267	0.905846	-3.362421	18546.719882
HLA B*4001	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.257934	0.895455	-3.362479	18110.651670
HLA A*0201	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.393504	1.031013	-3.362491	24745.946022
HLA B*3801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.529734	1.167129	-3.362605	33863.687688
HLA B*4402	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.383225	1.020365	-3.362860	24167.129228
HLA B*2705	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.363247	1.000328	-3.362919	23080.615886
HLA A*3101	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.383516	1.020365	-3.363151	24183.346612
HLA B*3501	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-3.227201	-0.136008	-3.363209	1687.333427
HLA A*2501	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.417434	1.054023	-3.363411	26147.704363
HLA B*1502	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.573651	1.210192	-3.363459	37467.164215
HLA A*2601	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.394564	1.031013	-3.363551	24806.396381
HLA A*3101	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.394693	1.031013	-3.363680	24813.778471
HLA B*5101	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.458608	1.094888	-3.363720	28748.043324
HLA A*6802	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.207185	0.843357	-3.363828	16113.326294
HLA B*5701	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.350633	0.986777	-3.363856	22419.865787
HLA B*4801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.426056	1.062125	-3.363931	26672.036449
HLA B*4501	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.633356	1.269415	-3.363941	42988.860816
HLA B*5801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.350158	0.986192	-3.363966	22395.378793
HLA B*5801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.353008	0.989026	-3.363982	22542.824904
HLA B*1502	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.476857	1.112802	-3.364055	29981.733581
HLA B*5801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.278154	0.914083	-3.364070	18973.774973
HLA A*6801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.235743	0.871584	-3.364159	17208.506960
HLA B*5101	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.278429	0.914083	-3.364345	18985.788359
HLA A*2601	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.332034	0.967687	-3.364347	21480.010294
HLA B*2705	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.381249	1.016861	-3.364389	24057.425385
HLA B*3501	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.469524	1.105060	-3.364464	29479.763697
HLA A*2403	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.351321	0.986777	-3.364545	22455.431641
HLA B*1517	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.456534	1.091927	-3.364607	28611.043353
HLA A*2601	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.391932	1.027215	-3.364718	24656.546977
HLA A*2603	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.502081	1.137355	-3.364726	31774.652649
HLA B*4403	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.592226	1.227496	-3.364729	39104.420311
HLA B*5101	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.424456	1.059725	-3.364731	26573.953864
HLA B*0803	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.480296	1.115540	-3.364756	30220.134070
HLA B*0802	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.477623	1.112802	-3.364821	30034.656736
HLA A*0202	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.541580	1.176703	-3.364877	34800.088911
HLA A*0201	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.383951	1.019055	-3.364896	24207.562134
HLA B*0801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.381764	1.016861	-3.364903	24085.944689
HLA B*5301	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.587365	1.222401	-3.364964	38669.162640
HLA A*0101	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.385330	1.020365	-3.364965	24284.557977
HLA B*3501	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.091097	0.726109	-3.364988	12333.806982
HLA A*0216	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.249260	0.883995	-3.365265	17752.510535
HLA A*3301	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.629996	1.264555	-3.365441	42657.575993
HLA B*5801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.358790	0.993286	-3.365504	22844.960967
HLA A*0250	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.547456	1.181912	-3.365545	35274.138478
HLA A*2603	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.596377	1.230828	-3.365549	39480.022566

HLA A*0301	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.352379	0.986777	-3.365602	22510.164865
HLA A*3001	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.248882	0.883265	-3.365617	17737.054969
HLA B*4002	1:429-437	9	EAALKDALI	1.091740	0.176549	-4.633941	1.268289	-3.365652	43046.808515
HLA A*0211	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.550156	1.184382	-3.365774	35494.084083
HLA B*5701	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.366189	1.000328	-3.365861	23237.475700
HLA A*0211	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.414638	1.048747	-3.365890	25979.912190
HLA B*5101	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.333470	0.967578	-3.365892	21551.128702
HLA B*7301	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.528642	1.162617	-3.366025	33778.607306
HLA A*2603	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.750774	0.384545	-3.366230	5633.447419
HLA A*8001	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.425983	1.059725	-3.366258	26667.563748
HLA A*1101	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.470880	1.104589	-3.366291	29571.928729
HLA B*4001	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.373252	1.006851	-3.366400	23618.455853
HLA A*2301	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.533543	1.167129	-3.366413	34161.958859
HLA B*1502	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.429181	1.062587	-3.366594	26864.637887
HLA A*8001	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.355764	0.989026	-3.366738	22686.332014
HLA B*5701	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.334429	0.967687	-3.366741	21598.749638
HLA A*0219	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.292504	0.925719	-3.366785	19611.210442
HLA A*0301	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.331847	0.965021	-3.366825	21470.715947
HLA A*3001	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.269146	0.902312	-3.366834	18584.283422
HLA B*7301	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.504193	1.137355	-3.366838	31929.564766
HLA B*2705	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.290385	0.923460	-3.366925	19515.746334
HLA A*3002	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.136475	0.769405	-3.367070	13692.258856
HLA B*1801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.356133	0.989026	-3.367107	22705.608894
HLA B*1509	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.292974	0.925719	-3.367255	19632.440820
HLA B*0802	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.387654	1.020365	-3.367289	24414.837812
HLA A*2501	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.322402	0.955018	-3.367383	21008.816929
HLA A*6802	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.394745	1.027215	-3.367530	24816.731922
HLA A*3301	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.625102	1.257536	-3.367566	42179.574648
HLA B*2705	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.462530	1.094888	-3.367641	29008.787798
HLA A*0101	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.358363	0.990658	-3.367705	22822.478892
HLA A*3301	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.388182	1.020365	-3.367818	24444.574259
HLA A*6901	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.320235	0.952354	-3.367881	20904.287586
HLA B*7301	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.602112	1.234192	-3.367920	40004.835149
HLA A*2301	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.523337	1.155314	-3.368022	33368.493703
HLA B*5301	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-3.733454	0.365377	-3.368077	5413.197115
HLA A*3201	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.578270	1.210192	-3.368078	37867.785753
HLA B*2705	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-3.668016	0.299836	-3.368180	4656.032310
HLA A*3002	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.358842	0.990658	-3.368184	22847.680080
HLA A*0206	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.230311	0.862113	-3.368198	16994.609212
HLA A*0301	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.357371	0.989026	-3.368345	22770.435214
HLA A*3301	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.602559	1.234192	-3.368367	40045.976417
HLA A*0301	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.354827	0.986192	-3.368635	22637.415341
HLA A*2902	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.395943	1.027215	-3.368728	24885.296908
HLA B*4402	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.431021	1.062125	-3.368895	26978.676327
HLA B*1503	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.029926	0.660945	-3.368981	10713.366351
HLA A*2603	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.492417	1.123062	-3.369356	31075.446675
HLA A*2602	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.579675	1.210192	-3.369483	37990.490721
HLA B*5701	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.396702	1.027215	-3.369487	24928.819345
HLA B*1501	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.284749	0.915076	-3.369672	19264.101153
HLA B*3501	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.388775	1.019055	-3.369719	24477.922079
HLA A*3002	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.551709	1.181912	-3.369797	35621.235890
HLA A*0211	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-3.845078	0.475212	-3.369866	6999.674972
HLA B*1501	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.358953	0.989026	-3.369927	22853.490180
HLA A*3301	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.230617	0.860662	-3.369955	17006.565479
HLA A*3002	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.376851	1.006851	-3.370000	23815.017861
HLA A*0211	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.525324	1.155314	-3.370010	33521.563513
HLA A*0203	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.389073	1.019055	-3.370018	24494.745559
HLA A*2602	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.592449	1.222401	-3.370048	39124.522781
HLA A*3201	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.325205	0.955018	-3.370186	21144.846281
HLA B*4403	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.612077	1.241782	-3.370295	40933.289876
HLA A*3101	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.322651	0.952354	-3.370297	21020.867853
HLA B*3501	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.254292	0.883995	-3.370298	17959.422850
HLA B*4002	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.597994	1.227496	-3.370497	39627.241161
HLA A*6802	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.296242	0.925719	-3.370523	19780.735266
HLA B*0702	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.419442	1.048747	-3.370695	26268.929544

HLA A*2501	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.419562	1.048747	-3.370815	26276.178255
HLA B*1501	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.336087	0.965021	-3.371066	21681.401247
HLA A*0219	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.048553	0.677348	-3.371204	11182.854472
HLA B*1517	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-3.993687	0.622434	-3.371254	9855.700546
HLA A*2602	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.471869	1.100571	-3.371297	29639.357427
HLA B*1501	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.165783	0.794424	-3.371358	14648.143198
HLA B*4001	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.390417	1.019055	-3.371361	24570.660884
HLA B*3501	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-3.583331	0.211872	-3.371459	3831.167571
HLA A*0202	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.487002	1.115540	-3.371462	30690.348281
HLA A*8001	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.421801	1.050133	-3.371668	26411.998177
HLA A*0202	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.420427	1.048747	-3.371680	26328.542008
HLA A*0216	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.339419	0.967687	-3.371732	21848.363691
HLA A*1101	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.487296	1.115540	-3.371755	30711.109222
HLA A*3001	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.259654	0.887847	-3.371807	18182.512746
HLA A*6801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.051757	0.679867	-3.371890	11265.678957
HLA A*0211	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.539116	1.167129	-3.371986	34603.158637
HLA B*0803	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.484897	1.112802	-3.372095	30541.944130
HLA B*0802	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.434700	1.062587	-3.372113	27208.207516
HLA A*3201	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.606323	1.234192	-3.372131	40394.548869
HLA A*0206	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.265831	0.893488	-3.372342	18442.963076
HLA B*1502	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.098522	0.726109	-3.372413	12546.469069
HLA A*2402	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.520787	1.148177	-3.372610	33173.203375
HLA B*1801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.435250	1.062587	-3.372663	27242.672579
HLA A*0211	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.325068	0.952354	-3.372714	21138.212628
HLA A*2403	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.298463	0.925719	-3.372744	19882.120150
HLA B*0802	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.473441	1.100571	-3.372869	29746.823012
HLA B*4403	1:268-276	9	FAHRDRGFI	1.022602	0.246813	-4.642324	1.269415	-3.372909	43885.790032
HLA A*0301	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.340669	0.967687	-3.372981	21911.335189
HLA A*0211	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.219529	0.846543	-3.372987	16577.895428
HLA B*1517	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.440529	1.067176	-3.373353	27575.856066
HLA B*3901	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.474023	1.100571	-3.373452	29786.759696
HLA B*4001	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.373780	1.000328	-3.373452	23647.222334
HLA B*0801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.312423	0.938712	-3.373711	20531.625489
HLA A*8001	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.427933	1.054023	-3.373911	26787.575894
HLA A*3201	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.574748	1.200757	-3.373991	37561.941615
HLA A*0206	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.827363	0.452989	-3.374373	6719.899179
HLA A*8001	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.401692	1.027215	-3.374477	25216.918597
HLA A*0203	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.405602	1.031013	-3.374589	25444.947523
HLA A*3001	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.300366	0.925719	-3.374647	19969.434971
HLA A*2402	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.457882	1.083182	-3.374701	28700.026637
HLA B*1509	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.424884	1.050133	-3.374751	26600.131460
HLA B*4801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.221353	0.846543	-3.374810	16647.636947
HLA B*4601	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.361683	0.986777	-3.374906	22997.606377
HLA B*4001	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.391777	1.016861	-3.374917	24647.744862
HLA A*2501	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.437068	1.062125	-3.374943	27356.983732
HLA A*6901	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.368294	0.993286	-3.375008	23350.387237
HLA B*4501	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.220136	0.844865	-3.375271	16601.050204
HLA A*2603	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.425450	1.050133	-3.375317	26634.834885
HLA B*5401	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.559803	1.184382	-3.375421	36291.336246
HLA B*4002	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.512778	1.137355	-3.375423	32567.019701
HLA A*2601	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.392299	1.016861	-3.375438	24677.364473
HLA A*0206	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.327812	0.952354	-3.375458	21272.202598
HLA A*3002	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.435294	1.059725	-3.375569	27245.472940
HLA B*0702	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.443915	1.067986	-3.375928	27791.667900
HLA B*5301	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.278250	0.902312	-3.375938	18977.983927
HLA A*2601	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.369311	0.993286	-3.376025	23405.149213
HLA B*4601	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.056080	0.679867	-3.376214	11378.379726
HLA B*1801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.291391	0.915076	-3.376314	19560.986083
HLA B*4801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.269933	0.893488	-3.376445	18617.994496
HLA B*4002	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.586726	1.210192	-3.376534	38612.303204
HLA A*2403	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.403898	1.027215	-3.376684	25345.343583
HLA A*0202	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.486215	1.109528	-3.376687	30634.778138
HLA B*2705	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.482094	1.105060	-3.377034	30345.461223
HLA A*0101	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.340688	0.963515	-3.377172	21912.283513
HLA B*2705	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-3.939978	0.562720	-3.377258	8709.200169

HLA A*2602	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.539771	1.162401	-3.377371	34655.426664
HLA A*0201	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.363630	0.986192	-3.377438	23100.977625
HLA B*1517	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.363736	0.986192	-3.377544	23106.602127
HLA A*2602	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.611830	1.234192	-3.377638	40910.044800
HLA A*3001	1:221-229	9	STPRQLALH	0.899770	-0.287449	-3.990126	0.612321	-3.377805	9775.200640
HLA B*1501	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.283882	0.905846	-3.378036	19225.683567
HLA B*5401	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.478666	1.100571	-3.378094	30106.886418
HLA B*0801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.284133	0.905846	-3.378287	19236.815732
HLA B*5401	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.562206	1.183813	-3.378394	36492.740794
HLA B*1509	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.473337	1.094888	-3.378449	29739.743066
HLA A*2301	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.473408	1.094888	-3.378520	29744.570119
HLA B*1509	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.501653	1.123062	-3.378591	31743.382728
HLA B*0801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.292993	0.914377	-3.378617	19633.290513
HLA B*3901	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.483762	1.105060	-3.378702	30462.242923
HLA A*0201	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.346573	0.967687	-3.378886	22211.255011
HLA B*1503	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.257333	0.878392	-3.378941	18085.587016
HLA A*2301	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.483802	1.104589	-3.379213	30465.044607
HLA A*3001	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.167230	0.787998	-3.379232	14697.039442
HLA A*2402	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.561243	1.181912	-3.379332	36411.887606
HLA A*8001	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.365538	0.986192	-3.379346	23202.679508
HLA B*0803	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.484004	1.104589	-3.379415	30479.221781
HLA B*4601	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.410545	1.031013	-3.379532	25736.226851
HLA A*3101	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.303084	0.923460	-3.379624	20094.820491
HLA B*4001	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.372953	0.993286	-3.379667	23602.234227
HLA A*0206	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.148246	0.768573	-3.379673	14068.442531
HLA B*3801	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.542121	1.162401	-3.379720	34843.416724
HLA A*6801	1:326-334	9	ALNAEHIRM	1.139293	0.102489	-4.621712	1.241782	-3.379930	41851.582957
HLA B*2705	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-3.738782	0.358727	-3.380055	5480.024166
HLA A*1101	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.485212	1.105060	-3.380151	30564.092780
HLA A*3001	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.226766	0.846543	-3.380223	16856.438082
HLA A*0212	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.411245	1.031013	-3.380232	25777.750894
HLA B*3801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.485009	1.104589	-3.380420	30549.876129
HLA B*0803	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.503512	1.123062	-3.380450	31879.510773
HLA B*5101	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.472390	1.091927	-3.380463	29674.975543
HLA A*3101	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.367317	0.986777	-3.380540	23297.895955
HLA A*8001	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.335462	0.954860	-3.380602	21650.223487
HLA B*5101	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.496148	1.115540	-3.380608	31343.562884
HLA B*3901	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.411628	1.031013	-3.380615	25800.492047
HLA B*5301	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.562566	1.181912	-3.380654	36522.958816
HLA B*7301	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.543061	1.162401	-3.380660	34918.897973
HLA B*1509	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.472588	1.091927	-3.380661	29688.463827
HLA A*0201	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.397658	1.016861	-3.380797	24983.768712
HLA A*0206	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.547978	1.167129	-3.380849	35316.528006
HLA B*0801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.335763	0.954860	-3.380903	21665.220719
HLA A*3001	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.259358	0.878392	-3.380966	18170.122932
HLA B*7301	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-3.626942	0.245974	-3.380968	4235.866738
HLA A*0211	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.464362	1.083182	-3.381181	29131.455201
HLA A*0202	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.333829	0.952354	-3.381475	21568.974237
HLA B*1801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.482451	1.100571	-3.381879	30370.424654
HLA A*0206	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.060544	0.678487	-3.382058	11495.938842
HLA A*0203	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.269916	0.887847	-3.382070	18617.289460
HLA A*0203	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.225770	0.843357	-3.382413	16817.817214
HLA B*4002	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.646983	1.264555	-3.382428	44359.122829
HLA B*0702	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.369396	0.986777	-3.382619	23409.707950
HLA B*1801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.450829	1.067986	-3.382843	28237.688680
HLA B*5101	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.483572	1.100571	-3.383000	30448.897261
HLA B*3901	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.466486	1.083182	-3.383305	29274.272684
HLA B*5101	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.492838	1.109528	-3.383310	31105.553785
HLA B*1801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.410780	1.027215	-3.383565	25750.153631
HLA B*5401	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.227198	0.843615	-3.383583	16873.225665
HLA B*1502	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.546343	1.162617	-3.383726	35183.801322
HLA B*3901	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.266991	0.883265	-3.383726	18492.317542
HLA B*3901	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.372993	0.989026	-3.383967	23604.404979
HLA B*3801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.507250	1.123062	-3.384188	32155.086238
HLA B*1501	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.272278	0.887847	-3.384431	18718.786185

HLA B*0802	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.467757	1.083182	-3.384576	29360.076665
HLA A*3001	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.280320	0.895455	-3.384865	19068.651023
HLA A*2301	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.544919	1.159900	-3.385019	35068.643869
HLA B*2705	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.375831	0.990658	-3.385173	23759.168364
HLA B*1502	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.533482	1.148177	-3.385304	34157.154074
HLA A*3002	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.485912	1.100571	-3.385340	30613.406329
HLA B*4403	1:367-375	9	ELVQTRIVV	1.078092	0.155925	-4.619684	1.234017	-3.385667	41656.644447
HLA A*2403	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.386000	1.000328	-3.385672	24322.029235
HLA A*6802	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.338087	0.952354	-3.385733	21781.448544
HLA B*4601	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.338305	0.952354	-3.385951	21792.409977
HLA A*8001	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.406419	1.020365	-3.386054	25492.896357
HLA B*3901	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.257727	0.871584	-3.386143	18102.031779
HLA B*5101	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.393133	1.006851	-3.386281	24724.803153
HLA B*0801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.373089	0.986777	-3.386313	23609.641146
HLA B*3901	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.446128	1.059725	-3.386403	27933.658945
HLA B*1517	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.481325	1.094888	-3.386437	30291.826533
HLA A*2402	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.570904	1.184382	-3.386522	37230.963532
HLA A*0206	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.481591	1.094888	-3.386703	30310.350117
HLA A*3101	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.375747	0.989026	-3.386721	23754.541574
HLA B*1503	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.181158	0.794424	-3.386733	15176.010095
HLA A*3101	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.354481	0.967687	-3.386794	22619.420009
HLA A*3201	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.435574	1.048747	-3.386827	27263.018591
HLA A*0301	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.354416	0.967578	-3.386837	22615.993949
HLA A*0216	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-3.565358	0.178488	-3.386869	3675.848365
HLA B*3801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.546972	1.159900	-3.387072	35234.849564
HLA B*5801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.352212	0.965021	-3.387191	22501.520323
HLA B*1501	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.342363	0.955018	-3.387344	21996.967909
HLA A*3101	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.352592	0.965021	-3.387571	22521.249345
HLA B*2705	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.177854	0.790220	-3.387635	15061.014646
HLA B*1503	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.289976	0.902312	-3.387664	19497.384402
HLA A*8001	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.272195	0.884477	-3.387718	18715.242191
HLA A*2601	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.388077	1.000328	-3.387749	24438.624073
HLA A*2301	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.470941	1.083182	-3.387759	29576.088524
HLA A*6801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.000727	0.612666	-3.388061	10016.743584
HLA B*1517	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.415321	1.027215	-3.388107	26020.843998
HLA A*6801	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.550779	1.162617	-3.388161	35545.005626
HLA A*3001	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.268746	0.880484	-3.388262	18567.199663
HLA A*6802	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-3.710034	0.321711	-3.388323	5129.017433
HLA B*4001	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.379043	0.990658	-3.388385	23935.526288
HLA A*0219	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.374706	0.986192	-3.388514	23697.680057
HLA B*4501	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.388887	1.000328	-3.388559	24484.279201
HLA A*1101	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.455944	1.067176	-3.388767	28572.219292
HLA B*0801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.407862	1.019055	-3.388806	25577.716189
HLA B*0802	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.483736	1.094888	-3.388848	30460.430206
HLA A*0219	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.395743	1.006851	-3.388892	24873.856269
HLA A*0216	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.272271	0.883265	-3.389006	18718.482388
HLA A*2501	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.483997	1.094888	-3.389109	30478.727117
HLA B*0803	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.282716	0.893488	-3.389228	19174.164345
HLA A*0212	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.408334	1.019055	-3.389279	25605.544210
HLA A*0212	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.396187	1.006851	-3.389336	24899.302024
HLA B*1509	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.380063	0.990658	-3.389405	23991.790341
HLA B*4801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.389801	1.000328	-3.389473	24535.859321
HLA A*3101	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.452084	1.062587	-3.389497	28319.381941
HLA A*2501	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.494656	1.105060	-3.389596	31236.073715
HLA B*4601	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.408726	1.019055	-3.389671	25628.688031
HLA B*0802	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.456935	1.067176	-3.389759	28637.523419
HLA A*0101	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.376548	0.986777	-3.389771	23798.403737
HLA A*0101	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.337441	0.947523	-3.389918	21749.067951
HLA B*3501	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.315640	0.925719	-3.389921	20684.250028
HLA B*1501	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.233321	0.843357	-3.389964	17112.792043
HLA A*2301	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.513109	1.123062	-3.390047	32591.871118
HLA B*5801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.305147	0.915076	-3.390071	20190.495574
HLA A*2902	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.440212	1.050133	-3.390079	27555.723805
HLA A*8001	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.357858	0.967687	-3.390170	22795.948902
HLA B*1801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.473767	1.083182	-3.390586	29769.200280

HLA B*3901	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.239373	0.848752	-3.390621	17352.943236
HLA A*3001	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.296672	0.905846	-3.390827	19800.328083
HLA B*4601	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.418174	1.027215	-3.390959	26192.301049
HLA A*0219	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.278812	0.887847	-3.390965	19002.537638
HLA A*3201	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.514103	1.123062	-3.391041	32666.539207
HLA A*0301	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.354573	0.963515	-3.391058	22624.192886
HLA B*5801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.305436	0.914377	-3.391059	20203.935131
HLA A*0203	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.274418	0.883265	-3.391153	18811.267726
HLA B*0702	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.358809	0.967578	-3.391231	22845.949698
HLA A*2301	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.539414	1.148177	-3.391237	34626.941111
HLA B*4601	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.408101	1.016861	-3.391241	25591.834090
HLA A*0216	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.441699	1.050133	-3.391566	27650.249031
HLA B*5401	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.514707	1.123062	-3.391645	32711.988440
HLA B*1502	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.573564	1.181912	-3.391652	37459.665317
HLA A*2501	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.297511	0.905846	-3.391665	19838.606010
HLA A*2301	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.445688	1.054023	-3.391666	27905.414169
HLA A*0212	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.212805	0.821048	-3.391757	16323.195035
HLA A*0250	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.275795	0.883995	-3.391800	18870.997742
HLA A*3201	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.459059	1.067176	-3.391883	28777.919393
HLA A*2402	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.559361	1.167129	-3.392232	36254.444574
HLA B*5801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.344597	0.952354	-3.392243	22110.429629
HLA A*2403	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.441029	1.048747	-3.392282	27607.650216
HLA B*1503	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.069675	0.677348	-3.392326	11740.174265
HLA A*8001	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.423371	1.031013	-3.392358	26507.618686
HLA A*2402	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.547882	1.155314	-3.392567	35308.695476
HLA B*5701	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.399420	1.006851	-3.392569	25085.344204
HLA B*5801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.347569	0.954860	-3.392709	22262.261509
HLA A*0250	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.552778	1.159900	-3.392878	35709.025549
HLA A*0211	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.498021	1.105060	-3.392961	31478.998116
HLA A*1101	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.360609	0.967578	-3.393031	22940.819177
HLA B*1509	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.555644	1.162401	-3.393244	35945.486902
HLA A*0301	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.345807	0.952354	-3.393453	22172.117234
HLA A*1101	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.420706	1.027215	-3.393492	26345.497170
HLA B*4001	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.379757	0.986192	-3.393565	23974.923193
HLA B*4801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.387142	0.993286	-3.393856	24386.061003
HLA A*2301	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.506787	1.112802	-3.393985	32120.835269
HLA A*6901	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.328160	0.934152	-3.394008	21289.241297
HLA A*3001	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.237508	0.843357	-3.394151	17278.564362
HLA B*4001	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.349127	0.954860	-3.394267	22342.254191
HLA B*4501	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.628509	1.234192	-3.394317	42511.746673
HLA B*1501	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.411189	1.016861	-3.394328	25774.404196
HLA B*5101	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.456966	1.062587	-3.394379	28639.537526
HLA B*4501	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.658989	1.264555	-3.394433	45602.517435
HLA B*4601	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.380819	0.986192	-3.394627	24033.620086
HLA A*6901	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.297027	0.902312	-3.394715	19816.509445
HLA A*2601	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.381515	0.986777	-3.394738	24072.136606
HLA A*3002	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.448773	1.054023	-3.394750	28104.337129
HLA B*4402	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.413825	1.019055	-3.394769	25931.327913
HLA A*0101	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.383935	0.989026	-3.394909	24206.645430
HLA B*1509	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.243788	0.848752	-3.395036	17530.238651
HLA B*4501	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.333754	0.938712	-3.395042	21565.240615
HLA B*4402	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.395473	1.000328	-3.395145	24858.386129
HLA B*5801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.352870	0.957710	-3.395159	22535.630755
HLA B*1501	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.242106	0.846543	-3.395563	17462.466952
HLA B*4001	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-3.807105	0.411532	-3.395573	6413.653562
HLA B*1509	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.363252	0.967578	-3.395674	23080.865615
HLA B*7301	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.445815	1.050133	-3.395682	27913.567480
HLA B*4002	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.396042	1.000328	-3.395714	24890.951871
HLA B*4402	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.363405	0.967578	-3.395827	23088.983262
HLA B*5301	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.455573	1.059725	-3.395848	28547.807266
HLA A*2403	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.386644	0.990658	-3.395986	24358.108747
HLA B*0802	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.446187	1.050133	-3.396053	27937.437151
HLA B*0702	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.389630	0.993286	-3.396344	24526.171485
HLA A*6801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.311458	0.915076	-3.396381	20486.024865
HLA A*6901	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.361443	0.965021	-3.396422	22984.919599

HLA B*1501	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.165942	0.769405	-3.396537	14653.532838
HLA A*0212	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.322289	0.925719	-3.396570	21003.362180
HLA A*0216	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.170815	0.774156	-3.396659	14818.872922
HLA A*2403	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.166370	0.769461	-3.396909	14667.967809
HLA A*2403	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.390393	0.993286	-3.397107	24569.331674
HLA B*5101	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.383552	0.986192	-3.397359	24185.309130
HLA B*1509	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.510215	1.112802	-3.397413	32375.369129
HLA B*1501	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.416569	1.019055	-3.397514	26095.700272
HLA B*5301	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.384522	0.986777	-3.397745	24239.406396
HLA A*2403	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.355797	0.957710	-3.398087	22688.050306
HLA B*5701	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.363116	0.965021	-3.398095	23073.624585
HLA A*2602	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.580121	1.181912	-3.398210	38029.560422
HLA A*2902	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.192656	0.794424	-3.398232	15583.176382
HLA B*2705	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.447037	1.048747	-3.398290	27992.202874
HLA B*1501	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.384501	0.986192	-3.398309	24238.226233
HLA A*3001	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.266211	0.867880	-3.398331	18459.133611
HLA A*3001	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.271625	0.872828	-3.398796	18690.655241
HLA B*5401	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.566104	1.167129	-3.398975	36821.737530
HLA B*4402	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.389764	0.990658	-3.399106	24533.735632
HLA A*3001	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-3.741508	0.342354	-3.399154	5514.522033
HLA A*0203	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.356965	0.957710	-3.399255	22749.134087
HLA A*0101	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.392576	0.993286	-3.399290	24693.122715
HLA B*1517	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.243217	0.843615	-3.399602	17507.208486
HLA A*2403	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.420072	1.020365	-3.399707	26307.043182
HLA A*3201	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.500335	1.100571	-3.399764	31647.189263
HLA B*0803	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.500394	1.100571	-3.399822	31651.469747
HLA A*6801	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.630767	1.230828	-3.399938	42733.336654
HLA A*0219	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.419074	1.019055	-3.400018	26246.627433
HLA B*2705	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.407011	1.006851	-3.400160	25527.674321
HLA B*3801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.483412	1.083182	-3.400230	30437.698010
HLA B*1801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.523409	1.123062	-3.400348	33374.090288
HLA A*0250	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.577126	1.176703	-3.400422	37768.149987
HLA A*0250	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.449422	1.048747	-3.400675	28146.331886
HLA B*0702	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.365938	0.965021	-3.400916	23224.028391
HLA B*5301	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.549155	1.148177	-3.400978	35412.378150
HLA A*0203	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.366008	0.965021	-3.400987	23227.797879
HLA B*5701	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.420197	1.019055	-3.401141	26314.587127
HLA B*1517	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.506221	1.105060	-3.401161	32078.983949
HLA B*4501	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.632207	1.230828	-3.401379	42875.286838
HLA B*2705	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.359096	0.957710	-3.401386	22861.033150
HLA A*0101	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.353814	0.952354	-3.401460	22584.694023
HLA B*1502	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.578265	1.176703	-3.401562	37867.376034
HLA B*0702	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.432637	1.031013	-3.401624	27079.278165
HLA A*0301	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.356746	0.955018	-3.401728	22737.691428
HLA A*2601	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.390776	0.989026	-3.401750	24591.006759
HLA B*1501	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.395064	0.993286	-3.401778	24834.997425
HLA A*0201	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.275146	0.872828	-3.402318	18842.841925
HLA A*8001	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.395903	0.993286	-3.402617	24883.008359
HLA A*0101	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.358034	0.955018	-3.403016	22805.200045
HLA A*2501	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.370705	0.967687	-3.403017	23480.355004
HLA B*7301	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.515933	1.112802	-3.403131	32804.496415
HLA A*0202	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.587764	1.184382	-3.403382	38704.742299
HLA A*1101	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.410235	1.006851	-3.403383	25717.855034
HLA B*4403	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.667966	1.264555	-3.403411	46554.985985
HLA B*0803	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.452572	1.048747	-3.403825	28351.266458
HLA A*2403	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.371536	0.967687	-3.403849	23525.365335
HLA B*5701	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.421000	1.016861	-3.404139	26363.318972
HLA B*7301	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.521471	1.117129	-3.404342	33225.468340
HLA A*3301	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.626756	1.222401	-3.404355	42340.524471
HLA B*1801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.519911	1.115540	-3.404371	33106.331038
HLA A*6801	1:34-42	9	ARHTGGTFV	0.979623	0.277913	-4.661994	1.257536	-3.404458	45919.146727
HLA A*0250	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.552771	1.148177	-3.404594	35708.446008
HLA A*2602	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.397895	0.993286	-3.404609	24997.423544
HLA B*1517	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.393741	0.989026	-3.404715	24759.470872
HLA A*0301	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.298331	0.893488	-3.404843	19876.097698

HLA B*0803	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.467529	1.062587	-3.404943	29344.673735
HLA A*3201	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.514613	1.109528	-3.405085	32704.910477
HLA B*0803	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.394141	0.989026	-3.405115	24782.252164
HLA B*0802	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.467240	1.062125	-3.405115	29325.153804
HLA A*3001	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.276702	0.871584	-3.405117	18910.445657
HLA B*3901	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.500025	1.094888	-3.405137	31624.597903
HLA A*1101	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.391998	0.986777	-3.405221	24660.282157
HLA B*5801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.360564	0.955018	-3.405546	22938.461260
HLA B*4002	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.518389	1.112802	-3.405587	32990.476403
HLA B*3801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.473666	1.067986	-3.405680	29762.276018
HLA B*0802	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.459802	1.054023	-3.405779	28827.158040
HLA B*0803	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.500690	1.094888	-3.405802	31673.052201
HLA B*4002	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.511007	1.105060	-3.405946	32434.447559
HLA B*0801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.360992	0.955018	-3.405974	22961.057587
HLA A*8001	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.412831	1.006851	-3.405980	25872.054946
HLA A*2603	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.554216	1.148177	-3.406038	35827.448786
HLA B*4601	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.284450	0.878392	-3.406058	19250.870184
HLA A*0201	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.160430	0.754283	-3.406147	14468.731256
HLA B*4801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.425570	1.019055	-3.406514	26642.184565
HLA A*3101	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.361438	0.954860	-3.406578	22984.670908
HLA A*2403	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.423498	1.016861	-3.406637	26515.363595
HLA B*1517	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-3.747823	0.340987	-3.406836	5595.298907
HLA B*1501	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.121114	0.714055	-3.407060	13216.430242
HLA A*6901	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.345868	0.938712	-3.407156	22175.236119
HLA B*0803	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.474528	1.067176	-3.407352	29821.425612
HLA B*7301	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.407758	1.000328	-3.407430	25571.628519
HLA B*3901	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.434693	1.027215	-3.407478	27207.765940
HLA A*0212	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.434806	1.027215	-3.407591	27214.832025
HLA A*8001	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.398292	0.990658	-3.407634	25020.288420
HLA B*4402	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.424646	1.016861	-3.407786	26585.601150
HLA B*0801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.438934	1.031013	-3.407921	27474.747084
HLA B*1502	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.592315	1.184382	-3.407933	39112.460059
HLA A*0250	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.592421	1.184382	-3.408039	39121.982952
HLA A*2603	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.525235	1.117129	-3.408106	33514.672999
HLA A*2603	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.517644	1.109528	-3.408116	32933.948370
HLA A*2301	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.517691	1.109528	-3.408163	32937.511943
HLA B*4403	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.568209	1.159900	-3.408309	37000.655371
HLA A*2403	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.363287	0.954860	-3.408427	23082.738664
HLA B*4601	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.397479	0.989026	-3.408453	24973.498708
HLA A*6802	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.439728	1.031013	-3.408715	27525.031788
HLA B*1501	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.239326	0.830606	-3.408720	17351.065788
HLA A*3001	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.253616	0.844865	-3.408751	17931.462993
HLA B*0803	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.347543	0.938712	-3.408831	22260.936748
HLA A*2603	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.314705	0.905846	-3.408859	20639.761938
HLA A*0301	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.366614	0.957710	-3.408904	23260.240746
HLA A*3301	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.590894	1.181912	-3.408982	38984.654911
HLA A*0201	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.402329	0.993286	-3.409043	25253.915730
HLA A*0201	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.361476	0.952354	-3.409122	22986.660507
HLA A*6802	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.426301	1.016861	-3.409440	26687.047118
HLA B*1501	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.348215	0.938712	-3.409503	22295.406159
HLA A*0201	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.398617	0.989026	-3.409591	25038.974659
HLA A*0202	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.230765	0.821048	-3.409716	17012.362696
HLA A*0219	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.426615	1.016861	-3.409755	26706.400243
HLA A*0202	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-3.503721	0.093574	-3.410148	3189.489657
HLA A*0211	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.298026	0.887847	-3.410179	19862.124040
HLA A*0219	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.293468	0.883265	-3.410203	19654.757453
HLA A*6802	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.293486	0.883265	-3.410222	19655.608112
HLA A*3301	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.514881	1.104589	-3.410292	32725.086711
HLA A*2402	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.459057	1.048747	-3.410310	28777.763708
HLA A*2501	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.282188	0.871584	-3.410604	19150.839271
HLA B*4501	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.502687	1.091927	-3.410760	31819.033129
HLA B*4801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.378453	0.967687	-3.410766	23903.046720
HLA B*4402	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.368506	0.957710	-3.410795	23361.759076
HLA A*6901	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.368616	0.957710	-3.410906	23367.699904
HLA A*0301	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.325035	0.914083	-3.410952	21136.611713

HLA A*3001	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.260013	0.848752	-3.411261	18197.568879
HLA B*1501	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.273377	0.862113	-3.411264	18766.238980
HLA B*2705	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.133938	0.722436	-3.411501	13612.492616
HLA A*3002	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.375103	0.963515	-3.411588	23719.356072
HLA B*0802	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.428481	1.016861	-3.411620	26821.363035
HLA B*5701	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.364051	0.952354	-3.411697	23123.358757
HLA B*5301	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.596114	1.184382	-3.411732	39456.108566
HLA B*4402	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.400900	0.989026	-3.411874	25170.986693
HLA B*4601	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.379550	0.967578	-3.411972	23963.512162
HLA B*5701	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.401065	0.989026	-3.412039	25180.520555
HLA B*1503	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.261101	0.848752	-3.412349	18243.206894
HLA B*1517	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.405656	0.993286	-3.412370	25448.113770
HLA B*4402	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.296985	0.884477	-3.412508	19814.579847
HLA B*5701	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.403193	0.990658	-3.412535	25304.242295
HLA B*3801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.517599	1.105060	-3.412539	32930.563332
HLA B*0803	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.466587	1.054023	-3.412564	29281.083411
HLA A*2602	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.233687	0.821048	-3.412639	17127.240355
HLA B*7301	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.535826	1.123062	-3.412765	34342.069655
HLA B*1501	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.256494	0.843615	-3.412879	18050.691480
HLA B*0802	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.401925	0.989026	-3.412899	25230.427867
HLA A*3001	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.116143	0.703210	-3.412933	13066.000118
HLA A*0201	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.119610	0.706599	-3.413012	13170.749738
HLA A*2301	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.530167	1.117129	-3.413038	33897.413049
HLA B*5801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.336597	0.923460	-3.413137	21706.868986
HLA A*2601	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.376698	0.963515	-3.413183	23806.644954
HLA B*0801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.286097	0.872828	-3.413269	19324.014487
HLA A*2403	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.360809	0.947523	-3.413285	22951.370722
HLA A*6901	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.273974	0.860662	-3.413312	18792.043617
HLA B*4801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.189113	0.775701	-3.413412	15456.564231
HLA A*6802	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-3.804972	0.391537	-3.413436	6382.225798
HLA B*0702	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.430328	1.016861	-3.413467	26935.654929
HLA A*0206	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.399707	0.986192	-3.413514	25101.906159
HLA B*5801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.361058	0.947523	-3.413535	22964.535920
HLA B*4403	1:85-93	9	YRQSQRAEI	0.995777	0.235051	-4.644464	1.230828	-3.413636	44102.611007
HLA B*4402	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.352484	0.938712	-3.413772	22515.645519
HLA A*0101	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.339527	0.925719	-3.413808	21853.801440
HLA B*1502	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.569361	1.155314	-3.414046	37098.868515
HLA A*0216	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.433264	1.019055	-3.414209	27118.420831
HLA B*3801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.529772	1.115540	-3.414232	33866.618995
HLA B*3501	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.441575	1.027215	-3.414360	27642.322174
HLA A*2601	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.400644	0.986192	-3.414452	25156.148293
HLA B*1517	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.799019	0.384545	-3.414474	6295.331007
HLA B*5401	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.027243	0.612666	-3.414577	10647.382211
HLA A*8001	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.415171	1.000328	-3.414843	26011.836285
HLA B*3501	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-3.552431	0.137558	-3.414873	3568.048271
HLA A*1101	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.515489	1.100571	-3.414918	32770.971974
HLA B*1503	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.369793	0.954860	-3.414933	23431.120561
HLA B*3801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.532589	1.117129	-3.415460	34087.007363
HLA B*5101	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.482705	1.067176	-3.415528	30388.174307
HLA B*2705	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.370500	0.954860	-3.415640	23469.306332
HLA B*4801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.422530	1.006851	-3.415678	26456.329995
HLA B*1501	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.296292	0.880484	-3.415808	19782.982636
HLA A*2602	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.616581	1.200757	-3.415823	41360.007969
HLA B*5301	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.599697	1.183813	-3.415884	39782.971123
HLA B*4001	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.404937	0.989026	-3.415911	25406.021149
HLA B*1503	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.422809	1.006851	-3.415958	26473.367450
HLA A*0219	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.028662	0.612666	-3.415996	10682.230213
HLA B*1517	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.447140	1.031013	-3.416128	27998.866794
HLA A*2603	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.643635	1.227496	-3.416138	44018.469022
HLA B*1517	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.470201	1.054023	-3.416178	29525.730386
HLA B*5401	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.531839	1.115540	-3.416299	34028.232282
HLA B*4001	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.384073	0.967687	-3.416386	24214.373024
HLA B*5401	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-3.433819	0.017415	-3.416404	2715.309383
HLA B*4501	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.299731	0.883265	-3.416467	19940.287507
HLA B*4402	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.403334	0.986777	-3.416558	25312.457217

HLA A*0202	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.869912	0.452989	-3.416923	7411.599282
HLA A*0301	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.300967	0.883995	-3.416973	19997.110432
HLA B*7301	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.601412	1.184382	-3.417030	39940.393434
HLA A*3002	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.331128	0.914083	-3.417044	21435.202167
HLA A*3301	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.644605	1.227496	-3.417109	44116.928745
HLA A*2601	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.382278	0.965021	-3.417257	24114.497802
HLA A*6801	1:201-209	9	PCDDALMKI	1.248268	0.016287	-4.681835	1.264555	-3.417280	48065.693217
HLA B*4601	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.340789	0.923460	-3.417328	21917.381456
HLA B*4001	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.384943	0.967578	-3.417364	24262.890483
HLA B*3501	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.434326	1.016861	-3.417466	27184.813831
HLA B*2705	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.301954	0.884477	-3.417477	20042.598594
HLA A*2403	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.381136	0.963515	-3.417621	24051.179092
HLA A*0212	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.404493	0.986777	-3.417716	25380.057555
HLA A*3002	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.530533	1.112802	-3.417731	33926.032598
HLA A*2402	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.485731	1.067986	-3.417744	30600.656619
HLA A*6801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.477475	1.059725	-3.417750	30024.421978
HLA B*1501	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.375472	0.957710	-3.417761	23739.510727
HLA A*0219	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.448780	1.031013	-3.417768	28104.793257
HLA B*2705	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.352038	0.934152	-3.417886	22492.514051
HLA A*0211	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.261761	0.843615	-3.418146	18270.960922
HLA B*5801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.356930	0.938712	-3.418217	22747.288107
HLA B*5401	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-3.686770	0.268538	-3.418232	4861.491992
HLA B*5301	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.501500	1.083182	-3.418319	31732.222358
HLA A*3002	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.585567	1.167129	-3.418438	38509.458491
HLA A*2601	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.373315	0.954860	-3.418455	23621.905982
HLA B*5801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.333012	0.914477	-3.418535	21528.405792
HLA B*3501	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.404739	0.986192	-3.418547	25394.478497
HLA A*6801	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.585737	1.167129	-3.418607	38524.461309
HLA A*0101	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.383657	0.965021	-3.418636	24191.197640
HLA A*0206	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.267480	0.848752	-3.418728	18513.137863
HLA B*1517	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.467510	1.048747	-3.418763	29343.403751
HLA B*5301	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.581663	1.162617	-3.419045	38164.762813
HLA B*1503	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.188455	0.769405	-3.419050	15433.168831
HLA B*2705	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.306970	0.887847	-3.419123	20275.434934
HLA B*7301	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.602977	1.183813	-3.419164	40084.557674
HLA A*0301	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.366689	0.947523	-3.419166	23264.267825
HLA A*2301	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.467999	1.048747	-3.419252	29376.441204
HLA A*0211	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.292164	0.872828	-3.419336	19595.832775
HLA A*2301	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.524417	1.105060	-3.419357	33451.636244
HLA B*1503	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.333566	0.914083	-3.419483	21555.909390
HLA A*3101	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.188967	0.769461	-3.419506	15451.380766
HLA B*1502	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.579409	1.159900	-3.419509	37967.273568
HLA A*2603	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.586676	1.167129	-3.419547	38607.916800
HLA A*0219	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.446772	1.027215	-3.419557	27975.095980
HLA B*4001	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.304160	0.884477	-3.419683	20144.671749
HLA B*5801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.345427	0.925719	-3.419707	22152.694058
HLA B*5301	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.596657	1.176703	-3.419954	39505.447072
HLA B*1502	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.582356	1.162401	-3.419955	38225.719246
HLA A*0250	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.482545	1.062587	-3.419958	30376.997390
HLA B*0802	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.479751	1.059725	-3.420026	30182.228745
HLA A*0216	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.372476	0.952354	-3.420122	23576.328304
HLA A*0219	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.126908	0.706599	-3.420309	13393.929173
HLA B*2705	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.334830	0.914477	-3.420353	21618.739693
HLA A*0212	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.406779	0.986192	-3.420586	25514.005895
HLA A*2902	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.251276	0.830606	-3.420670	17835.103632
HLA B*4601	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.385708	0.965021	-3.420687	24305.718851
HLA B*4402	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.384207	0.963515	-3.420692	24221.841009
HLA A*2601	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.378688	0.957710	-3.420978	23915.981502
HLA B*4001	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.376139	0.955018	-3.421121	23776.012347
HLA B*1801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.471303	1.050133	-3.421169	29600.739309
HLA B*4002	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.071291	0.650029	-3.421262	11783.952659
HLA B*4601	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.414664	0.993286	-3.421377	25981.458269
HLA A*0206	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.360125	0.938712	-3.421413	22915.267316
HLA B*5101	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.389160	0.967687	-3.421472	24499.649063
HLA A*0216	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.407751	0.986192	-3.421559	25571.213503

HLA A*1101	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.475814	1.054023	-3.421791	29909.804155
HLA A*0250	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.589019	1.167129	-3.421889	38816.717349
HLA B*4001	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.293536	0.871584	-3.421952	19657.841267
HLA B*4601	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.385586	0.963515	-3.422071	24298.882268
HLA A*6901	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.369636	0.947523	-3.422112	23422.629195
HLA A*0101	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.380067	0.957710	-3.422357	23992.049928
HLA A*0216	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.369889	0.947523	-3.422366	23436.318287
HLA A*6901	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.138904	0.716494	-3.422411	13769.065582
HLA A*0101	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.350184	0.927578	-3.422607	22396.711555
HLA A*3201	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.585027	1.162401	-3.422626	38461.571951
HLA B*4501	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.585168	1.162401	-3.422767	38474.058348
HLA B*2705	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.409243	0.986192	-3.423051	25659.208829
HLA B*7301	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.538615	1.115540	-3.423075	34563.308160
HLA B*5301	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.590243	1.167129	-3.423113	38926.278625
HLA A*2601	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.391129	0.967578	-3.423550	24610.970051
HLA B*4801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.410451	0.986777	-3.423674	25730.658248
HLA A*8001	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.440581	1.016861	-3.423720	27579.138273
HLA B*2705	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.442940	1.019055	-3.423884	27729.342704
HLA B*4403	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.541071	1.117129	-3.423942	34759.259458
HLA B*5101	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.414624	0.990658	-3.423966	25979.068913
HLA B*1509	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.150112	0.726109	-3.424003	14129.002825
HLA B*4002	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.491536	1.067176	-3.424360	31012.467559
HLA A*3002	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.376771	0.952354	-3.424417	23810.637819
HLA A*2501	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.484173	1.059725	-3.424448	30491.096116
HLA A*0211	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.392440	0.967687	-3.424752	24685.375881
HLA B*5801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.359009	0.934152	-3.424857	22856.457609
HLA B*1801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.484626	1.059725	-3.424902	30522.948758
HLA A*1101	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.339983	0.915076	-3.424906	21876.749448
HLA B*5701	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.348406	0.923460	-3.424945	22305.178169
HLA A*6901	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.200687	0.775701	-3.424986	15874.005488
HLA B*1801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.379884	0.954860	-3.425024	23981.928106
HLA B*3901	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.431904	1.006851	-3.425053	27033.609999
HLA A*0201	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.372631	0.947523	-3.425108	23584.747798
HLA A*2402	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.534727	1.109528	-3.425199	34255.231414
HLA B*5701	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.418862	0.993286	-3.425576	26233.851322
HLA B*3801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.526177	1.100571	-3.425606	33587.457496
HLA B*1501	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.304099	0.878392	-3.425707	20141.838457
HLA A*2402	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.585671	1.159900	-3.425771	38518.626185
HLA A*2902	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.442634	1.016861	-3.425774	27709.847913
HLA A*0301	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.364516	0.938712	-3.425804	23148.140799
HLA A*6802	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.349376	0.923460	-3.425916	22355.069992
HLA A*0216	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.442860	1.016861	-3.425999	27724.242743
HLA B*5101	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.360266	0.934152	-3.426114	22922.706667
HLA A*3002	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.148636	0.722436	-3.426200	14081.082253
HLA A*3101	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.389797	0.963515	-3.426281	24535.593850
HLA A*3301	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.627055	1.200757	-3.426297	42369.624774
HLA B*4403	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.588946	1.162617	-3.426329	38810.208077
HLA A*3001	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.247472	0.821048	-3.426424	17679.575007
HLA B*1517	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.247700	0.821048	-3.426652	17688.854962
HLA B*4501	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.493923	1.067176	-3.426747	31183.395272
HLA B*5401	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.518692	1.091927	-3.426765	33013.507690
HLA B*4001	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.350335	0.923460	-3.426874	22404.467376
HLA A*6802	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.030105	0.603125	-3.426980	10717.772074
HLA B*3901	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.489177	1.062125	-3.427052	30844.479081
HLA B*2705	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.394735	0.967578	-3.427157	24816.194905
HLA A*2603	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.420455	0.993286	-3.427169	26330.251277
HLA B*1509	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.544461	1.117129	-3.427332	35031.668468
HLA B*4402	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.434214	1.006851	-3.427362	27177.755539
HLA B*4402	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.379809	0.952354	-3.427455	23977.776799
HLA B*0702	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.321236	0.893488	-3.427748	20952.519431
HLA B*0803	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.477883	1.050133	-3.427750	30052.697895
HLA B*1501	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.311890	0.883995	-3.427895	20506.427208
HLA A*0203	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.308410	0.880484	-3.427926	20342.785203
HLA B*4403	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.565289	1.137355	-3.427934	36752.679443
HLA A*8001	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.383126	0.955018	-3.428108	24161.638710

HLA B*0702	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.312165	0.883995	-3.428170	20519.411004
HLA B*1503	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.393206	0.965021	-3.428184	24728.950012
HLA A*6801	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.612128	1.183813	-3.428315	40938.161947
HLA A*6901	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.343415	0.915076	-3.428339	22050.345085
HLA A*0201	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.393394	0.965021	-3.428372	24739.654799
HLA A*3002	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.031862	0.603125	-3.428737	10761.230449
HLA A*2902	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.343164	0.914377	-3.428787	22037.584757
HLA B*5401	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.533449	1.104589	-3.428860	34154.567162
HLA B*4402	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.415056	0.986192	-3.428864	26004.941863
HLA B*4001	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.393892	0.965021	-3.428870	24768.044899
HLA A*0202	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.596009	1.167129	-3.428879	39446.504343
HLA B*3901	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.429237	1.000328	-3.428909	26868.126147
HLA A*0219	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.203149	0.774156	-3.428993	15964.259784
HLA A*1101	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.491713	1.062587	-3.429126	31025.053163
HLA B*1517	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.491713	1.062587	-3.429126	31025.053163
HLA B*1517	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.219365	0.790220	-3.429145	16571.618697
HLA B*1502	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.529767	1.100571	-3.429196	33866.252568
HLA B*0702	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.376736	0.947523	-3.429213	23808.705704
HLA A*6901	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.343796	0.914477	-3.429319	22069.678523
HLA B*0801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.394479	0.965021	-3.429458	24801.565656
HLA B*5801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.357047	0.927578	-3.429469	22753.441955
HLA A*0101	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.343662	0.914083	-3.429579	22062.874085
HLA A*0250	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.584957	1.155314	-3.429642	38455.330273
HLA A*3301	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.448701	1.019055	-3.429645	28099.624243
HLA A*0219	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.397355	0.967687	-3.429667	24966.339230
HLA B*0802	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.423063	0.993286	-3.429777	26488.839512
HLA B*3801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.480021	1.050133	-3.429888	30201.012076
HLA A*0206	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.387621	0.957710	-3.429911	24412.988740
HLA A*6802	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.155078	0.725139	-3.429940	14291.516770
HLA B*4001	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.416825	0.986777	-3.430048	26111.092868
HLA B*0702	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.437028	1.006851	-3.430177	27354.467878
HLA A*6901	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.125884	0.695627	-3.430256	13362.373986
HLA A*1101	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.479054	1.048747	-3.430306	30133.772777
HLA A*0212	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.388027	0.957710	-3.430317	24435.847816
HLA A*6801	1:162-170	9	DDDLAWNDL	1.228018	0.006174	-4.664564	1.234192	-3.430372	46191.721274
HLA A*2601	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.382814	0.952354	-3.430460	24144.260295
HLA B*5801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.351173	0.920689	-3.430484	22447.779617
HLA A*0203	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.423975	0.993286	-3.430688	26544.498961
HLA A*2902	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.461874	1.031013	-3.430861	28965.036148
HLA B*3901	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.378409	0.947523	-3.430885	23900.589903
HLA B*3501	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.462022	1.031013	-3.431009	28974.909781
HLA A*0201	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.356735	0.925719	-3.431016	22737.076395
HLA A*0203	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.333355	0.902312	-3.431043	21545.416587
HLA A*3201	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.354524	0.923460	-3.431063	22621.622750
HLA A*3002	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.493193	1.062125	-3.431067	31130.974084
HLA A*3301	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.498256	1.067176	-3.431079	31496.032512
HLA A*2301	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.499120	1.067986	-3.431134	31558.798506
HLA A*0202	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.450209	1.019055	-3.431153	28197.388096
HLA B*5701	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.345760	0.914377	-3.431384	22169.718390
HLA A*0201	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.314768	0.883265	-3.431503	20642.776947
HLA A*0216	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.304409	0.872828	-3.431581	20156.226988
HLA A*3101	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.389294	0.957710	-3.431583	24507.205029
HLA A*2501	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.458864	1.027215	-3.431650	28765.000409
HLA A*2301	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.547266	1.115540	-3.431726	35258.684701
HLA B*0803	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.491471	1.059725	-3.431746	31007.770242
HLA A*3301	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.448611	1.016861	-3.431751	28093.848234
HLA B*4402	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.280600	0.848752	-3.431848	19080.930931
HLA A*0206	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.523926	1.091927	-3.431999	33413.834963
HLA A*0202	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.389726	0.957710	-3.432016	24531.612127
HLA A*2602	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.387088	0.955018	-3.432069	24383.026896
HLA B*2705	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-3.972505	0.540290	-3.432214	9386.518549
HLA B*2705	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.419031	0.986777	-3.432255	26244.071713
HLA B*5301	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.346362	0.914083	-3.432278	22200.443205
HLA B*5301	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.549444	1.117129	-3.432315	35435.949968
HLA B*4001	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.396009	0.963515	-3.432493	24889.066741

HLA A*3001	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-3.514698	0.082100	-3.432598	3271.131416
HLA B*4601	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.387496	0.954860	-3.432636	24405.989951
HLA A*0301	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.356319	0.923460	-3.432858	22715.314919
HLA A*0101	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.347257	0.914377	-3.432880	22246.249233
HLA A*3002	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.433217	1.000328	-3.432889	27115.486837
HLA B*7301	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.600021	1.167129	-3.432892	39812.682775
HLA A*0201	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.390720	0.957710	-3.433010	24587.814135
HLA A*2902	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.398321	0.965021	-3.433299	25021.912757
HLA A*6802	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.426641	0.993286	-3.433355	26707.989556
HLA A*0212	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.450333	1.016861	-3.433473	28205.474126
HLA A*8001	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.347952	0.914477	-3.433475	22281.901295
HLA A*1101	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.434098	1.000328	-3.433770	27170.552091
HLA A*1101	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.207932	0.774156	-3.433777	16141.070628
HLA B*0803	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.450683	1.016861	-3.433823	28228.218977
HLA A*0203	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.450834	1.016861	-3.433973	28237.994207
HLA A*2902	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.294666	0.860662	-3.434004	19709.060661
HLA B*7301	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.610714	1.176703	-3.434011	40805.053323
HLA B*1517	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.389007	0.954860	-3.434147	24491.035452
HLA B*4402	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.354860	0.920689	-3.434170	22639.129929
HLA A*3301	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.071521	0.637330	-3.434191	11790.201803
HLA B*4801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.399239	0.965021	-3.434218	25074.896793
HLA A*3101	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.224553	0.790220	-3.434333	16770.754238
HLA B*4801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.305946	0.871584	-3.434362	20227.667386
HLA A*6801	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.616529	1.181912	-3.434617	41355.085695
HLA B*3801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.488752	1.054023	-3.434729	30814.291260
HLA A*2602	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.349233	0.914377	-3.434856	22347.693964
HLA A*6802	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.362714	0.927578	-3.435136	23052.289252
HLA B*1501	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.360893	0.925719	-3.435174	22955.841075
HLA A*0211	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.337610	0.902312	-3.435298	21757.541124
HLA B*4601	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.390436	0.955018	-3.435417	24571.724303
HLA A*0250	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.387933	0.952354	-3.435579	24430.560579
HLA A*2602	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.495364	1.059725	-3.435639	31286.979243
HLA A*2603	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.320179	0.884477	-3.435702	20901.573605
HLA A*0216	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.462988	1.027215	-3.435773	29039.406139
HLA A*1101	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.466871	1.031013	-3.435859	29300.256983
HLA B*4403	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.646179	1.210192	-3.435988	44277.126253
HLA A*0201	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.323872	0.887847	-3.436025	21080.085802
HLA B*5101	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.150196	0.714055	-3.436141	14131.754801
HLA B*3501	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.391234	0.955018	-3.436216	24616.962198
HLA A*3002	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.591563	1.155314	-3.436249	39044.808531
HLA A*0212	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.048994	0.612666	-3.436329	11194.233882
HLA A*6802	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.401481	0.965021	-3.436459	25204.643720
HLA A*2501	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.404060	0.967578	-3.436482	25354.806318
HLA B*4002	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.490510	1.054023	-3.436487	30939.236913
HLA B*3901	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.453374	1.016861	-3.436513	28403.616358
HLA B*5301	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.559622	1.123062	-3.436560	36276.221822
HLA B*0802	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.330056	0.893488	-3.436568	21382.388635
HLA A*2602	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.599448	1.162617	-3.436831	39760.164188
HLA A*2402	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.490942	1.054023	-3.436919	30970.049769
HLA A*2603	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.637698	1.200757	-3.436940	43420.796419
HLA A*3101	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.280557	0.843615	-3.436942	19079.072959
HLA B*4801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.371200	0.934152	-3.437048	23507.172818
HLA A*3002	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.499708	1.062587	-3.437121	31601.509783
HLA B*4001	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.384806	0.947523	-3.437283	24255.278623
HLA A*3101	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.384849	0.947523	-3.437325	24257.640669
HLA A*3101	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.351756	0.914377	-3.437380	22477.916949
HLA B*5401	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.389794	0.952354	-3.437440	24535.461115
HLA A*0202	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.592839	1.155314	-3.437525	39159.674011
HLA B*1503	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.423768	0.986192	-3.437575	26531.864923
HLA B*2705	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.389961	0.952354	-3.437607	24544.887048
HLA B*0803	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.428427	0.990658	-3.437769	26818.025929
HLA A*2902	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.424158	0.986192	-3.437965	26555.702343
HLA A*3201	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.622412	1.184382	-3.438030	41919.108275
HLA A*2402	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.542652	1.104589	-3.438063	34886.043556
HLA B*3501	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.431352	0.993286	-3.438066	26999.263360

HLA B*3901	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.372239	0.934152	-3.438087	23563.449745
HLA B*0702	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.226207	0.787998	-3.438209	16834.748481
HLA B*2705	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.164373	0.726109	-3.438264	14600.673383
HLA B*4601	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.352473	0.914083	-3.438389	22515.036491
HLA A*3002	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.533315	1.094888	-3.438427	34144.036758
HLA A*0301	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.366161	0.927578	-3.438583	23235.967203
HLA A*2501	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.455474	1.016861	-3.438613	28541.321503
HLA B*4501	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.539431	1.100571	-3.438859	34628.252431
HLA A*3001	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.273525	0.834602	-3.438923	18772.636037
HLA A*0250	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.554491	1.115540	-3.438951	35850.133200
HLA A*3002	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.142307	0.703210	-3.439097	13877.349394
HLA B*5101	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.489243	1.050133	-3.439110	30849.151661
HLA B*3801	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.501799	1.062587	-3.439212	31754.031661
HLA A*0250	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-3.619443	0.180214	-3.439229	4163.348181
HLA B*1517	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.301442	0.862113	-3.439328	20018.975172
HLA A*2403	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.391798	0.952354	-3.439444	24648.944965
HLA B*4601	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.397360	0.957710	-3.439649	24966.609361
HLA A*3002	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.123515	0.683810	-3.439705	13289.705030
HLA A*0212	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.363475	0.923460	-3.440015	23092.730831
HLA B*4501	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.534924	1.094888	-3.440036	34270.801580
HLA A*2501	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.363506	0.923460	-3.440046	23094.354967
HLA A*3002	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.555588	1.115540	-3.440048	35940.820138
HLA B*0702	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.403576	0.963515	-3.440061	25326.565719
HLA A*2902	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.427003	0.986777	-3.440226	26730.249866
HLA A*2602	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.553098	1.112802	-3.440296	35735.307951
HLA A*2603	1:111-119	9	FSTPEEVEA	1.413854	-0.203662	-4.650500	1.210192	-3.440308	44719.828436
HLA B*1502	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.489058	1.048747	-3.440310	30835.970129
HLA B*4601	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.234778	0.794424	-3.440353	17170.286963
HLA A*2603	1:91-99	9	AEIYRDVLA	1.321993	-0.140081	-4.622344	1.181912	-3.440432	41912.532237
HLA B*4402	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.387962	0.947523	-3.440438	24432.146630
HLA A*3201	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.607775	1.167129	-3.440645	40529.826440
HLA B*3801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.553466	1.112802	-3.440664	35765.672721
HLA B*4403	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.603090	1.162401	-3.440689	40094.967971
HLA B*4402	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.405743	0.965021	-3.440721	25453.208125
HLA A*0203	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.285616	0.844865	-3.440751	19302.595507
HLA B*1502	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.447629	1.006851	-3.440778	28030.390446
HLA B*4001	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.321375	0.880484	-3.440891	20959.208196
HLA A*2501	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.053759	0.612666	-3.441094	11317.724866
HLA B*1503	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.022887	0.581735	-3.441152	10541.123440
HLA A*3301	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.608487	1.167129	-3.441357	40596.317267
HLA A*0206	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.472419	1.031013	-3.441406	29676.902065
HLA A*0216	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.210846	0.769405	-3.441440	16249.713162
HLA B*4801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.356166	0.914477	-3.441689	22707.328646
HLA B*0802	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.448748	1.006851	-3.441896	28102.664724
HLA B*4402	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.396822	0.954860	-3.441962	24935.698264
HLA B*1503	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.263040	0.821048	-3.441991	18324.811190
HLA A*8001	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.389710	0.947523	-3.442186	24530.683152
HLA B*4801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.431249	0.989026	-3.442223	26992.837352
HLA A*0301	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.368047	0.925719	-3.442328	23337.127088
HLA A*8001	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.366104	0.923460	-3.442644	23232.950503
HLA B*5301	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.602648	1.159900	-3.442748	40054.209747
HLA B*0801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.338270	0.895455	-3.442815	21790.641631
HLA B*2705	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.406520	0.963515	-3.443005	25498.827337
HLA A*0301	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.357503	0.914377	-3.443126	22777.334649
HLA B*5301	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.505791	1.062587	-3.443204	32047.241159
HLA B*0801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.129638	0.686428	-3.443210	13478.392515
HLA A*2602	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.603259	1.159900	-3.443359	40110.588485
HLA A*0216	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.211955	0.768573	-3.443382	16291.259300
HLA B*0802	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.470626	1.027215	-3.443411	29554.655843
HLA A*0250	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.548591	1.105060	-3.443531	35366.429496
HLA B*0802	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.408682	0.965021	-3.443660	25626.053847
HLA A*1101	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.462753	1.019055	-3.443697	29023.700391
HLA A*2601	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.358783	0.915076	-3.443707	22844.590204
HLA A*2403	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.315722	0.871584	-3.444138	20688.166881
HLA B*1502	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.536165	1.091927	-3.444238	34368.833376

HLA B*1509	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.411940	0.967687	-3.444253	25819.062575
HLA A*8001	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.463335	1.019055	-3.444280	29062.666245
HLA B*2705	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.437646	0.993286	-3.444360	27393.415538
HLA A*3201	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.080308	0.635887	-3.444421	12031.182442
HLA B*4002	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.628448	1.183813	-3.444635	42505.767514
HLA A*6802	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-3.892772	0.448098	-3.444674	7812.183209
HLA B*4801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.412279	0.967578	-3.444701	25839.184082
HLA A*1101	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.408224	0.963515	-3.444708	25599.034450
HLA A*2402	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.561964	1.117129	-3.444836	36472.412025
HLA A*6802	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.236770	0.791821	-3.444949	17249.238090
HLA B*5101	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.400000	0.955018	-3.444982	25118.886716
HLA A*2902	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.279646	0.834602	-3.445044	19039.067280
HLA B*4601	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.392571	0.947523	-3.445048	24692.855543
HLA B*1502	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.554597	1.109528	-3.445068	35858.861798
HLA B*1509	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.504919	1.059725	-3.445194	31982.984644
HLA A*2501	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.445609	1.000328	-3.445281	27900.281824
HLA B*5801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.351143	0.905846	-3.445297	22446.200952
HLA B*3901	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.432094	0.986777	-3.445318	27045.458750
HLA A*2602	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.600745	1.155314	-3.445431	39879.075790
HLA A*3101	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.400466	0.955018	-3.445447	25145.807429
HLA B*4402	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.438776	0.993286	-3.445490	27464.790321
HLA B*5401	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.472989	1.027215	-3.445775	29715.941067
HLA B*5101	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.432578	0.986777	-3.445802	27075.616016
HLA B*0801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.439192	0.993286	-3.445906	27491.101837
HLA A*0301	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.330519	0.884477	-3.446042	21405.189024
HLA B*1502	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.613176	1.167129	-3.446047	41037.057236
HLA B*0801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.371783	0.925719	-3.446064	23538.732441
HLA A*6901	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.200456	0.754283	-3.446173	15865.591810
HLA B*7301	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.601572	1.155314	-3.446258	39955.089108
HLA A*0211	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.465443	1.019055	-3.446388	29204.040534
HLA B*1517	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.463319	1.016861	-3.446458	29061.565685
HLA A*0101	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.380685	0.934152	-3.446533	24026.210133
HLA A*2402	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.496703	1.050133	-3.446570	31383.605828
HLA B*4501	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.551340	1.104589	-3.446751	35590.993746
HLA B*5701	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.401770	0.955018	-3.446751	25221.420883
HLA A*2403	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.433001	0.986192	-3.446809	27101.994551
HLA B*4501	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.433612	0.986777	-3.446836	27140.142258
HLA A*0203	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.435865	0.989026	-3.446839	27281.313475
HLA A*2601	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.394392	0.947523	-3.446869	24796.601726
HLA B*3801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.514117	1.067176	-3.446941	32667.599558
HLA A*2602	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.433748	0.986777	-3.446972	27148.659454
HLA A*2902	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.404695	0.957710	-3.446984	25391.868386
HLA B*4001	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.367768	0.920689	-3.447078	23322.108021
HLA A*0202	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.290799	0.843615	-3.447184	19534.336916
HLA B*0802	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.415063	0.967687	-3.447376	26005.363917
HLA A*3101	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.268514	0.821048	-3.447466	18557.258123
HLA A*0301	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.368200	0.920689	-3.447511	23345.334863
HLA A*2602	1:252-260	9	GEGTKKLSK	1.151343	0.015786	-4.614694	1.167129	-3.447564	41180.723963
HLA B*5701	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.405646	0.957710	-3.447936	25447.563090
HLA A*2501	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.479044	1.031013	-3.448031	30133.120703
HLA B*5801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.350370	0.902312	-3.448058	22406.285535
HLA A*0212	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.441441	0.993286	-3.448155	27633.799600
HLA A*6801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.060488	0.612321	-3.448167	11494.446337
HLA A*0202	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.475475	1.027215	-3.448261	29886.512772
HLA A*3201	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.608205	1.159900	-3.448305	40569.971231
HLA A*3002	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.336195	0.887847	-3.448349	21686.797441
HLA A*6802	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.310551	0.862113	-3.448437	20443.290230
HLA B*0702	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.467520	1.019055	-3.448464	29344.038736
HLA B*5101	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.468854	1.020365	-3.448489	29434.346276
HLA A*0250	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.549096	1.100571	-3.448525	35407.589048
HLA B*1501	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.396161	0.947523	-3.448638	24897.820341
HLA A*2501	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.455556	1.006851	-3.448705	28546.726203
HLA B*4002	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.372178	0.923460	-3.448718	23560.135611
HLA A*3002	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.396471	0.947523	-3.448948	24915.606357
HLA B*0802	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.480083	1.031013	-3.449070	30205.260362

HLA A*2301	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.363619	0.914477	-3.449142	23100.352765
HLA A*0250	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.435553	0.986192	-3.449360	27261.691214
HLA A*3002	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.333851	0.884477	-3.449373	21570.024434
HLA B*5401	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.468441	1.019055	-3.449385	29406.333981
HLA A*2602	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.516579	1.067176	-3.449403	32853.336625
HLA B*4402	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.337269	0.887847	-3.449422	21740.480463
HLA A*0211	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.541479	1.091927	-3.449552	34791.994473
HLA A*0212	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.417377	0.967687	-3.449690	26144.309635
HLA A*6802	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.438797	0.989026	-3.449771	27466.127587
HLA A*0219	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.373848	0.923460	-3.450388	23650.932561
HLA A*0201	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.389174	0.938712	-3.450462	24500.444318
HLA B*1502	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.573606	1.123062	-3.450544	37463.313242
HLA A*2601	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.389322	0.938712	-3.450610	24508.796056
HLA B*4501	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.331381	0.880484	-3.450897	21447.729730
HLA B*5401	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.556006	1.105060	-3.450946	35975.446389
HLA B*0803	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.481965	1.031013	-3.450952	30336.433459
HLA B*1801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.467973	1.016861	-3.451113	29374.693100
HLA A*3301	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.599317	1.148177	-3.451139	39748.120520
HLA A*0212	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.440214	0.989026	-3.451188	27555.872879
HLA A*3002	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.177314	0.726109	-3.451205	15042.286264
HLA A*2601	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.357122	0.905846	-3.451276	22757.381291
HLA B*5401	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.519338	1.067986	-3.451351	33062.659082
HLA A*2601	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.365439	0.914083	-3.451356	23197.408102
HLA B*0801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-3.815991	0.364577	-3.451414	6546.229845
HLA A*8001	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.414943	0.963515	-3.451428	25998.189914
HLA A*0101	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.241969	0.790220	-3.451750	17456.988551
HLA B*4501	1:109-117	9	HAFSTPEEV	0.992700	0.144655	-4.589146	1.137355	-3.451791	38828.058689
HLA B*1801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.419541	0.967687	-3.451854	26274.898926
HLA A*2402	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.419480	0.967578	-3.451902	26271.203434
HLA B*0802	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.442632	0.990658	-3.451974	27709.698006
HLA A*8001	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.417001	0.965021	-3.451980	26121.689376
HLA A*3101	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.323644	0.871584	-3.452060	21069.026734
HLA A*3002	1:323-331	9	KADALNAEH	0.661781	-0.194938	-3.919148	0.466843	-3.452304	8301.331142
HLA A*2403	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.386479	0.934152	-3.452327	24348.886267
HLA A*6901	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.380037	0.927578	-3.452459	23990.362661
HLA A*3101	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.391263	0.938712	-3.452550	24618.560351
HLA B*7301	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.600825	1.148177	-3.452648	39886.411672
HLA B*1509	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.445947	0.993286	-3.452661	27922.025283
HLA B*5401	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.562350	1.109528	-3.452822	36504.785504
HLA A*3002	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.446140	0.993286	-3.452853	27934.414545
HLA B*7301	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.553448	1.100571	-3.452876	35764.124848
HLA B*4801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.416496	0.963515	-3.452981	26091.324218
HLA A*2603	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.608306	1.155314	-3.452991	40579.409927
HLA B*5401	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-3.590694	0.137558	-3.453136	3896.677232
HLA A*6901	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.296625	0.843357	-3.453268	19798.185847
HLA B*4402	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.420962	0.967687	-3.453275	26361.037109
HLA A*2601	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.376743	0.923460	-3.453283	23809.092115
HLA B*3901	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.108718	0.655319	-3.453399	12844.532004
HLA A*0219	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.392256	0.938712	-3.453544	24674.961557
HLA A*2301	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.545492	1.091927	-3.453565	35114.965499
HLA B*3501	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.315696	0.862113	-3.453583	20686.935790
HLA B*7301	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.367704	0.914083	-3.453621	23318.701680
HLA B*1503	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.388107	0.934152	-3.453955	24440.342867
HLA B*4801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.440374	0.986192	-3.454182	27566.011791
HLA A*6801	1:137-145	9	RHLTDAQRA	1.402106	-0.174610	-4.681753	1.227496	-3.454257	48056.593027
HLA B*5401	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.441121	0.986777	-3.454344	27613.475649
HLA B*2705	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.422067	0.967687	-3.454379	26428.149229
HLA B*1517	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.113032	0.658550	-3.454482	12972.746739
HLA A*8001	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.441321	0.986777	-3.454544	27626.176366
HLA A*0216	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.380309	0.925719	-3.454590	24005.422470
HLA B*3501	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.134506	0.679867	-3.454639	13630.325670
HLA B*0803	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.481885	1.027215	-3.454670	30330.854003
HLA B*4402	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.298106	0.843357	-3.454749	19865.777740
HLA A*2403	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.443851	0.989026	-3.454825	27787.608750
HLA B*0801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.224351	0.769405	-3.454945	16762.953452

HLA A*0101	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.393845	0.938712	-3.455133	24765.365197
HLA A*0202	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.560202	1.105060	-3.455142	36324.728056
HLA A*0201	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.276199	0.821048	-3.455151	18888.565395
HLA B*1502	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.410040	0.954860	-3.455180	25706.309774
HLA B*5801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.352590	0.897326	-3.455264	22521.127508
HLA B*1509	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.517395	1.062125	-3.455269	32915.067869
HLA B*4002	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.632115	1.176703	-3.455412	42866.241721
HLA B*4001	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.369967	0.914477	-3.455490	23440.502661
HLA B*1502	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.327157	0.871584	-3.455573	21240.119425
HLA B*4402	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.336148	0.880484	-3.455664	21684.451105
HLA A*3001	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.229881	0.774156	-3.455725	16977.792709
HLA B*4001	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.408116	0.952354	-3.455761	25592.664797
HLA A*0301	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.358095	0.902312	-3.455783	22808.407985
HLA B*3501	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.148105	0.692320	-3.455785	14063.876750
HLA B*1503	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.444833	0.989026	-3.455807	27850.516907
HLA A*6801	1:329-337	9	AEHIRMLDV	1.009089	0.213312	-4.678212	1.222401	-3.455812	47666.394646
HLA B*4402	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.334295	0.878392	-3.455903	21592.090395
HLA A*0101	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.379600	0.923460	-3.456140	23966.234755
HLA B*1503	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.376914	0.920689	-3.456225	23818.496704
HLA A*0216	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.487246	1.031013	-3.456234	30707.620403
HLA A*6901	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.381963	0.925719	-3.456244	24097.022931
HLA B*0702	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.318659	0.862113	-3.456545	20828.541841
HLA A*3001	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-3.730174	0.273594	-3.456580	5372.469524
HLA A*2403	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.337182	0.880484	-3.456698	21736.129196
HLA A*0201	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.390936	0.934152	-3.456784	24600.054777
HLA B*5801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.340065	0.883265	-3.456800	21880.892118
HLA A*2601	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.390953	0.934152	-3.456800	24600.986380
HLA B*5701	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.411675	0.954860	-3.456815	25803.283754
HLA B*4402	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.371908	0.915076	-3.456831	23545.482532
HLA B*4501	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.641410	1.184382	-3.457028	43793.531829
HLA B*4402	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-3.960151	0.502859	-3.457292	9123.278880
HLA A*0201	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.378035	0.920689	-3.457346	23880.040115
HLA B*4002	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.642018	1.184382	-3.457637	43854.936639
HLA B*4501	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.634484	1.176703	-3.457780	43100.637067
HLA A*0202	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.227363	0.769405	-3.457957	16879.616635
HLA A*2601	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.329699	0.871584	-3.458115	21364.813056
HLA A*2402	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.451640	0.993286	-3.458354	28290.441048
HLA A*2602	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.248726	0.790220	-3.458507	17730.723037
HLA B*1517	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.477592	1.019055	-3.458537	30032.544517
HLA A*2403	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.307424	0.848752	-3.458672	20296.615745
HLA A*3101	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.346688	0.887847	-3.458841	22217.143652
HLA B*4501	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.642719	1.183813	-3.458906	43925.694263
HLA A*2403	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.414013	0.955018	-3.458994	25942.553190
HLA A*0219	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.416874	0.957710	-3.459164	26114.059457
HLA B*5701	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.406703	0.947523	-3.459180	25509.589383
HLA B*0801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.342501	0.883265	-3.459237	22003.990098
HLA A*2501	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.319899	0.860662	-3.459237	20888.121987
HLA A*0216	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.452655	0.993286	-3.459369	28356.635169
HLA A*2301	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.521962	1.062587	-3.459375	33263.056521
HLA A*0211	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.120353	0.660945	-3.459408	13193.284720
HLA A*0201	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.382873	0.923460	-3.459412	24147.525960
HLA A*2501	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.124761	0.665274	-3.459486	13327.864501
HLA A*3201	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-3.712440	0.252948	-3.459492	5157.509633
HLA A*3002	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.427285	0.967687	-3.459598	26747.608423
HLA B*4801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.414642	0.955018	-3.459624	25980.193288
HLA A*0219	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.365580	0.905846	-3.459735	23204.939049
HLA A*2602	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.514089	1.054023	-3.460066	32665.478890
HLA B*5801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.355609	0.895455	-3.460154	22678.233244
HLA B*0802	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.446523	0.986192	-3.460330	27959.058309
HLA A*6802	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.399103	0.938712	-3.460391	25067.030187
HLA B*4001	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.394578	0.934152	-3.460425	24807.201593
HLA A*0212	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.333437	0.872828	-3.460609	21549.496515
HLA A*0219	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.453905	0.993286	-3.460619	28438.364850
HLA B*5401	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.381881	0.920689	-3.461192	24092.460685
HLA A*0203	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.367051	0.905846	-3.461205	23283.657896

HLA B*4601	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.387229	0.925719	-3.461510	24390.942749
HLA B*4001	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.400306	0.938712	-3.461594	25136.558680
HLA A*0212	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.308157	0.846543	-3.461614	20330.903035
HLA A*2601	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.376010	0.914377	-3.461633	23768.938992
HLA B*4601	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.400426	0.938712	-3.461713	25143.494923
HLA A*1101	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.482129	1.020365	-3.461764	30347.923807
HLA B*1502	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.515837	1.054023	-3.461814	32797.221005
HLA B*1503	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.376921	0.915076	-3.461845	23818.883273
HLA A*6801	1:70-78	9	LDWDEGPEV	1.135549	0.065208	-4.662694	1.200757	-3.461937	45993.234844
HLA B*4801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.400982	0.938712	-3.462270	25175.753172
HLA A*6901	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.383091	0.920689	-3.462402	24159.678112
HLA A*0301	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.368249	0.905846	-3.462404	23347.987223
HLA B*3501	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.306073	0.843615	-3.462458	20233.577439
HLA B*0801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.396732	0.934152	-3.462580	24930.572615
HLA A*0216	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.383394	0.920689	-3.462705	24176.544449
HLA A*6801	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.579938	1.117129	-3.462809	38013.516423
HLA B*1502	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.430501	0.967687	-3.462814	26946.440287
HLA A*0216	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.377295	0.914477	-3.462818	23839.380433
HLA A*0216	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.323553	0.860662	-3.462891	21064.581940
HLA B*5801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.350861	0.887847	-3.463014	22431.633906
HLA A*3002	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.386540	0.923460	-3.463080	24352.311352
HLA A*6901	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.346409	0.883265	-3.463144	22202.845373
HLA A*0212	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.383866	0.920689	-3.463177	24202.848025
HLA A*0212	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.343690	0.880484	-3.463206	22064.306424
HLA A*2501	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.452286	0.989026	-3.463260	28332.560612
HLA B*5101	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.180039	0.716494	-3.463546	15136.980516
HLA A*0101	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.346822	0.883265	-3.463557	22223.995669
HLA B*1509	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.391148	0.927578	-3.463570	24612.035215
HLA A*6801	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.568240	1.104589	-3.463651	37003.257665
HLA A*2501	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.482707	1.019055	-3.463652	30388.338704
HLA B*4001	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.378879	0.915076	-3.463802	23926.463806
HLA A*1101	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.258232	0.794424	-3.463808	18123.098976
HLA A*0101	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.369690	0.905846	-3.463844	23425.543795
HLA B*5101	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.480947	1.016861	-3.464087	30265.454077
HLA B*4001	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.378195	0.914083	-3.464111	23888.826540
HLA B*1503	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.190307	0.726109	-3.464198	15499.100750
HLA A*0201	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.307858	0.843615	-3.464243	20316.939366
HLA A*1101	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.450599	0.986192	-3.464407	28222.721897
HLA A*0219	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.337293	0.872828	-3.464465	21741.656631
HLA B*7301	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.531729	1.067176	-3.464552	34019.581201
HLA A*0219	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.218857	0.754283	-3.464574	16552.265472
HLA A*0216	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.367176	0.902312	-3.464864	23290.334840
HLA A*0219	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.233525	0.768573	-3.464952	17120.848252
HLA A*3101	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.392555	0.927578	-3.464977	24691.920461
HLA B*4001	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.422711	0.957710	-3.465000	26467.352978
HLA B*4002	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.627466	1.162401	-3.465065	42409.756389
HLA B*5801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.349592	0.884477	-3.465115	22366.199099
HLA A*2403	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.430182	0.965021	-3.465161	26926.621872
HLA B*5401	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.371008	0.905846	-3.465162	23496.747092
HLA B*2705	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.325846	0.860662	-3.465184	21176.098171
HLA B*3501	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.257192	0.791821	-3.465371	18079.717507
HLA B*4002	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-3.487289	0.021903	-3.465386	3071.064233
HLA A*0201	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.379903	0.914477	-3.465426	23982.966045
HLA B*5101	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.492965	1.027215	-3.465750	31114.642103
HLA B*4402	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.391655	0.925719	-3.465936	24640.812076
HLA A*3002	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.256167	0.790220	-3.465948	18037.122921
HLA B*1501	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.322162	0.856154	-3.466008	20997.227279
HLA B*5801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.337647	0.871584	-3.466063	21759.424500
HLA B*5801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.346594	0.880484	-3.466110	22212.336481
HLA B*0801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.180180	0.714055	-3.466126	15141.894677
HLA B*0802	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.485190	1.019055	-3.466135	30562.604681
HLA B*4601	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.349404	0.883265	-3.466139	22356.521301
HLA A*3201	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.621536	1.155314	-3.466221	41834.605470
HLA A*1101	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.434195	0.967687	-3.466507	27176.579336
HLA B*5101	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.497596	1.031013	-3.466583	31448.189284

HLA B*1502	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.582128	1.115540	-3.466588	38205.665208
HLA B*0801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.311465	0.844865	-3.466600	20486.357349
HLA B*5801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.360186	0.893488	-3.466698	22918.490738
HLA A*2902	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.392567	0.925719	-3.466848	24692.588373
HLA A*2902	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.401001	0.934152	-3.466849	25176.842780
HLA B*4002	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.582548	1.115540	-3.467008	38242.680354
HLA B*4501	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.579828	1.112802	-3.467026	38003.852153
HLA A*0212	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.369415	0.902312	-3.467103	23410.721124
HLA B*5101	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.414647	0.947523	-3.467124	25980.474390
HLA B*3801	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.559063	1.091927	-3.467136	36229.544298
HLA B*1503	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.364570	0.897326	-3.467244	23151.021243
HLA B*1517	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.133632	0.666384	-3.467248	13602.922512
HLA B*0801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.302111	0.834835	-3.467276	20049.864603
HLA B*0702	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.350593	0.883265	-3.467328	22417.803969
HLA A*8001	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.406102	0.938712	-3.467390	25474.284799
HLA A*0216	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.432423	0.965021	-3.467402	27065.950320
HLA A*2402	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.364838	0.897326	-3.467512	23165.303514
HLA A*0202	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-3.720574	0.252948	-3.467626	5255.015059
HLA A*2402	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.580485	1.112802	-3.467684	38061.462831
HLA A*3201	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.458357	0.990658	-3.467699	28731.407100
HLA A*3101	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.351697	0.883995	-3.467703	22474.877079
HLA B*4801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.422570	0.954860	-3.467710	26458.763246
HLA A*2402	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.468072	1.000328	-3.467744	29381.368239
HLA A*3301	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.516544	1.048747	-3.467797	32850.670740
HLA A*0301	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.365266	0.897326	-3.467939	23188.123301
HLA A*0101	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.348789	0.880484	-3.468304	22324.855816
HLA A*0212	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.415850	0.947523	-3.468327	26052.536506
HLA B*5801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.352353	0.883995	-3.468358	22508.825352
HLA B*5101	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.420723	0.952354	-3.468369	26346.494872
HLA A*0101	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.352447	0.883995	-3.468452	22513.696689
HLA A*3301	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.468812	1.000328	-3.468484	29431.480158
HLA A*3002	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.454739	0.986192	-3.468546	28493.033512
HLA A*0101	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.389254	0.920689	-3.468564	24504.951252
HLA B*1501	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.194686	0.726109	-3.468577	15656.184889
HLA A*0101	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.383669	0.915076	-3.468593	24191.852007
HLA B*0802	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.436239	0.967578	-3.468661	27304.790203
HLA B*0802	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.455493	0.986777	-3.468716	28542.556773
HLA A*0203	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.256717	0.787998	-3.468720	18059.970827
HLA B*7301	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.459384	0.990658	-3.468726	28799.411993
HLA A*0101	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.340328	0.871584	-3.468744	21894.153934
HLA B*1503	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.487873	1.019055	-3.468818	30752.007780
HLA B*1509	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.475738	1.006851	-3.468887	29904.626724
HLA A*3301	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.436528	0.967578	-3.468950	27322.965303
HLA A*0206	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.257015	0.787998	-3.469018	18072.383300
HLA A*0250	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.352336	0.883265	-3.469071	22507.972976
HLA A*0211	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.416646	0.947523	-3.469123	26100.359457
HLA A*3101	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.337929	0.868794	-3.469135	21773.555015
HLA B*5101	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.209803	0.740545	-3.469257	16210.728340
HLA A*2603	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.318151	0.848752	-3.469399	20804.217154
HLA B*5701	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.384498	0.915076	-3.469422	24238.095107
HLA B*4001	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.383829	0.914377	-3.469452	24200.753160
HLA A*0201	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.397061	0.927578	-3.469484	24949.461796
HLA A*1101	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.434775	0.965021	-3.469754	27212.918113
HLA A*2601	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.397517	0.927578	-3.469939	24975.660463
HLA A*2601	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.395980	0.925719	-3.470261	24887.451028
HLA B*1801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.477167	1.006851	-3.470316	30003.151344
HLA B*7301	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-3.576579	0.106226	-3.470353	3772.061180
HLA B*3801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.565270	1.094888	-3.470382	36751.088854
HLA B*0702	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.396338	0.925719	-3.470618	24907.924474
HLA B*1502	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.106651	0.635887	-3.470764	12783.528334
HLA B*1517	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.425817	0.955018	-3.470798	26657.322647
HLA B*1501	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.373174	0.902312	-3.470862	23614.239713
HLA B*5401	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.385279	0.914377	-3.470902	24281.667861
HLA B*0803	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.425976	0.955018	-3.470958	26667.130946
HLA B*4402	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.343810	0.872828	-3.470982	22070.394902

HLA B*2705	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.460020	0.989026	-3.470994	28841.665200
HLA A*3301	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.259001	0.787998	-3.471003	18155.187724
HLA A*2601	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.391763	0.920689	-3.471074	24646.944826
HLA B*1801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.351646	0.880484	-3.471161	22472.202333
HLA A*6801	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.538364	1.067176	-3.471187	34543.306698
HLA B*0802	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.471523	1.000328	-3.471195	29615.795988
HLA A*2603	1:355-363	9	IALDEAAFA	1.363244	-0.200843	-4.633633	1.162401	-3.471233	43016.312244
HLA A*1101	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-3.855820	0.384545	-3.471275	7174.963887
HLA B*0702	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.377347	0.905846	-3.471501	23842.217907
HLA B*1801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.502593	1.031013	-3.471580	31812.148377
HLA B*0801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.386761	0.915076	-3.471685	24364.698372
HLA B*1517	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.320459	0.848752	-3.471707	20915.033886
HLA A*2402	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.576837	1.105060	-3.471777	37743.026802
HLA B*4403	1:253-261	9	EGTKKLSKR	0.773761	0.410621	-4.656179	1.184382	-3.471797	45308.411269
HLA A*3201	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.584705	1.112802	-3.471903	38433.076533
HLA B*5801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.246130	0.774156	-3.471975	17625.046239
HLA A*0301	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.367528	0.895455	-3.472073	23309.242230
HLA B*4801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.344997	0.872828	-3.472168	22130.773528
HLA A*0212	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.410958	0.938712	-3.472246	25760.743024
HLA A*0101	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.374626	0.902312	-3.472314	23693.321596
HLA B*4402	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.365813	0.893488	-3.472325	23217.370456
HLA B*5301	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.577452	1.105060	-3.472392	37796.561357
HLA B*5101	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.491752	1.019055	-3.472697	31027.906610
HLA A*2301	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.540004	1.067176	-3.472827	34673.992354
HLA A*3001	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.264788	0.791821	-3.472967	18398.716410
HLA A*2902	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.356347	0.883265	-3.473082	22716.789615
HLA A*6802	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.430870	0.957710	-3.473160	26969.337039
HLA B*4501	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.621383	1.148177	-3.473206	41819.897218
HLA A*2902	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.420911	0.947523	-3.473388	26357.899869
HLA B*2705	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.134361	0.660945	-3.473416	13625.754646
HLA B*5401	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.152174	0.678719	-3.473455	14196.273568
HLA B*5701	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.412180	0.938712	-3.473468	25833.313690
HLA A*3201	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.535660	1.062125	-3.473534	34328.881326
HLA A*6801	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.586460	1.112802	-3.473658	38588.706042
HLA B*0803	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.441293	0.967578	-3.473714	27624.382970
HLA A*2902	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.352160	0.878392	-3.473768	22498.842406
HLA B*4001	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.401438	0.927578	-3.473861	25202.189461
HLA B*4601	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.389190	0.915076	-3.474114	24501.372148
HLA B*1501	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.395125	0.920689	-3.474436	24838.490890
HLA B*1501	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.357891	0.883265	-3.474626	22797.675497
HLA B*0801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.432346	0.957710	-3.474635	27061.118766
HLA B*5301	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.569551	1.094888	-3.474663	37115.128839
HLA B*4402	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.408825	0.934152	-3.474673	25634.511923
HLA A*0202	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.362749	0.887847	-3.474902	23054.159982
HLA B*1501	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.359390	0.884477	-3.474912	22876.497835
HLA B*4001	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.362940	0.887847	-3.475093	23064.264553
HLA B*0803	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.481995	1.006851	-3.475144	30338.567052
HLA A*0301	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.362994	0.887847	-3.475147	23067.134559
HLA B*4402	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.389360	0.914083	-3.475276	24510.917586
HLA B*1501	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.324229	0.848752	-3.475478	21097.427152
HLA A*0212	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.182722	0.707098	-3.475624	15230.787672
HLA A*0301	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.088052	0.612321	-3.475731	12247.634434
HLA B*4402	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.430891	0.955018	-3.475873	26970.650181
HLA B*4403	1:343-351	9	RLRDHLDTH	1.259062	-0.075249	-4.659724	1.183813	-3.475911	45679.801377
HLA B*4403	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.567885	1.091927	-3.475958	36973.042297
HLA A*0211	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.244730	0.768573	-3.476157	17568.309426
HLA B*0803	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.469566	0.993286	-3.476280	29482.634517
HLA B*5801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.354914	0.878392	-3.476522	22641.947033
HLA B*0803	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.495592	1.019055	-3.476536	31303.401683
HLA B*5701	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.410803	0.934152	-3.476651	25751.546724
HLA A*8001	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.391782	0.915076	-3.476705	24648.011547
HLA B*2705	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.431815	0.955018	-3.476796	27028.053114
HLA A*0211	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.072771	0.595974	-3.476797	11824.183601
HLA B*1517	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.410956	0.934152	-3.476804	25760.603662
HLA A*8001	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.360830	0.883995	-3.476835	22952.488229

HLA A*2402	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.483703	1.006851	-3.476852	30458.123268
HLA B*0802	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.429251	0.952354	-3.476897	26868.998283
HLA A*0216	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.465934	0.989026	-3.476908	29237.079248
HLA B*5301	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.581500	1.104589	-3.476911	38150.519239
HLA B*5701	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.402707	0.925719	-3.476988	25275.921274
HLA A*2403	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.391129	0.914083	-3.477045	24610.970051
HLA B*4801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.434808	0.957710	-3.477098	27214.979255
HLA A*2601	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.391620	0.914477	-3.477143	24638.812596
HLA B*3501	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.391627	0.914477	-3.477150	24639.212479
HLA A*2603	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.348749	0.871584	-3.477164	22322.802736
HLA B*5801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.350076	0.872828	-3.477248	22391.138717
HLA B*0803	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.429656	0.952354	-3.477301	26894.011546
HLA A*8001	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.391772	0.914377	-3.477396	24647.478180
HLA A*6901	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.357923	0.880484	-3.477439	22799.402223
HLA A*0212	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.383286	0.905846	-3.477440	24170.528746
HLA A*8001	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.360846	0.883265	-3.477581	22953.357438
HLA A*0201	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.392708	0.915076	-3.477631	24700.604724
HLA A*3201	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.361746	0.883995	-3.477751	23000.965814
HLA A*0203	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.393076	0.915076	-3.478000	24721.593158
HLA B*4601	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.412281	0.934152	-3.478129	25839.323869
HLA B*0702	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.412382	0.934152	-3.478230	25845.335447
HLA B*5401	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.561426	1.083182	-3.478245	36427.255622
HLA B*4001	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.340366	0.862113	-3.478252	21896.049135
HLA B*7301	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.582856	1.104589	-3.478267	38269.792374
HLA B*4002	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.626512	1.148177	-3.478334	42316.709186
HLA A*3201	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.392715	0.914377	-3.478338	24701.005610
HLA A*0219	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.426122	0.947523	-3.478599	26676.076952
HLA A*3001	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.248019	0.769405	-3.478614	17701.874236
HLA A*0203	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.101435	0.622672	-3.478763	12630.917010
HLA B*0702	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.406379	0.927578	-3.478802	25490.551931
HLA B*4801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.404631	0.925719	-3.478912	25388.159742
HLA B*4501	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.233290	0.754283	-3.479007	17111.588568
HLA A*2403	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.417852	0.938712	-3.479140	26172.895691
HLA A*3002	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.527951	1.048747	-3.479204	33724.924883
HLA A*3001	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.173202	0.693953	-3.479249	14900.548334
HLA A*2602	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.571226	1.091927	-3.479299	37258.567668
HLA A*0206	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.400069	0.920689	-3.479379	25122.827846
HLA B*5101	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.405125	0.925719	-3.479406	25417.019030
HLA A*6901	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.373026	0.893488	-3.479538	23606.192808
HLA A*0203	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.407155	0.927578	-3.479577	25536.099926
HLA A*0212	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.413947	0.934152	-3.479795	25938.623791
HLA A*0212	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.432207	0.952354	-3.479853	27052.482683
HLA B*5401	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.528809	1.048747	-3.480061	33791.584233
HLA A*0250	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.353034	0.872828	-3.480206	22544.166440
HLA B*7301	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.585285	1.105060	-3.480225	38484.466775
HLA B*0801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.358675	0.878392	-3.480283	22838.905923
HLA A*3301	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.640259	1.159900	-3.480359	43677.595666
HLA B*7301	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.511397	1.031013	-3.480384	32463.588125
HLA A*3101	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.360957	0.880484	-3.480472	22959.194411
HLA A*2603	1:447-455	9	AFSPIRVAA	1.216390	-0.053773	-4.643102	1.162617	-3.480484	43964.445547
HLA B*4601	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.329260	0.848752	-3.480508	21343.210288
HLA B*3901	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.499621	1.019055	-3.480565	31595.184871
HLA A*3101	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.386613	0.905846	-3.480767	24356.395737
HLA B*2705	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.361309	0.880484	-3.480825	22977.832977
HLA A*3001	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.130648	0.649772	-3.480877	13509.783154
HLA B*4801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.361377	0.880484	-3.480893	22981.438178
HLA B*0803	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.481246	1.000328	-3.480918	30286.255281
HLA B*7301	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.575831	1.094888	-3.480943	37655.736465
HLA A*2601	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.374513	0.893488	-3.481025	23687.169839
HLA B*0802	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.435891	0.954860	-3.481031	27282.937001
HLA A*2301	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.396131	0.915076	-3.481054	24896.069374
HLA B*4801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.396319	0.915076	-3.481242	24906.846504
HLA A*3002	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.364549	0.883265	-3.481284	23149.894070
HLA A*0301	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.352896	0.871584	-3.481311	22536.971863
HLA B*0803	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.415467	0.934152	-3.481315	26029.573194

HLA B*0802	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.415580	0.934152	-3.481427	26036.333293
HLA A*2301	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.531581	1.050133	-3.481448	34007.988520
HLA A*6802	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.257154	0.775701	-3.481453	18078.152627
HLA B*1801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.326389	0.844865	-3.481524	21202.578153
HLA A*2301	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.543690	1.062125	-3.481565	34969.561866
HLA A*6901	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.359979	0.878392	-3.481587	22907.582524
HLA B*1801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.375093	0.893488	-3.481605	23718.842802
HLA B*5801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.350457	0.868794	-3.481663	22410.770958
HLA B*1501	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.415843	0.934152	-3.481691	26052.113685
HLA B*4403	1:314-322	9	SSPARFDQK	0.878945	0.297758	-4.658752	1.176703	-3.482048	45577.607080
HLA A*2902	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.434437	0.952354	-3.482083	27191.726851
HLA B*3501	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.137410	0.655319	-3.482091	13721.771911
HLA A*2902	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.189315	0.707098	-3.482217	15463.757078
HLA A*0301	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.365545	0.883265	-3.482280	23203.056083
HLA A*2402	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.597930	1.115540	-3.482390	39621.453352
HLA A*2603	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.405876	0.923460	-3.482416	25461.058180
HLA B*4403	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.637731	1.155314	-3.482416	43424.085167
HLA A*2602	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.598175	1.115540	-3.482635	39643.751782
HLA A*0250	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.532854	1.050133	-3.482721	34107.851717
HLA B*4403	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.510034	1.027215	-3.482819	32361.885607
HLA A*2301	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.542574	1.059725	-3.482849	34879.816035
HLA A*3301	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.595691	1.112802	-3.482889	39417.705696
HLA B*4601	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.403586	0.920689	-3.482896	25327.113780
HLA B*3901	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.376390	0.893488	-3.482902	23789.779269
HLA A*3101	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.367413	0.884477	-3.482936	23303.064128
HLA A*3301	1:408-416	9	AVLDAALAA	1.150749	-0.033620	-4.600127	1.117129	-3.482998	39822.376153
HLA A*2902	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.421804	0.938712	-3.483091	26412.141064
HLA B*1501	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.274956	0.791821	-3.483135	18834.586782
HLA A*0201	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.385544	0.902312	-3.483232	24296.516206
HLA B*5801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.351209	0.867880	-3.483328	22449.601291
HLA B*5301	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.583974	1.100571	-3.483403	38368.468189
HLA B*7301	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.545549	1.062125	-3.483423	35119.525029
HLA B*1503	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.476735	0.993286	-3.483448	29973.300479
HLA A*0101	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.318224	0.834602	-3.483622	20807.706450
HLA A*0212	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.448703	0.965021	-3.483682	28099.776259
HLA B*4001	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.327206	0.843357	-3.483849	21242.532603
HLA A*3101	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.379402	0.895455	-3.483948	23955.346237
HLA B*5301	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.599610	1.115540	-3.484070	39775.008726
HLA B*5401	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.515264	1.031013	-3.484251	32753.956810
HLA A*0203	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.362759	0.878392	-3.484367	23054.658870
HLA A*3001	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.278861	0.794424	-3.484437	19004.696594
HLA B*5401	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.368459	0.883995	-3.484464	23359.231522
HLA A*3101	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.278936	0.794424	-3.484512	19007.986905
HLA A*0219	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.436873	0.952354	-3.484519	27344.702635
HLA A*2402	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.576512	1.091927	-3.484586	37714.859706
HLA B*1503	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.501569	1.016861	-3.484708	31737.201115
HLA B*5301	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.552848	1.067986	-3.484862	35714.821475
HLA B*1501	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.399521	0.914477	-3.485044	25091.180367
HLA A*2603	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.645061	1.159900	-3.485161	44163.254583
HLA B*5301	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.594773	1.109528	-3.485244	39334.414860
HLA A*3001	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.262833	0.777400	-3.485432	18316.089369
HLA B*1501	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.381042	0.895455	-3.485588	24045.975087
HLA A*2603	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.097948	0.612321	-3.485627	12529.918493
HLA B*4801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.433163	0.947523	-3.485640	27112.113136
HLA B*0803	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.471970	0.986192	-3.485777	29646.253091
HLA A*0301	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.316410	0.830606	-3.485805	20720.985646
HLA A*0206	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.450871	0.965021	-3.485850	28240.438544
HLA B*1509	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.503147	1.016861	-3.486287	31852.789962
HLA A*2601	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.388608	0.902312	-3.486296	24468.521863
HLA B*3501	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.369643	0.883265	-3.486378	23423.009340
HLA A*2402	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.548561	1.062125	-3.486435	35363.942314
HLA A*0301	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.367014	0.880484	-3.486529	23281.642591
HLA B*4801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.438950	0.952354	-3.486596	27475.787551
HLA A*0101	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.374501	0.887847	-3.486655	23686.529123
HLA B*5801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.347363	0.860662	-3.486701	22251.665631

HLA B*5701	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.401203	0.914477	-3.486726	25188.559043
HLA B*3901	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.454320	0.967578	-3.486742	28465.609059
HLA B*1509	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.475776	0.989026	-3.486750	29907.215328
HLA A*0201	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.392632	0.905846	-3.486787	24696.329013
HLA A*0216	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.410256	0.923460	-3.486796	25719.107241
HLA B*1501	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.209286	0.722436	-3.486849	16191.446203
HLA A*6901	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.331748	0.844865	-3.486883	21465.838025
HLA A*8001	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.401039	0.914083	-3.486956	25179.022137
HLA B*0803	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.441840	0.954860	-3.486980	27659.225575
HLA A*0301	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.365454	0.878392	-3.487061	23198.161087
HLA B*1502	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.555191	1.067986	-3.487204	35907.975496
HLA B*0702	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.473412	0.986192	-3.487220	29744.891951
HLA B*1503	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.371724	0.884477	-3.487247	23535.549108
HLA A*0211	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.445045	0.957710	-3.487334	27864.080347
HLA B*1509	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.389665	0.902312	-3.487353	24528.161824
HLA A*2501	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.442270	0.954860	-3.487410	27686.622036
HLA B*5701	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.415072	0.927578	-3.487495	26005.926668
HLA B*4501	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.642878	1.155314	-3.487564	43941.856288
HLA A*6901	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.349745	0.862113	-3.487631	22374.065395
HLA A*0202	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.579574	1.091927	-3.487647	37981.654202
HLA B*4601	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.415230	0.927578	-3.487652	26015.354552
HLA A*0250	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.570928	1.083182	-3.487746	37232.977740
HLA A*2601	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.383223	0.895455	-3.487768	24166.998487
HLA A*3002	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.263968	0.776187	-3.487781	18364.011462
HLA A*2902	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.263533	0.775701	-3.487832	18345.641412
HLA A*2601	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.360682	0.872828	-3.487854	22944.666826
HLA A*3101	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-3.875010	0.387024	-3.487986	7499.120170
HLA A*3301	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.583103	1.094888	-3.488215	38291.537260
HLA A*2902	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.337001	0.848752	-3.488249	21727.076648
HLA A*6901	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.385697	0.897326	-3.488370	24305.061404
HLA A*8001	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.422525	0.934152	-3.488373	26456.043745
HLA A*0301	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.350490	0.862113	-3.488376	22412.468379
HLA A*2902	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.368997	0.880484	-3.488512	23388.188380
HLA B*0702	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.369029	0.880484	-3.488545	23389.959832
HLA A*3001	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.167117	0.678487	-3.488630	14693.223488
HLA B*3501	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.182614	0.693953	-3.488661	15226.997887
HLA B*3801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.537473	1.048747	-3.488726	34472.553457
HLA A*2403	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.349484	0.860662	-3.488822	22360.633853
HLA B*7301	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.516091	1.027215	-3.488876	32816.388972
HLA B*4402	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.403257	0.914377	-3.488880	25307.938680
HLA B*4403	1:481-489	9	RAARQLVGH	1.222490	-0.074313	-4.637075	1.148177	-3.488898	43358.592069
HLA A*3201	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.604509	1.115540	-3.488969	40226.195488
HLA A*0201	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.382546	0.893488	-3.489058	24129.374460
HLA A*2403	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.394944	0.905846	-3.489099	24828.146287
HLA B*4002	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-3.962900	0.473598	-3.489302	9181.208456
HLA A*6901	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.373884	0.884477	-3.489406	23652.851873
HLA A*2902	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.386923	0.897326	-3.489597	24373.794982
HLA B*1801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.453230	0.963515	-3.489715	28394.244619
HLA B*3901	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.453284	0.963515	-3.489769	28397.777863
HLA B*0702	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.404159	0.914377	-3.489782	25360.567974
HLA B*5701	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.410531	0.920689	-3.489841	25735.391484
HLA A*0219	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.454906	0.965021	-3.489884	28503.979849
HLA B*1501	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.417495	0.927578	-3.489917	26151.382483
HLA A*0219	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.478990	0.989026	-3.489964	30129.371549
HLA B*5801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.352094	0.862113	-3.489981	22495.434609
HLA A*0301	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.346141	0.856154	-3.489987	22189.156493
HLA B*1502	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.336564	0.846543	-3.490022	21705.225003
HLA A*8001	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.415751	0.925719	-3.490032	26046.617642
HLA B*0702	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.405155	0.915076	-3.490079	25418.806635
HLA B*4001	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.415904	0.925719	-3.490185	26055.778358
HLA A*0202	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.320853	0.830606	-3.490247	20934.051393
HLA A*3001	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.289121	0.798809	-3.490312	19459.027937
HLA A*2403	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.000492	0.510101	-3.490391	10011.326103
HLA A*0203	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.259901	0.769461	-3.490440	18192.844045
HLA A*8001	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.443010	0.952354	-3.490656	27733.843450

HLA A*3002	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.595774	1.105060	-3.490714	39425.169993
HLA A*0250	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.438276	0.947523	-3.490753	27433.160695
HLA B*4002	1:200-208	9	NPCDDALMK	1.044498	0.110816	-4.646109	1.155314	-3.490795	44269.940805
HLA B*3501	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.443186	0.952354	-3.490832	27745.098509
HLA B*7301	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.582793	1.091927	-3.490866	38264.202828
HLA A*0101	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.386366	0.895455	-3.490912	24342.564299
HLA A*2603	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.279016	0.787998	-3.491019	19011.483484
HLA A*2902	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.384513	0.893488	-3.491024	24238.881872
HLA A*2301	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.518250	1.027215	-3.491035	32979.948069
HLA B*1801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.405183	0.914083	-3.491100	25420.456844
HLA B*5801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.351549	0.860349	-3.491200	22467.218429
HLA B*1501	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.279223	0.787998	-3.491225	19020.536440
HLA A*2602	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.601137	1.109528	-3.491609	39915.120881
HLA B*7301	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.551545	1.059725	-3.491820	35607.748958
HLA B*3801	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.554000	1.062125	-3.491874	35809.621550
HLA B*1503	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.042552	0.550534	-3.492018	11029.405107
HLA A*2501	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.478997	0.986777	-3.492221	30129.860542
HLA A*2601	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.380204	0.887847	-3.492357	23999.579181
HLA A*3101	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.188051	0.695627	-3.492424	15418.814933
HLA A*2301	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.523661	1.031013	-3.492648	33393.414744
HLA A*0203	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.341454	0.848752	-3.492702	21950.962637
HLA A*6901	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.388222	0.895455	-3.492768	24446.822484
HLA A*0301	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.365728	0.872828	-3.492900	23212.849174
HLA B*5701	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.386406	0.893488	-3.492918	24344.803141
HLA B*7301	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.395480	0.902312	-3.493168	24858.789576
HLA A*0206	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.089213	0.595974	-3.493238	12280.409832
HLA B*1503	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.102812	0.609548	-3.493264	12671.023019
HLA A*0201	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.373846	0.880484	-3.493362	23650.804613
HLA B*0702	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.337131	0.843615	-3.493516	21733.542369
HLA A*2603	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.594101	1.100571	-3.493529	39273.602598
HLA B*3801	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.553382	1.059725	-3.493657	35758.707819
HLA B*4001	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.366487	0.872828	-3.493659	23253.446631
HLA B*4601	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.355783	0.862113	-3.493670	22687.313879
HLA B*1502	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.598828	1.105060	-3.493768	39703.418826
HLA A*2602	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.407970	0.914083	-3.493886	25584.082121
HLA A*0203	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.263310	0.769405	-3.493904	18336.215285
HLA A*2501	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.381844	0.887847	-3.493997	24090.375375
HLA B*1503	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.338874	0.844865	-3.494009	21820.959136
HLA A*2402	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.513076	1.019055	-3.494021	32589.402753
HLA A*0216	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.451839	0.957710	-3.494129	28303.453132
HLA B*4402	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.421717	0.927578	-3.494139	26406.854783
HLA B*1509	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.400007	0.905846	-3.494162	25119.294390
HLA A*0201	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.389625	0.895455	-3.494170	24525.906119
HLA A*0101	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.337528	0.843357	-3.494171	21753.421808
HLA A*0219	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.337906	0.843615	-3.494291	21772.377122
HLA A*0212	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.409469	0.915076	-3.494392	25672.538384
HLA A*6901	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.155393	0.660945	-3.494448	14301.880806
HLA B*2705	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.459480	0.965021	-3.494459	28805.800569
HLA B*4001	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.388023	0.893488	-3.494534	24435.583427
HLA B*0702	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.452295	0.957710	-3.494585	28333.173723
HLA B*0702	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.408851	0.914083	-3.494768	25636.037447
HLA A*0101	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.388281	0.893488	-3.494793	24450.129072
HLA B*5801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.350988	0.856154	-3.494834	22438.187907
HLA A*0211	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.522216	1.027215	-3.495001	33282.496740
HLA B*0702	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.433767	0.938712	-3.495055	27149.834449
HLA B*5301	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.557193	1.062125	-3.495067	36073.865472
HLA B*1502	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.590001	1.094888	-3.495113	38904.594221
HLA A*0212	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.343897	0.848752	-3.495145	22074.813084
HLA A*3001	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.153772	0.658550	-3.495222	14248.593926
HLA A*0202	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.373672	0.878392	-3.495280	23641.338339
HLA A*0101	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.373745	0.878392	-3.495353	23645.303479
HLA B*1801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.366938	0.871584	-3.495354	23277.612505
HLA A*6802	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.373879	0.878392	-3.495487	23652.595956
HLA A*0101	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.368360	0.872828	-3.495532	23353.924549
HLA A*2301	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.512400	1.016861	-3.495539	32538.666432

HLA B*1501	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.393018	0.897326	-3.495691	24718.249858
HLA B*0801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.363769	0.867880	-3.495889	23108.352252
HLA B*4001	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.393302	0.897326	-3.495976	24734.435637
HLA A*3001	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.073373	0.577123	-3.496250	11840.570632
HLA A*2601	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.270499	0.774156	-3.496343	18642.284157
HLA B*3801	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.513278	1.016861	-3.496418	32604.568516
HLA B*3501	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.380946	0.884477	-3.496469	24040.642150
HLA B*4801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.417170	0.920689	-3.496481	26131.866070
HLA A*2403	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.358962	0.862113	-3.496849	22853.984724
HLA A*0301	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.365679	0.868794	-3.496885	23210.212166
HLA B*5301	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.487676	0.990658	-3.497018	30738.036299
HLA A*2902	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.381559	0.884477	-3.497082	24074.611057
HLA B*4601	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.402940	0.905846	-3.497094	25289.462153
HLA A*3101	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.380479	0.883265	-3.497214	24014.774692
HLA A*3001	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-3.844655	0.347215	-3.497440	6992.862146
HLA B*5801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.273297	0.775701	-3.497597	18762.787507
HLA B*5401	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.504736	1.006851	-3.497884	31969.491588
HLA B*0801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.385826	0.887847	-3.497979	24312.294302
HLA A*1101	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.273723	0.775701	-3.498022	18781.168837
HLA A*3201	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.590034	1.091927	-3.498107	38907.540906
HLA A*2301	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.504968	1.006851	-3.498117	31986.618363
HLA A*2301	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.465701	0.967578	-3.498123	29221.424674
HLA A*1101	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.456151	0.957710	-3.498440	28585.824914
HLA B*2705	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.412580	0.914083	-3.498496	25857.083030
HLA A*3101	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.358870	0.860349	-3.498521	22849.163370
HLA A*3002	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.134455	0.635887	-3.498568	13628.703518
HLA A*1101	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.383159	0.884477	-3.498682	24163.468744
HLA B*5801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.347471	0.848752	-3.498719	22257.203756
HLA A*2501	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.463967	0.965021	-3.498946	29104.990775
HLA A*0301	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.274679	0.775701	-3.498978	18822.567241
HLA A*2501	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.485202	0.986192	-3.499010	30563.431394
HLA A*0101	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.383643	0.884477	-3.499166	24190.412422
HLA A*2301	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.492469	0.993286	-3.499183	31079.145419
HLA B*4403	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.254870	0.755651	-3.499219	17983.339749
HLA A*2602	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.451604	0.952354	-3.499250	28288.145419
HLA A*0301	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.367291	0.867880	-3.499411	23296.509566
HLA B*4601	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.401849	0.902312	-3.499537	25226.060443
HLA B*1509	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.464628	0.965021	-3.499606	29149.269213
HLA B*4801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.413771	0.914083	-3.499687	25928.101544
HLA B*5801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.294142	0.794424	-3.499718	19685.297883
HLA A*3301	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.600294	1.100571	-3.499723	39837.674951
HLA A*0211	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.516657	1.016861	-3.499796	32859.202335
HLA A*2301	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.518896	1.019055	-3.499841	33029.049496
HLA A*2601	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.226080	0.726109	-3.499971	16829.831196
HLA B*3501	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.290714	0.790719	-3.499996	19530.532857
HLA A*6801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.486833	0.986777	-3.500056	30678.396349
HLA B*1503	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.457887	0.957710	-3.500177	28700.337166
HLA A*2902	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.112510	0.612321	-3.500190	12957.175882
HLA A*2402	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.520703	1.020365	-3.500338	33166.743324
HLA B*1801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.493700	0.993286	-3.500414	31167.373012
HLA B*3901	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.493717	0.993286	-3.500431	31168.553318
HLA A*0211	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.465459	0.965021	-3.500438	29205.146489
HLA A*0201	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.397775	0.897326	-3.500449	24990.527597
HLA B*1509	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.527709	1.027215	-3.500494	33706.137963
HLA A*2301	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.361177	0.860662	-3.500516	22970.872810
HLA A*0203	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.434683	0.934152	-3.500531	27207.177182
HLA B*4801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.428274	0.927578	-3.500696	26808.597221
HLA A*0203	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.123172	0.622434	-3.500739	13279.212383
HLA A*0216	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.331346	0.830606	-3.500740	21445.989353
HLA B*5101	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.465812	0.965021	-3.500791	29228.855598
HLA B*4402	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.269484	0.768573	-3.500911	18598.766666
HLA A*0206	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.292751	0.791821	-3.500930	19622.353526
HLA A*3301	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.624007	1.123062	-3.500946	42073.373512
HLA B*0803	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.291276	0.790220	-3.501056	19555.801455
HLA B*5801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.347626	0.846543	-3.501083	22265.152169

HLA B*5401	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-3.798563	0.297408	-3.501155	6288.727406
HLA A*3002	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.520219	1.019055	-3.501163	33129.801661
HLA A*6802	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.421954	0.920689	-3.501265	26421.287399
HLA A*3101	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.363435	0.862113	-3.501322	23090.607134
HLA A*3101	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.403736	0.902312	-3.501424	25335.884379
HLA B*1502	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.551700	1.050133	-3.501566	35620.465070
HLA B*5701	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.407467	0.905846	-3.501621	25554.480151
HLA B*1501	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.346561	0.844865	-3.501697	22210.654217
HLA A*2902	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.429294	0.927578	-3.501716	26871.614859
HLA B*7301	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.440435	0.938712	-3.501723	27569.889419
HLA A*0101	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.399108	0.897326	-3.501781	25067.301408
HLA A*2603	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.520893	1.019055	-3.501838	33181.280209
HLA A*0202	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.363985	0.862113	-3.501872	23119.856368
HLA B*4601	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.395360	0.893488	-3.501872	24851.931874
HLA B*5401	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-3.950067	0.448098	-3.501969	8913.883647
HLA A*2603	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.550757	1.048747	-3.502010	35543.275018
HLA B*0802	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.465544	0.963515	-3.502029	29210.834921
HLA A*0219	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.422722	0.920689	-3.502033	26468.068915
HLA B*1509	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.385396	0.883265	-3.502131	24288.236806
HLA B*4001	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.404565	0.902312	-3.502254	25384.314314
HLA A*0203	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.348819	0.846543	-3.502276	22326.425946
HLA A*2603	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.519321	1.016861	-3.502461	33061.407049
HLA B*3501	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.450016	0.947523	-3.502493	28184.882201
HLA A*0203	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.301334	0.798809	-3.502524	20013.993971
HLA A*2403	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.346228	0.843615	-3.502613	22193.598450
HLA B*5701	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.404981	0.902312	-3.502669	25408.632715
HLA B*4601	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.417224	0.914477	-3.502747	26135.117794
HLA A*3101	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.423446	0.920689	-3.502756	26512.207988
HLA B*0803	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.417262	0.914477	-3.502785	26137.380101
HLA B*4402	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.426301	0.923460	-3.502840	26687.047118
HLA B*2705	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.417939	0.915076	-3.502862	26178.135136
HLA B*1801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.430469	0.927578	-3.502891	26944.399483
HLA A*0301	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.297673	0.794424	-3.503249	19846.012794
HLA B*4403	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.618789	1.115540	-3.503249	41570.871541
HLA B*1801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.458350	0.955018	-3.503332	28730.940803
HLA A*2603	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.492427	0.989026	-3.503401	31076.119141
HLA A*2501	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.466923	0.963515	-3.503408	29303.744436
HLA A*2902	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.279784	0.776187	-3.503598	19045.145205
HLA A*0219	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.418080	0.914477	-3.503603	26186.633764
HLA B*3501	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.348479	0.844865	-3.503614	22308.919208
HLA A*2902	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.348584	0.844865	-3.503720	22314.350864
HLA B*4001	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.360005	0.856154	-3.503851	22908.945767
HLA B*4402	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.387139	0.883265	-3.503874	24385.929078
HLA A*0216	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.442709	0.938712	-3.503997	27714.645359
HLA B*3901	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.418425	0.914377	-3.504049	26207.467065
HLA A*2603	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.571273	1.067176	-3.504097	37262.599180
HLA A*0206	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.218195	0.714055	-3.504140	16527.032775
HLA A*8001	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.376985	0.872828	-3.504157	23822.362680
HLA A*6802	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.438313	0.934152	-3.504161	27435.535364
HLA A*2601	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.401509	0.897326	-3.504182	25206.280025
HLA B*0803	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.451741	0.947523	-3.504218	28297.022884
HLA B*7301	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.587501	1.083182	-3.504319	38681.297905
HLA A*8001	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.462055	0.957710	-3.504345	28977.104379
HLA A*0216	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.353173	0.848752	-3.504421	22551.363313
HLA A*2402	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.564554	1.059725	-3.504829	36690.498963
HLA B*0803	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.472567	0.967687	-3.504879	29687.018361
HLA B*5301	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.558920	1.054023	-3.504897	36217.590403
HLA A*2301	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.525343	1.020365	-3.504978	33523.014328
HLA A*3001	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.021670	0.516619	-3.505050	10511.625163
HLA A*1101	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.494093	0.989026	-3.505067	31195.543945
HLA A*2902	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.213153	0.707963	-3.505190	16336.269656
HLA A*0206	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.294718	0.789406	-3.505312	19711.406525
HLA A*2902	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.393177	0.887847	-3.505331	24727.344694
HLA B*3801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.428887	0.923460	-3.505427	26846.477189
HLA A*2601	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.366163	0.860662	-3.505501	23236.092907

HLA A*3001	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.281711	0.776187	-3.505524	19129.819220
HLA A*0301	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.365886	0.860349	-3.505537	23221.264488
HLA A*0203	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-3.616948	0.111406	-3.505542	4139.497069
HLA A*0206	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.671855	0.166266	-3.505589	4697.372964
HLA A*0201	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.390067	0.884477	-3.505590	24550.863106
HLA A*0212	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.420096	0.914477	-3.505619	26308.466402
HLA B*4601	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.378498	0.872828	-3.505670	23905.503790
HLA A*0301	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.349442	0.843615	-3.505827	22358.456525
HLA B*4001	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.389092	0.883265	-3.505827	24495.805693
HLA B*4402	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.408198	0.902312	-3.505886	25597.511128
HLA B*5101	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.499177	0.993286	-3.505891	31562.896283
HLA A*0201	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.280057	0.774156	-3.505901	19057.100683
HLA A*1101	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.453437	0.947523	-3.505914	28407.765492
HLA A*0216	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.352538	0.846543	-3.505996	22518.447258
HLA B*4001	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.390008	0.883995	-3.506013	24547.542894
HLA A*2601	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.390558	0.884477	-3.506081	24578.637651
HLA A*0211	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.426803	0.920689	-3.506114	26717.961038
HLA B*4601	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.350079	0.843615	-3.506464	22391.259851
HLA B*3901	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.432264	0.925719	-3.506544	27055.995333
HLA A*3002	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.527046	1.020365	-3.506682	33654.755463
HLA A*2602	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.525738	1.019055	-3.506682	33553.495950
HLA A*0301	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.341310	0.834602	-3.506708	21943.719943
HLA B*1801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.275332	0.768573	-3.506759	18850.896724
HLA A*0250	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.598689	1.091927	-3.506762	39690.748174
HLA A*3201	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.569659	1.062587	-3.507072	37124.366270
HLA A*2403	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.402533	0.895455	-3.507078	25265.804544
HLA B*5701	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.404502	0.897326	-3.507176	25380.606774
HLA B*4403	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.561288	1.054023	-3.507265	36415.630500
HLA B*1502	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.400757	0.893488	-3.507269	25162.681556
HLA B*4601	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.404612	0.897326	-3.507286	25387.060989
HLA A*3101	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.363532	0.856154	-3.507378	23095.729324
HLA B*1503	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.462398	0.955018	-3.507380	29000.000807
HLA A*0219	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.422478	0.915076	-3.507402	26453.181415
HLA B*0702	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.353965	0.846543	-3.507422	22592.514941
HLA B*4801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.421851	0.914377	-3.507474	26414.998953
HLA B*1517	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.422555	0.915076	-3.507479	26457.904426
HLA B*5301	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.599422	1.091927	-3.507495	39757.798179
HLA A*0211	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.538521	1.031013	-3.507509	34555.829623
HLA B*0801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-3.618931	0.111406	-3.507525	4158.441006
HLA B*0801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.388124	0.880484	-3.507640	24441.268421
HLA A*0101	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.338380	0.830606	-3.507775	21796.182928
HLA B*3901	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.493982	0.986192	-3.507790	31187.613025
HLA B*0802	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.462812	0.955018	-3.507793	29027.626031
HLA A*2601	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.386272	0.878392	-3.507880	24337.297246
HLA B*5301	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.556749	1.048747	-3.508001	36036.999912
HLA A*0250	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.527422	1.019055	-3.508367	33683.899034
HLA A*8001	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.282533	0.774156	-3.508377	19166.075104
HLA A*8001	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.410747	0.902312	-3.508435	25748.203428
HLA B*4402	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.405893	0.897326	-3.508567	25462.022389
HLA A*6801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.303002	0.794424	-3.508577	20091.015975
HLA B*0801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.423126	0.914477	-3.508649	26492.708940
HLA A*0219	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.442843	0.934152	-3.508691	27723.192867
HLA A*2601	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.389298	0.880484	-3.508814	24507.470193
HLA B*5801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.353967	0.844865	-3.509102	22592.637164
HLA B*4801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.357921	0.848752	-3.509169	22799.278881
HLA A*6901	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.355727	0.846543	-3.509184	22684.368410
HLA A*0211	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.174504	0.665274	-3.509230	14945.273437
HLA A*6802	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.424308	0.915076	-3.509232	26564.898393
HLA A*3101	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.435012	0.925719	-3.509293	27227.791281
HLA A*0219	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.231831	0.722436	-3.509395	17054.197939
HLA B*3501	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.285400	0.775701	-3.509699	19292.990806
HLA A*3002	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.381486	0.871584	-3.509902	24070.573926
HLA A*3101	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.407277	0.897326	-3.509950	25543.284605
HLA A*8001	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.390508	0.880484	-3.510024	24575.845488
HLA A*0101	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.354893	0.844865	-3.510028	22640.844646

HLA B*4601	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.394061	0.883995	-3.510066	24777.694230
HLA B*1502	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.397994	0.887847	-3.510147	25003.103987
HLA B*7301	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.403656	0.893488	-3.510168	25331.224620
HLA A*6901	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.378244	0.867880	-3.510364	23891.540648
HLA B*4601	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.381961	0.871584	-3.510377	24096.892569
HLA A*1101	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.462807	0.952354	-3.510453	29027.311961
HLA A*3201	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.578542	1.067986	-3.510556	37891.557032
HLA B*3801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.517630	1.006851	-3.510778	32932.879373
HLA A*2301	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.408118	0.897326	-3.510792	25592.803251
HLA B*4601	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.395273	0.884477	-3.510796	24846.957862
HLA B*4501	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.478443	0.967578	-3.510864	30091.417276
HLA A*3101	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.383848	0.872828	-3.511020	24201.800570
HLA B*3801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.500049	0.989026	-3.511023	31626.308805
HLA B*4002	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.606259	1.094888	-3.511371	40388.648989
HLA B*3901	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.438997	0.927578	-3.511419	27478.760532
HLA A*2403	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.371783	0.860349	-3.511434	23538.732441
HLA B*4801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.417330	0.905846	-3.511484	26141.481032
HLA B*4402	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.356366	0.844865	-3.511501	22717.772799
HLA B*4403	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.014368	0.502859	-3.511509	10336.360945
HLA B*1509	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.435008	0.923460	-3.511547	27227.496684
HLA A*3201	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.498345	0.986777	-3.511569	31502.507999
HLA A*0301	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.280994	0.769405	-3.511589	19098.280735
HLA B*4601	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.392076	0.880484	-3.511591	24664.685060
HLA A*2902	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.383211	0.871584	-3.511627	24166.344792
HLA A*0201	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.390137	0.878392	-3.511745	24554.847953
HLA A*2603	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.624606	1.112802	-3.511805	42131.454698
HLA A*0206	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.134633	0.622672	-3.511961	13634.308133
HLA A*0202	1:410-418	9	LDAALAALT	0.811732	-0.410998	-3.912781	0.400734	-3.512046	8180.514786
HLA B*4601	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.407538	0.895455	-3.512083	25558.627895
HLA A*2403	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.395553	0.883265	-3.512288	24862.958907
HLA B*1517	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.470177	0.957710	-3.512467	29524.133120
HLA A*2403	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.440221	0.927578	-3.512644	27556.320105
HLA A*2601	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.333719	0.821048	-3.512671	21563.490703
HLA B*3801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.540058	1.027215	-3.512843	34678.307019
HLA A*2403	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.397439	0.884477	-3.512962	24971.202048
HLA B*5701	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.393741	0.880484	-3.513257	24759.470872
HLA A*6801	1:99-107	9	ARLLAAGEA	1.210175	-0.050275	-4.673180	1.159900	-3.513280	47117.225325
HLA A*3002	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.530181	1.016861	-3.513320	33898.513354
HLA B*0803	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.471319	0.957710	-3.513609	29601.860287
HLA B*0702	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.428119	0.914477	-3.513642	26799.026848
HLA B*5801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.357353	0.843615	-3.513738	22769.449751
HLA A*3201	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.618813	1.105060	-3.513753	41573.120540
HLA A*6801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.428164	0.914377	-3.513787	26801.781605
HLA B*4002	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.576456	1.062587	-3.513869	37709.963227
HLA B*1509	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.461421	0.947523	-3.513897	28934.809287
HLA A*2403	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.428340	0.914377	-3.513963	26812.658412
HLA B*4001	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.358868	0.844865	-3.514003	22849.039758
HLA A*2403	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.428500	0.914477	-3.514023	26822.523865
HLA A*2402	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.545142	1.031013	-3.514130	35086.671662
HLA A*0216	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.448393	0.934152	-3.514240	28079.717221
HLA A*0101	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.376383	0.862113	-3.514270	23789.393172
HLA B*5301	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.363165	0.848752	-3.514413	23076.246075
HLA A*3001	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.301061	0.786321	-3.514740	20001.438187
HLA B*3501	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.472454	0.957710	-3.514743	29679.310394
HLA A*3201	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.609657	1.094888	-3.514769	40705.836275
HLA B*5301	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.535178	1.020365	-3.514813	34290.830764
HLA A*0101	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.363680	0.848752	-3.514928	23103.602222
HLA B*0801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.371257	0.856154	-3.515103	23510.225125
HLA A*2902	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.137593	0.622434	-3.515160	13727.563328
HLA B*3901	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.480280	0.965021	-3.515259	30218.989678
HLA A*0101	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.375646	0.860349	-3.515296	23749.016311
HLA B*1509	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.534459	1.019055	-3.515404	34234.111788
HLA A*6802	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.364190	0.848752	-3.515438	23130.740529
HLA B*1517	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.462964	0.947523	-3.515441	29037.835182
HLA A*2602	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.241553	0.726109	-3.515445	17440.280605

HLA A*0216	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.421327	0.905846	-3.515481	26383.150974
HLA B*4402	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-3.923466	0.407915	-3.515551	8384.286143
HLA A*1101	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.429963	0.914377	-3.515587	26913.077966
HLA B*1503	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.362223	0.846543	-3.515680	23026.239522
HLA B*1501	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.376083	0.860349	-3.515733	23772.925533
HLA B*5701	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.411238	0.895455	-3.515783	25777.332533
HLA B*3901	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.470807	0.955018	-3.515788	29566.969738
HLA A*0211	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.441528	0.925719	-3.515808	27639.331498
HLA A*8001	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.443402	0.927578	-3.515825	27758.910954
HLA B*0802	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.430274	0.914377	-3.515897	26932.303603
HLA A*3001	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.182436	0.666384	-3.516052	15220.738570
HLA A*0101	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.304127	0.787998	-3.516130	20143.146080
HLA B*1801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.450449	0.934152	-3.516296	28212.951953
HLA A*0201	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.365061	0.848752	-3.516309	23177.212138
HLA A*2602	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.195203	0.678719	-3.516484	15674.829592
HLA A*2501	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.464029	0.947523	-3.516505	29109.084887
HLA A*2602	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.611407	1.094888	-3.516519	40870.226805
HLA B*1517	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.418855	0.902312	-3.516543	26233.425559
HLA B*4501	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.578672	1.062125	-3.516546	37902.833111
HLA B*0803	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.481629	0.965021	-3.516607	30312.973841
HLA A*2501	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.431061	0.914083	-3.516977	26981.157619
HLA B*1501	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.384863	0.867880	-3.516982	24258.428069
HLA B*7301	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.626580	1.109528	-3.517052	42323.348640
HLA B*4002	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.471937	0.954860	-3.517077	29644.007815
HLA A*0212	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.291236	0.774156	-3.517080	19554.003028
HLA A*0101	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.385067	0.867880	-3.517187	24269.848236
HLA A*6802	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.362209	0.844865	-3.517344	23025.492118
HLA B*0801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.438071	0.920689	-3.517382	27420.252032
HLA B*3801	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.510703	0.993286	-3.517417	32411.820243
HLA A*6802	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.432005	0.914477	-3.517528	27039.899430
HLA B*0802	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.338608	0.821048	-3.517560	21807.623679
HLA B*2705	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.380011	0.862113	-3.517898	23988.935067
HLA B*1502	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.366661	0.848752	-3.517909	23262.757589
HLA B*3901	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.456691	0.938712	-3.517979	28621.415665
HLA A*2402	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.580617	1.062587	-3.518030	38072.995442
HLA A*0101	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.378792	0.860662	-3.518130	23921.675023
HLA B*4801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.402171	0.883995	-3.518177	25244.763789
HLA B*0702	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.396695	0.878392	-3.518303	24928.414762
HLA A*2403	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.420704	0.902312	-3.518392	26345.354644
HLA B*5701	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.380589	0.862113	-3.518476	24020.881580
HLA A*2601	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.310297	0.791821	-3.518476	20431.349358
HLA A*0212	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.446111	0.927578	-3.518534	27932.601139
HLA B*7301	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.179612	0.660945	-3.518667	15122.083982
HLA B*4801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.397082	0.878392	-3.518690	24950.676590
HLA A*6901	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.205216	0.686428	-3.518788	16040.442072
HLA B*5801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.349395	0.830606	-3.518789	22356.037521
HLA A*0301	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.365428	0.846543	-3.518885	23196.780633
HLA B*1509	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.519232	1.000328	-3.518904	33054.611123
HLA A*6901	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.353506	0.834602	-3.518905	22568.694023
HLA A*0301	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.367662	0.848752	-3.518910	23316.431062
HLA A*0203	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.349691	0.830606	-3.519085	22371.281620
HLA B*1801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.476805	0.957710	-3.519095	29978.165441
HLA A*2301	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.509872	0.990658	-3.519214	32349.807740
HLA B*1801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.340295	0.821048	-3.519247	21892.495768
HLA A*2402	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.586488	1.067176	-3.519312	38591.211251
HLA B*7301	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.486929	0.967578	-3.519351	30685.201739
HLA A*6801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.226451	0.707098	-3.519353	16844.222854
HLA A*0219	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.421724	0.902312	-3.519412	26407.283361
HLA B*5701	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.403898	0.884477	-3.519421	25345.343583
HLA B*0802	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.477146	0.957710	-3.519435	30001.690556
HLA A*2601	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.241873	0.722436	-3.519437	17453.116925
HLA B*4501	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.407352	0.887847	-3.519505	25547.706951
HLA A*8001	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.413134	0.893488	-3.519646	25890.116726
HLA A*0206	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.536606	1.016861	-3.519746	34403.806295
HLA A*3201	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.602975	1.083182	-3.519793	40084.340822

HLA B*1501	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.392642	0.872828	-3.519814	24696.863436
HLA A*6802	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.422290	0.902312	-3.519978	26441.735189
HLA A*6801	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.568729	1.048747	-3.519981	37044.919273
HLA A*0212	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.415451	0.895455	-3.519996	26028.587493
HLA B*0803	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.483525	0.963515	-3.520009	30445.602936
HLA A*6802	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.415498	0.895455	-3.520043	26031.403881
HLA A*0301	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.363421	0.843357	-3.520064	23089.857640
HLA B*1509	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.506371	0.986192	-3.520179	32090.092672
HLA B*0702	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.389197	0.868794	-3.520403	24501.769800
HLA A*8001	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.426275	0.905846	-3.520429	26685.459052
HLA A*1101	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.404575	0.883995	-3.520580	25384.863625
HLA B*5401	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.403976	0.883265	-3.520711	25349.868798
HLA B*3801	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.488315	0.967578	-3.520737	30783.300302
HLA A*0212	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.414281	0.893488	-3.520792	25958.557608
HLA A*0219	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.401325	0.880484	-3.520841	25195.645940
HLA A*0212	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.275170	0.754283	-3.520886	18843.861330
HLA B*5701	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.381623	0.860662	-3.520961	24078.127821
HLA B*4801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.418326	0.897326	-3.521000	26201.513002
HLA B*4002	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.644065	1.123062	-3.521003	44062.069313
HLA B*5101	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.475917	0.954860	-3.521057	29916.924586
HLA B*4601	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.408935	0.887847	-3.521089	25641.030706
HLA B*1517	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.435583	0.914477	-3.521106	27263.608557
HLA B*1517	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.381799	0.860662	-3.521137	24087.899303
HLA A*0203	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.117186	0.595974	-3.521211	13097.422253
HLA B*1501	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.342276	0.821048	-3.521228	21992.565307
HLA A*3002	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.508079	0.986777	-3.521302	32216.551184
HLA A*3101	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.370155	0.848752	-3.521403	23450.649698
HLA A*3001	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.228100	0.706599	-3.521502	16908.314495
HLA A*1101	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.447441	0.925719	-3.521722	28018.261767
HLA B*0801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.383845	0.862113	-3.521732	24201.669641
HLA A*6802	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.389717	0.867880	-3.521836	24531.081280
HLA B*3801	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.512501	0.990658	-3.521843	32546.236628
HLA A*0301	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.366746	0.844865	-3.521881	23267.288592
HLA A*3002	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.436467	0.914477	-3.521990	27319.122404
HLA B*1509	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.508831	0.986777	-3.522054	32272.371637
HLA A*2603	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.469712	0.947523	-3.522189	29492.525038
HLA A*3201	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.402787	0.880484	-3.522303	25280.570860
HLA B*0802	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.469886	0.947523	-3.522363	29504.334198
HLA A*3001	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.275426	0.752921	-3.522505	18854.976415
HLA B*4801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.424992	0.902312	-3.522680	26606.751857
HLA B*4403	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.582457	1.059725	-3.522732	38234.612547
HLA A*2601	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.371513	0.848752	-3.522761	23524.092674
HLA B*5301	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.284678	0.761813	-3.522865	19260.974907
HLA B*5401	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.487895	0.965021	-3.522873	30753.505101
HLA A*0203	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.437416	0.914477	-3.522939	27378.896244
HLA A*2602	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.488010	0.965021	-3.522988	30761.658461
HLA B*1517	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.461750	0.938712	-3.523037	28956.732364
HLA B*3901	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.407561	0.884477	-3.523084	25560.010626
HLA B*0702	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.407582	0.884477	-3.523105	25561.255148
HLA B*5701	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.406384	0.883265	-3.523119	25490.827734
HLA B*3501	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.461938	0.938712	-3.523225	28969.267293
HLA B*3901	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.437724	0.914477	-3.523247	27398.306421
HLA A*2301	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.523604	1.000328	-3.523276	33389.079313
HLA B*5801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.358015	0.834602	-3.523413	22804.213078
HLA B*1801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.401967	0.878392	-3.523575	25232.884876
HLA A*2602	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.628664	1.105060	-3.523604	42526.928317
HLA B*1509	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.276617	0.752921	-3.523696	18906.763093
HLA A*0250	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.311714	0.787998	-3.523716	20498.108584
HLA A*8001	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.444415	0.920689	-3.523726	27823.710874
HLA B*0801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.264376	0.740545	-3.523831	18381.306025
HLA B*0801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.392637	0.868794	-3.523843	24696.596223
HLA A*0219	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.372730	0.848752	-3.523978	23590.107223
HLA A*2301	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.438083	0.914083	-3.524000	27420.993745
HLA B*1503	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.367404	0.843357	-3.524047	23302.559866
HLA A*0203	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.408555	0.884477	-3.524078	25618.568698

HLA A*3301	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.574367	1.050133	-3.524234	37529.036674
HLA A*0201	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-3.977368	0.452989	-3.524379	9492.223965
HLA B*4001	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.385051	0.860662	-3.524389	24268.929173
HLA B*0801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.286309	0.761813	-3.524495	19333.425447
HLA A*2501	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.450239	0.925719	-3.524520	28199.371247
HLA B*5401	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.479538	0.954860	-3.524678	30167.373693
HLA B*4001	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.403109	0.878392	-3.524717	25299.314621
HLA A*2601	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.386857	0.862113	-3.524744	24370.103194
HLA A*1101	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.463458	0.938712	-3.524745	29070.843136
HLA B*1509	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.385485	0.860662	-3.524823	24293.230392
HLA A*0201	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.392712	0.867880	-3.524832	24700.871980
HLA A*3002	1:216-224	9	EDLLPSTPR	0.675449	0.416478	-4.616935	1.091927	-3.525008	41393.808485
HLA B*5301	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.592480	1.067176	-3.525303	39127.274449
HLA B*3501	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.294252	0.768573	-3.525680	19690.303798
HLA B*4801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.410171	0.884477	-3.525694	25714.098778
HLA A*0201	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.203102	0.677348	-3.525753	15962.532580
HLA B*4001	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.313779	0.787998	-3.525781	20595.815214
HLA A*2601	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.409227	0.883265	-3.525962	25658.237153
HLA A*3002	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.557049	1.031013	-3.526037	36061.962944
HLA B*4801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.316575	0.790220	-3.526355	20728.834009
HLA B*4001	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.386707	0.860349	-3.526358	24361.666923
HLA A*8001	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.404807	0.878392	-3.526415	25398.462867
HLA B*0802	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.410963	0.884477	-3.526486	25761.021751
HLA B*5401	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.543366	1.016861	-3.526505	34943.464568
HLA B*2705	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.398252	0.871584	-3.526668	25017.987457
HLA B*5801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.370028	0.843357	-3.526671	23443.799967
HLA A*2902	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.447436	0.920689	-3.526747	28017.958617
HLA A*2402	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.553981	1.027215	-3.526766	35808.071775
HLA B*1801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.513605	0.986777	-3.526828	32629.095544
HLA B*4002	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.627487	1.100571	-3.526915	42411.821328
HLA A*2601	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.394834	0.867880	-3.526954	24821.834166
HLA A*2501	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.395851	0.868794	-3.527057	24880.047020
HLA B*3801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.481922	0.954860	-3.527062	30333.479502
HLA B*4801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.387915	0.860662	-3.527253	24429.503269
HLA B*0801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.411785	0.884477	-3.527308	25809.845455
HLA A*3002	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.554620	1.027215	-3.527405	35860.801776
HLA A*2902	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-3.992480	0.464975	-3.527504	9828.333034
HLA B*1503	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.249976	0.722436	-3.527540	17781.826644
HLA B*0803	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.514427	0.986777	-3.527651	32690.935998
HLA A*2402	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.514023	0.986192	-3.527831	32660.531199
HLA B*2705	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.425199	0.897326	-3.527872	26619.421555
HLA B*1502	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.482984	0.955018	-3.527966	30407.743807
HLA B*0802	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.434042	0.905846	-3.528196	27167.024567
HLA A*8001	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.318464	0.790220	-3.528244	20819.191492
HLA B*5701	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.416174	0.887847	-3.528327	26071.993672
HLA A*2501	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.462551	0.934152	-3.528398	29010.200241
HLA A*2501	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.480825	0.952354	-3.528471	30256.941171
HLA B*5101	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.314871	0.786321	-3.528550	20647.691238
HLA A*0219	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.375267	0.846543	-3.528725	23728.340110
HLA A*2603	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.644269	1.115540	-3.528729	44082.812463
HLA B*1801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.514930	0.986192	-3.528738	32728.804743
HLA A*0202	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.493792	0.965021	-3.528771	31173.949575
HLA A*0212	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.413261	0.884477	-3.528784	25897.681214
HLA B*2705	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.443179	0.914377	-3.528803	27744.648219
HLA A*1101	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.452272	0.923460	-3.528811	28331.640971
HLA A*0203	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.318544	0.789406	-3.529138	20823.021248
HLA B*4601	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.389543	0.860349	-3.529193	24521.262674
HLA B*5401	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.484274	0.955018	-3.529256	30498.189940
HLA B*0802	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.457022	0.927578	-3.529445	28643.256248
HLA B*1517	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.413512	0.883995	-3.529518	25912.676637
HLA A*3001	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.291341	0.761813	-3.529528	19558.763931
HLA A*0201	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.376130	0.846543	-3.529587	23775.497850
HLA B*2705	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.378369	0.848752	-3.529617	23898.391912
HLA B*4501	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.652744	1.123062	-3.529682	44951.468794
HLA A*2301	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.515924	0.986192	-3.529732	32803.786547

HLA B*1501	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.390396	0.860662	-3.529734	24569.464592
HLA B*4501	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.373369	0.843615	-3.529754	23624.845379
HLA A*3301	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.645305	1.115540	-3.529765	44188.109079
HLA A*0101	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.385927	0.856154	-3.529773	24317.950613
HLA A*2403	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.320137	0.790220	-3.529917	20899.538351
HLA B*4002	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.634524	1.104589	-3.529935	43104.601134
HLA B*4402	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.444502	0.914477	-3.530025	27829.280790
HLA A*2601	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.399007	0.868794	-3.530212	25061.470799
HLA A*0203	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.392329	0.862113	-3.530216	24679.100057
HLA A*6802	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.423801	0.893488	-3.530312	26533.874481
HLA B*1517	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.304597	0.774156	-3.530441	20164.952313
HLA B*3501	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.451139	0.920689	-3.530450	28257.860567
HLA A*8001	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.425906	0.895455	-3.530451	26662.803310
HLA B*0702	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.166375	0.635887	-3.530488	14668.126514
HLA A*2603	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.252995	0.722436	-3.530559	17905.871364
HLA A*8001	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.361239	0.830606	-3.530633	22974.104054
HLA A*2602	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.318699	0.787998	-3.530701	20830.457491
HLA B*3501	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.458345	0.927578	-3.530767	28730.629942
HLA A*0101	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.374424	0.843615	-3.530809	23682.300831
HLA B*5101	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.403673	0.872828	-3.530845	25332.183912
HLA B*3801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.403677	0.872828	-3.530849	25332.458002
HLA B*1503	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.374466	0.843615	-3.530851	23684.607079
HLA A*0203	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.365698	0.834835	-3.530862	23211.216705
HLA A*3001	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.256015	0.725139	-3.530876	18030.781411
HLA A*3101	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-3.910032	0.379131	-3.530901	8128.899167
HLA A*2902	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.433220	0.902312	-3.530908	27115.633529
HLA A*0211	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.361582	0.830606	-3.530976	22992.257176
HLA A*6801	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.654053	1.123062	-3.530991	45087.125711
HLA B*1503	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.391904	0.860662	-3.531242	24654.946358
HLA A*0212	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.374671	0.843357	-3.531314	23695.757108
HLA B*5401	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.419381	0.887847	-3.531534	26265.234892
HLA A*6901	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.391939	0.860349	-3.531590	24656.947148
HLA A*2602	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.323539	0.791821	-3.531718	21063.898209
HLA A*3002	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.326187	0.794424	-3.531762	21192.715938
HLA B*4402	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.415768	0.883995	-3.531773	26047.604026
HLA A*0206	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.293588	0.761813	-3.531774	19660.181035
HLA A*2602	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.144487	0.612666	-3.531821	13947.194098
HLA B*1503	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.415913	0.883995	-3.531919	26056.342200
HLA A*0301	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.366880	0.834835	-3.532044	23274.464485
HLA A*1101	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.415444	0.883265	-3.532179	26028.165062
HLA A*0216	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.459816	0.927578	-3.532238	28828.093766
HLA A*3201	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.592007	1.059725	-3.532282	39084.751055
HLA B*5301	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.539196	1.006851	-3.532344	34609.523997
HLA A*2902	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.455982	0.923460	-3.532521	28574.692560
HLA B*5801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.353694	0.821048	-3.532646	22578.463667
HLA B*3901	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.435031	0.902312	-3.532719	27228.969702
HLA B*4601	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.393419	0.860662	-3.532757	24741.127069
HLA A*6901	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.273368	0.740545	-3.532823	18765.832892
HLA A*0201	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.394989	0.862113	-3.532876	24830.698451
HLA B*4403	1:13-21	9	PSPTGTPHV	1.188362	-0.065300	-4.655949	1.123062	-3.532887	45284.396514
HLA A*3001	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.301595	0.768573	-3.533022	20026.015938
HLA A*8001	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.420880	0.887847	-3.533033	26356.046221
HLA B*5701	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.417072	0.883995	-3.533077	26125.929183
HLA B*4001	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.401889	0.868794	-3.533095	25228.380543
HLA A*1101	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.488278	0.955018	-3.533259	30780.635869
HLA A*3101	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.411760	0.878392	-3.533367	25808.309588
HLA A*0203	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.428850	0.895455	-3.533395	26844.153507
HLA B*4501	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.587426	1.054023	-3.533403	38674.602116
HLA B*4002	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.564443	1.031013	-3.533431	36681.171047
HLA B*3901	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.454198	0.920689	-3.533509	28457.602404
HLA A*6901	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.325367	0.791821	-3.533546	21152.740752
HLA A*0206	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.008818	0.475212	-3.533606	10205.121575
HLA B*5101	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.378568	0.844865	-3.533704	23909.383889
HLA A*0206	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.207049	0.673165	-3.533884	16108.271151
HLA A*3002	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.402691	0.868794	-3.533896	25274.964113

HLA B*0802	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.472616	0.938712	-3.533904	29690.391225
HLA A*2402	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.550870	1.016861	-3.534010	35552.505905
HLA A*3301	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.427522	0.893488	-3.534034	26762.227277
HLA B*0802	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.436439	0.902312	-3.534127	27317.348941
HLA B*1509	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.448548	0.914377	-3.534171	28089.744950
HLA A*2603	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.602218	1.067986	-3.534232	40014.575312
HLA A*2902	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.407178	0.872828	-3.534350	25537.481438
HLA A*0201	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.403278	0.868794	-3.534484	25309.170928
HLA B*0702	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.455180	0.920689	-3.534491	28522.027354
HLA A*6901	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.403346	0.868794	-3.534552	25313.141914
HLA B*0702	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.378204	0.843357	-3.534847	23889.343489
HLA B*4402	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.395402	0.860349	-3.535053	24854.352023
HLA B*0802	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.449220	0.914083	-3.535136	28133.239837
HLA B*4002	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.597324	1.062125	-3.535199	39566.190228
HLA B*4403	1:298-306	9	FGLDEMVAA	1.472143	-0.359341	-4.648033	1.112802	-3.535231	44466.522773
HLA A*3001	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.275795	0.740545	-3.535250	18870.997742
HLA B*4402	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.324739	0.789406	-3.535334	21122.208935
HLA A*2403	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.381881	0.846543	-3.535338	24092.460685
HLA A*2601	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.379113	0.843615	-3.535498	23939.411260
HLA B*0702	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.423378	0.887847	-3.535531	26508.048900
HLA B*0803	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.408416	0.872828	-3.535588	25610.392980
HLA A*3301	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.249720	0.714055	-3.535666	17771.344184
HLA A*2501	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.474390	0.938712	-3.535678	29811.908626
HLA A*0101	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.382353	0.846543	-3.535811	24118.672780
HLA B*4601	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.403710	0.867880	-3.535830	25334.376716
HLA A*0201	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.396500	0.860662	-3.535838	24917.223898
HLA A*2601	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.392038	0.856154	-3.535884	24662.550221
HLA B*1501	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.404857	0.868794	-3.536062	25401.348491
HLA B*3501	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.382638	0.846543	-3.536095	24134.465949
HLA A*6801	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.630988	1.094888	-3.536100	42755.073346
HLA B*0702	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.407770	0.871584	-3.536186	25572.320226
HLA B*5301	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.522477	0.986192	-3.536284	33302.488804
HLA B*5701	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.407930	0.871584	-3.536346	25581.729309
HLA A*0212	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.433887	0.897326	-3.536561	27157.326240
HLA A*0202	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.371179	0.834602	-3.536577	23506.028305
HLA A*3101	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.381573	0.844865	-3.536709	24075.392516
HLA B*1517	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.421193	0.884477	-3.536716	26375.016623
HLA A*3101	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.380107	0.843357	-3.536750	23994.256534
HLA A*3001	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-3.948930	0.412011	-3.536918	8890.574185
HLA B*0802	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.451574	0.914477	-3.537097	28286.156024
HLA A*0206	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.526165	0.989026	-3.537139	33586.548986
HLA B*5301	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.587433	1.050133	-3.537300	38675.229797
HLA B*0801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.386155	0.848752	-3.537403	24330.715032
HLA A*0201	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.382299	0.844865	-3.537435	24115.671941
HLA A*3301	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.642514	1.105060	-3.537454	43905.025044
HLA A*3002	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.430957	0.893488	-3.537469	26974.735920
HLA B*0801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.397851	0.860349	-3.537501	24994.854243
HLA A*0216	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.431082	0.893488	-3.537593	26982.471337
HLA A*3101	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.384160	0.846543	-3.537617	24219.220401
HLA B*0802	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.416043	0.878392	-3.537651	26064.096259
HLA B*5401	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.399845	0.862113	-3.537732	25109.919551
HLA B*3501	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.431227	0.893488	-3.537739	26991.523130
HLA B*0702	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.393899	0.856154	-3.537745	24768.446880
HLA B*0803	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.452276	0.914377	-3.537900	28331.947515
HLA B*1801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.502983	0.965021	-3.537962	31840.729841
HLA B*1801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.490326	0.952354	-3.537972	30926.184196
HLA B*5101	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.381625	0.843615	-3.538010	24078.258081
HLA B*2705	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.422050	0.883995	-3.538056	26427.148435
HLA B*4501	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.606100	1.067986	-3.538113	40373.793850
HLA B*1503	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.224590	0.686428	-3.538162	16772.205948
HLA A*2601	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.398638	0.860349	-3.538288	25040.193811
HLA B*3801	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.472477	0.934152	-3.538325	29680.916056
HLA B*4801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.421609	0.883265	-3.538344	26400.284125
HLA B*4501	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.501867	0.963515	-3.538352	31759.013840
HLA A*3002	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.496125	0.957710	-3.538415	31341.867278

HLA A*2602	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-3.929998	0.391537	-3.538461	8511.334523
HLA B*1503	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.093719	0.555221	-3.538498	12408.496797
HLA B*1501	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.327923	0.789406	-3.538517	21277.612058
HLA B*5801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.308018	0.769461	-3.538557	20324.414783
HLA B*4002	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.307149	0.768573	-3.538576	20283.772925
HLA B*4402	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.410195	0.871584	-3.538611	25715.489920
HLA B*2705	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.382363	0.843615	-3.538748	24119.194703
HLA A*2501	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.419259	0.880484	-3.538775	26257.847146
HLA A*0202	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.569788	1.031013	-3.538776	37135.414043
HLA A*2501	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.417269	0.878392	-3.538877	26137.804305
HLA B*4402	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.401048	0.862113	-3.538935	25179.567006
HLA A*0201	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.382466	0.843357	-3.539109	24124.936601
HLA A*0219	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.466766	0.927578	-3.539188	29293.124850
HLA A*0201	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.399627	0.860349	-3.539277	25097.289433
HLA A*1101	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.401412	0.862113	-3.539299	25200.689754
HLA B*4403	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.639885	1.100571	-3.539314	43640.041559
HLA A*3101	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.006159	0.466843	-3.539315	10142.816439
HLA B*5401	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.532782	0.993286	-3.539495	34102.132086
HLA B*5701	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.412338	0.872828	-3.539509	25842.678996
HLA B*1502	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.441882	0.902312	-3.539570	27661.919106
HLA B*1501	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.374219	0.834602	-3.539618	23671.157134
HLA B*1517	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.334046	0.794424	-3.539621	21579.711998
HLA A*0202	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.478351	0.938712	-3.539639	30085.069088
HLA A*0250	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.065276	0.525631	-3.539645	11621.877875
HLA A*2601	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.383089	0.843357	-3.539732	24159.547412
HLA A*2603	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.400428	0.860662	-3.539766	25143.630947
HLA A*6901	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.374635	0.834835	-3.539800	23693.834315
HLA B*4002	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.607855	1.067986	-3.539868	40537.282029
HLA B*5801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.330434	0.790220	-3.540215	21401.020640
HLA B*4403	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.590398	1.050133	-3.540265	38940.179838
HLA B*3901	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.492622	0.952354	-3.540268	31090.076098
HLA B*1509	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.424745	0.884477	-3.540268	26591.642493
HLA B*5701	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.408167	0.867880	-3.540287	25595.710955
HLA A*0216	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.455397	0.915076	-3.540320	28536.226580
HLA A*0211	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.533623	0.993286	-3.540337	34168.243059
HLA B*4001	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.374960	0.834602	-3.540358	23711.529900
HLA B*3801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.559434	1.019055	-3.540379	36260.525192
HLA A*0206	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-3.983148	0.442758	-3.540390	9619.393921
HLA A*0212	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.328470	0.787998	-3.540473	21304.449488
HLA A*3301	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.608644	1.067986	-3.540658	40611.034580
HLA A*0206	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.385535	0.844865	-3.540670	24295.990446
HLA B*1502	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.571938	1.031013	-3.540925	37319.691862
HLA B*5101	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.446915	0.905846	-3.541069	27984.329376
HLA B*1517	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.468652	0.927578	-3.541075	29420.655118
HLA B*4002	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.650801	1.109528	-3.541273	44750.806112
HLA B*2705	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.462154	0.920689	-3.541464	28983.689170
HLA B*1502	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.601191	1.059725	-3.541467	39920.087726
HLA B*5701	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.419940	0.878392	-3.541548	26299.074570
HLA A*2501	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.499323	0.957710	-3.541612	31573.484668
HLA A*6901	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.331048	0.789406	-3.541642	21431.259820
HLA A*2601	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.329692	0.787998	-3.541695	21364.466315
HLA A*6801	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.624933	1.083182	-3.541751	42163.148396
HLA A*6802	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.426293	0.884477	-3.541816	26686.614000
HLA B*0802	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.456997	0.915076	-3.541920	28641.551774
HLA B*5101	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.413569	0.871584	-3.541984	25916.041289
HLA A*0219	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.404185	0.862113	-3.542071	25362.077195
HLA A*1101	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.462783	0.920689	-3.542094	29025.741658
HLA A*3101	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.311570	0.769405	-3.542165	20491.345257
HLA A*0212	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.420678	0.878392	-3.542286	26343.786911
HLA A*2501	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.469926	0.927578	-3.542348	29507.047780
HLA A*0212	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.387280	0.844865	-3.542416	24393.845873
HLA B*3801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.528637	0.986192	-3.542445	33778.241831
HLA A*2601	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.377058	0.834602	-3.542456	23826.358182
HLA B*5801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.377365	0.834835	-3.542530	23843.249799
HLA B*4403	1:401-409	9	ELGPDGAAV	1.076274	0.028315	-4.647133	1.104589	-3.542544	44374.484077

HLA B*5801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.296891	0.754283	-3.542607	19810.292524
HLA A*0301	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.332890	0.790220	-3.542670	21522.350397
HLA A*8001	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.391437	0.848752	-3.542685	24628.417916
HLA B*5101	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.463472	0.920689	-3.542782	29071.786772
HLA A*0101	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.363835	0.821048	-3.542787	23111.852898
HLA B*5701	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.411612	0.868794	-3.542817	25799.515021
HLA A*3001	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.250009	0.707098	-3.542911	17783.173463
HLA A*2301	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.531983	0.989026	-3.542957	34039.463562
HLA B*5401	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.563510	1.020365	-3.543146	36602.474483
HLA A*2603	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.597345	1.054023	-3.543322	39568.116714
HLA A*6801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.449206	0.905846	-3.543360	28132.326666
HLA B*5701	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.403724	0.860349	-3.543375	25335.199066
HLA B*5701	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.399533	0.856154	-3.543379	25091.859079
HLA B*4601	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.386893	0.843357	-3.543536	24372.080868
HLA A*0211	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.467017	0.923460	-3.543557	29310.086322
HLA A*8001	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.415241	0.871584	-3.543657	26016.058262
HLA A*2403	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.437268	0.893488	-3.543780	27369.566476
HLA B*4001	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.125559	0.581735	-3.543824	13352.401832
HLA A*0203	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.312430	0.768573	-3.543857	20531.958714
HLA A*2402	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.458293	0.914377	-3.543917	28727.210696
HLA B*1501	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-3.832790	0.288865	-3.543925	6804.403629
HLA B*1509	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.478137	0.934152	-3.543985	30070.261856
HLA B*4501	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.653552	1.109528	-3.544024	45035.201450
HLA B*1517	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-3.925717	0.381582	-3.544135	8427.851960
HLA B*1801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.491717	0.947523	-3.544194	31025.388849
HLA A*2403	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.400348	0.856154	-3.544194	25139.006547
HLA A*0216	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.389165	0.844865	-3.544300	24499.914145
HLA A*0211	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.458801	0.914477	-3.544324	28760.799099
HLA A*3001	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.299983	0.755651	-3.544331	19951.833446
HLA B*0801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.441746	0.897326	-3.544420	27653.240888
HLA B*1509	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.416130	0.871584	-3.544545	26069.313925
HLA B*5801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.336454	0.791821	-3.544633	21699.706831
HLA B*5101	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.483372	0.938712	-3.544660	30434.898841
HLA B*0801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.379323	0.834602	-3.544721	23950.940386
HLA A*6801	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.565089	1.020365	-3.544724	36735.782955
HLA A*8001	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.442077	0.897326	-3.544751	27674.342672
HLA A*0301	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.365808	0.821048	-3.544760	23217.119250
HLA A*0203	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.442218	0.897326	-3.544892	27683.327038
HLA A*2301	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.531670	0.986777	-3.544894	34014.980458
HLA A*2902	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.314395	0.769405	-3.544989	20625.028235
HLA A*0101	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.413825	0.868794	-3.545030	25931.327913
HLA B*4002	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.628319	1.083182	-3.545137	42493.122063
HLA B*4001	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.335439	0.790220	-3.545219	21649.052266
HLA B*3901	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.459388	0.914083	-3.545305	28799.723598
HLA B*5101	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.503046	0.957710	-3.545336	31845.381061
HLA A*2602	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.534492	0.989026	-3.545466	34236.704725
HLA A*3301	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.628810	1.083182	-3.545628	42541.194799
HLA A*2602	1:301-309	9	DEMVAAFDV	1.060770	-0.012023	-4.594620	1.048747	-3.545873	39320.585628
HLA B*1503	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-3.932963	0.387024	-3.545939	8569.642604
HLA A*8001	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.321673	0.775701	-3.545972	20973.613292
HLA B*5101	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.394747	0.848752	-3.545995	24816.866178
HLA B*3901	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.503831	0.957710	-3.546121	31902.974592
HLA A*6802	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.168757	0.622434	-3.546323	14748.811495
HLA A*3301	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.608949	1.062587	-3.546363	40639.605781
HLA A*0212	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.408487	0.862113	-3.546373	25614.549799
HLA B*1801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.407077	0.860662	-3.546415	25531.541467
HLA A*0212	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.315858	0.769405	-3.546453	20694.659299
HLA A*2301	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.514230	0.967687	-3.546543	32676.083608
HLA A*6801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.240520	0.693953	-3.546567	17398.815982
HLA A*0101	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.381418	0.834835	-3.546583	24066.797867
HLA B*4601	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.391493	0.844865	-3.546628	24631.615812
HLA B*1503	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.415429	0.868794	-3.546635	26027.320218
HLA B*1503	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.345659	0.798809	-3.546850	22164.561754
HLA A*2501	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.462069	0.915076	-3.546993	28978.044972
HLA A*1101	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.474604	0.927578	-3.547026	29826.588639

HLA B*4403	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.630283	1.083182	-3.547101	42685.739562
HLA A*0206	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.449424	0.902312	-3.547112	28146.484155
HLA B*5301	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.263613	0.716494	-3.547119	18349.016150
HLA B*1503	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.316598	0.769461	-3.547137	20729.955446
HLA A*2501	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.461597	0.914377	-3.547220	28946.551728
HLA B*7301	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.510807	0.963515	-3.547292	32419.536313
HLA B*1509	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.510868	0.963515	-3.547353	32424.096672
HLA B*0802	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.473231	0.925719	-3.547512	29732.503955
HLA B*4601	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.394249	0.846543	-3.547706	24788.420117
HLA A*0101	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.316359	0.768573	-3.547786	20718.519632
HLA B*2705	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.450397	0.902312	-3.548085	28209.594317
HLA A*0212	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.391707	0.843615	-3.548092	24643.744940
HLA B*5401	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.347038	0.798809	-3.548229	22235.059522
HLA B*4402	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.416205	0.867880	-3.548325	26073.827342
HLA A*2602	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.516081	0.967687	-3.548394	32815.678847
HLA B*4801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.444006	0.895455	-3.548552	27797.532162
HLA A*2403	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.393560	0.844865	-3.548696	24749.159178
HLA B*0702	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.221902	0.673165	-3.548737	16668.724770
HLA A*2501	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.463333	0.914477	-3.548856	29062.509019
HLA B*4601	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.417770	0.868794	-3.548975	26167.940424
HLA A*3001	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.131706	0.582728	-3.548978	13542.712113
HLA A*2402	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.504038	0.955018	-3.549020	31918.166265
HLA A*3001	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.186914	0.637857	-3.549057	15378.495327
HLA A*0219	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.433807	0.884477	-3.549330	27152.331483
HLA A*0201	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.405510	0.856154	-3.549356	25439.579570
HLA B*3801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.410000	0.860349	-3.549650	25703.945722
HLA A*0203	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.410348	0.860662	-3.549686	25724.534177
HLA B*7301	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.617852	1.067986	-3.549865	41481.235689
HLA B*1517	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.162277	0.612321	-3.549956	14530.385792
HLA B*4402	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.418808	0.868794	-3.550014	26230.587314
HLA A*0250	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.475757	0.925719	-3.550038	29905.920998
HLA A*2403	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.434063	0.883995	-3.550069	27168.347335
HLA B*4002	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-3.781369	0.231300	-3.550069	6044.623271
HLA A*0216	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.430685	0.880484	-3.550200	26957.813313
HLA A*0201	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.318854	0.768573	-3.550281	20837.896389
HLA A*8001	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.419137	0.868794	-3.550343	26250.461479
HLA B*4403	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.613345	1.062587	-3.550759	41053.044776
HLA A*0216	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.448160	0.897326	-3.550834	28064.682340
HLA B*0801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.229477	0.678487	-3.550990	16962.002205
HLA A*2403	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.423831	0.872828	-3.551003	26535.740636
HLA A*6901	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.407462	0.856154	-3.551309	25554.203659
HLA A*3301	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.611144	1.059725	-3.551419	40845.470725
HLA B*0802	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.424397	0.872828	-3.551569	26570.360054
HLA A*6901	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.346028	0.794424	-3.551604	22183.395279
HLA A*0219	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.449029	0.897326	-3.551703	28120.914524
HLA B*3901	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.292262	0.740545	-3.551717	19600.285755
HLA A*0250	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.578998	1.027215	-3.551784	37931.345798
HLA A*2402	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.465875	0.914083	-3.551792	29233.125281
HLA B*1801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.189188	0.637330	-3.551858	15459.240249
HLA A*0211	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.457725	0.905846	-3.551879	28689.625836
HLA A*2301	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.515555	0.963515	-3.552040	32775.936395
HLA B*4801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.419955	0.867880	-3.552074	26299.928235
HLA B*2705	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.457922	0.905846	-3.552076	28702.666246
HLA B*4601	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.343953	0.791821	-3.552133	22077.679405
HLA B*0802	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.447589	0.895455	-3.552134	28027.812663
HLA B*1502	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.571196	1.019055	-3.552140	37255.947418
HLA B*4001	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.420032	0.867880	-3.552152	26304.623884
HLA A*2603	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.647105	1.094888	-3.552217	44371.603438
HLA B*1501	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.343014	0.790719	-3.552295	22029.955940
HLA A*3301	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.342732	0.790220	-3.552512	22015.659027
HLA B*1517	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.383176	0.830606	-3.552570	24164.383813
HLA A*1101	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.448038	0.895455	-3.552583	28056.788456
HLA B*2705	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.342003	0.789406	-3.552598	21978.768265
HLA A*0202	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.446142	0.893488	-3.552654	27934.565668
HLA B*7301	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.399202	0.846543	-3.552659	25072.726448

HLA A*2402	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.516267	0.963515	-3.552752	32829.706650
HLA B*1503	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.408943	0.856154	-3.552789	25641.446855
HLA B*2705	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.256031	0.703210	-3.552821	18031.464236
HLA A*0216	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.448560	0.895455	-3.553105	28090.504772
HLA A*0203	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.413529	0.860349	-3.553179	25913.657949
HLA B*0702	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.413844	0.860662	-3.553182	25932.450222
HLA B*5301	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.570178	1.016861	-3.553318	37168.778168
HLA A*3101	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.135126	0.581735	-3.553392	13649.806555
HLA A*6802	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.450754	0.897326	-3.553428	28232.800695
HLA B*1801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.467842	0.914377	-3.553465	29365.795273
HLA B*0702	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.426308	0.872828	-3.553479	26687.480243
HLA A*3001	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.267623	0.714055	-3.553569	18519.248266
HLA A*2301	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.501249	0.947523	-3.553726	31713.859219
HLA A*2402	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.521471	0.967687	-3.553784	33225.468340
HLA A*2601	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.398739	0.844865	-3.553874	25046.019470
HLA A*0201	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.388493	0.834602	-3.553891	24462.036495
HLA A*0212	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.414257	0.860349	-3.553908	25957.153316
HLA A*0206	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.237747	0.683810	-3.553937	17288.101455
HLA A*6802	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.291337	0.737370	-3.553967	19558.552311
HLA A*3201	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.585102	1.031013	-3.554090	38468.230859
HLA A*6801	1:390-398	9	QYVIDPKAA	1.238097	-0.137526	-4.654959	1.100571	-3.554388	45181.375796
HLA A*2902	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.460298	0.905846	-3.554452	28860.082643
HLA A*0101	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.343866	0.789406	-3.554461	22073.260649
HLA A*2501	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.449983	0.895455	-3.554529	28182.747603
HLA B*1501	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.308822	0.754283	-3.554538	20362.053460
HLA A*2603	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.659658	1.105060	-3.554598	45672.882466
HLA A*0203	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.192468	0.637857	-3.554611	15576.433581
HLA B*5801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.353483	0.798809	-3.554673	22567.473114
HLA B*3901	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.416787	0.862113	-3.554674	26108.832836
HLA B*0802	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.442575	0.887847	-3.554729	27706.100487
HLA B*0702	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.415101	0.860349	-3.554751	26007.614993
HLA B*0803	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.457152	0.902312	-3.554840	28651.780143
HLA B*1503	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.344311	0.789406	-3.554905	22095.841417
HLA B*1517	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.480630	0.925719	-3.554911	30243.358225
HLA A*2403	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.442803	0.887847	-3.554956	27720.643334
HLA B*1501	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.324706	0.769461	-3.555246	21120.609232
HLA A*1101	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.457650	0.902312	-3.555338	28684.659620
HLA A*3002	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.309623	0.754283	-3.555339	20399.651479
HLA B*7301	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.435856	0.880484	-3.555372	27280.723126
HLA A*3002	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.544632	0.989026	-3.555606	35045.505974
HLA A*0101	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.350055	0.794424	-3.555631	22390.048541
HLA B*0803	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.470732	0.915076	-3.555655	29561.851653
HLA B*5801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.346416	0.790719	-3.555697	22203.205721
HLA B*3501	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.453139	0.897326	-3.555812	28388.254472
HLA A*2601	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.402376	0.846543	-3.555833	25256.648295
HLA A*2601	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.386460	0.830606	-3.555854	24347.832492
HLA A*0203	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.317757	0.761813	-3.555943	20785.317594
HLA A*8001	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.416621	0.860662	-3.555959	26098.806303
HLA A*0219	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.399408	0.843357	-3.556051	25084.665669
HLA B*5101	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.470635	0.914477	-3.556158	29555.295400
HLA B*3501	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.416952	0.860662	-3.556290	26118.721920
HLA B*1517	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.476993	0.920689	-3.556304	29991.142533
HLA A*2403	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.259574	0.703210	-3.556364	18179.168631
HLA B*5401	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.391281	0.834835	-3.556446	24619.625843
HLA A*0101	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.229736	0.673165	-3.556570	16972.099089
HLA A*2601	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.169373	0.612666	-3.556707	14769.731149
HLA B*5701	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.405526	0.848752	-3.556774	25440.542966
HLA A*8001	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.403318	0.846543	-3.556775	25311.498672
HLA B*5301	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.584071	1.027215	-3.556856	38376.979468
HLA A*6802	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.243323	0.686428	-3.556894	17511.471048
HLA A*0211	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.545957	0.989026	-3.556931	35152.599330
HLA A*2501	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.450420	0.893488	-3.556932	28211.120466
HLA A*0301	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.345065	0.787998	-3.557067	22134.245826
HLA B*5701	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.400853	0.843615	-3.557238	25168.263395
HLA B*0702	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.452793	0.895455	-3.557339	28365.687582

HLA A*2603	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.588394	1.031013	-3.557381	38760.899080
HLA A*6901	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.343718	0.786321	-3.557397	22065.738856
HLA B*1509	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.451022	0.893488	-3.557533	28250.218006
HLA B*4001	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.401267	0.843615	-3.557652	25192.238530
HLA B*1503	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-3.900140	0.342354	-3.557787	7945.850775
HLA A*0219	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.451417	0.893488	-3.557928	28275.905209
HLA A*0101	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.312473	0.754283	-3.558189	20533.958172
HLA B*5301	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.589343	1.031013	-3.558330	38845.707360
HLA B*0802	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.441598	0.883265	-3.558333	27643.817633
HLA B*1503	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.472884	0.914477	-3.558407	29708.707749
HLA A*2403	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.401913	0.843357	-3.558556	25229.745407
HLA B*4402	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.357383	0.798809	-3.558574	22771.051150
HLA B*4801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.421042	0.862113	-3.558929	26365.886305
HLA A*2601	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.393784	0.834835	-3.558948	24761.882017
HLA A*0203	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.426834	0.867880	-3.558954	26719.840140
HLA A*2902	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.220060	0.660945	-3.559116	16598.176538
HLA A*3101	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.347118	0.787998	-3.559121	22239.149732
HLA B*4001	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.380173	0.821048	-3.559125	23997.891384
HLA A*0212	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.427019	0.867880	-3.559139	26731.262139
HLA A*0219	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.454656	0.895455	-3.559202	28487.638977
HLA B*5101	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.443212	0.883995	-3.559217	27746.749635
HLA B*3901	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.419745	0.860349	-3.559396	26287.268390
HLA A*3201	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.420063	0.860662	-3.559401	26306.473915
HLA B*5101	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.447291	0.887847	-3.559444	28008.562602
HLA B*1502	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.548490	0.989026	-3.559464	35358.203329
HLA A*2501	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.408226	0.848752	-3.559474	25599.172938
HLA A*2902	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.421620	0.862113	-3.559507	26400.998248
HLA A*0211	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.474601	0.915076	-3.559525	29826.427281
HLA B*3901	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.427426	0.867880	-3.559546	26756.291928
HLA A*0216	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.403182	0.843615	-3.559567	25303.557838
HLA B*4801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.428375	0.868794	-3.559581	26814.834303
HLA B*7301	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.578803	1.019055	-3.559748	37914.317658
HLA B*1517	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.394467	0.834602	-3.559865	24800.894797
HLA B*4601	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.416148	0.856154	-3.559995	26070.442206
HLA A*0206	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.455498	0.895455	-3.560043	28542.865598
HLA A*2403	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.438447	0.878392	-3.560055	27443.996791
HLA A*0219	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.420749	0.860662	-3.560087	26348.062766
HLA B*5801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.349606	0.789406	-3.560201	22366.925103
HLA A*0206	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.553680	0.993286	-3.560394	35783.284493
HLA B*1517	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.466303	0.905846	-3.560457	29261.922386
HLA B*0803	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.481408	0.920689	-3.560718	30297.562716
HLA B*1509	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.515839	0.954860	-3.560979	32797.398435
HLA B*7301	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.526191	0.965021	-3.561170	33588.547740
HLA B*4403	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.629164	1.067986	-3.561178	42575.960612
HLA B*4001	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.353093	0.791821	-3.561272	22547.215682
HLA B*5101	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.476429	0.915076	-3.561353	29952.228099
HLA B*5701	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.337119	0.775701	-3.561418	21732.954496
HLA B*5701	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.392038	0.830606	-3.561432	24662.550221
HLA A*2602	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.268608	0.707098	-3.561510	18561.274266
HLA A*0212	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.330190	0.768573	-3.561617	21388.983203
HLA A*2602	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.568656	1.006851	-3.561804	37038.707118
HLA A*3201	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.589230	1.027215	-3.562016	38835.621423
HLA B*4002	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.621768	1.059725	-3.562043	41857.017208
HLA A*3001	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.299682	0.737370	-3.562312	19938.022266
HLA A*2603	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.440724	0.878392	-3.562332	27588.240980
HLA B*4403	1:297-305	9	LFGLDEMVA	1.382315	-0.287427	-4.657231	1.094888	-3.562343	45418.355287
HLA B*0802	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.483041	0.920689	-3.562351	30411.692124
HLA B*5401	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.455892	0.893488	-3.562404	28568.818899
HLA B*3901	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.440811	0.878392	-3.562419	27593.763757
HLA A*3101	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.430311	0.867880	-3.562431	26934.634916
HLA A*0219	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.430363	0.867880	-3.562483	26937.840802
HLA A*1101	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.316775	0.754283	-3.562491	20738.368160
HLA A*3301	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.616524	1.054023	-3.562501	41354.638244
HLA B*0702	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.430424	0.867880	-3.562544	26941.630067
HLA B*4403	1:392-400	9	VIDPKAAAK	0.923137	0.186391	-4.672212	1.109528	-3.562683	47012.323900

HLA B*3801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.563165	1.000328	-3.562837	36573.377800
HLA B*4601	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.383968	0.821048	-3.562919	24208.478873
HLA B*1517	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.434655	0.871584	-3.563071	27205.410986
HLA B*7301	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.483764	0.920689	-3.563075	30462.407721
HLA A*2602	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.594183	1.031013	-3.563170	39281.039606
HLA A*1101	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.469052	0.905846	-3.563206	29447.725186
HLA A*2602	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.580206	1.016861	-3.563345	38036.967629
HLA A*0250	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.528388	0.965021	-3.563367	33758.877310
HLA B*3801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.443865	0.880484	-3.563381	27788.510732
HLA B*7301	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.583775	1.020365	-3.563410	38350.828866
HLA B*3901	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.199319	0.635887	-3.563432	15824.103901
HLA B*5401	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.351528	0.787998	-3.563531	22466.124549
HLA B*1501	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-3.950659	0.387024	-3.563635	8926.044161
HLA A*0201	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.398591	0.834835	-3.563755	25037.484664
HLA B*4601	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.398372	0.834602	-3.563770	25024.890981
HLA B*1502	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.531435	0.967578	-3.563857	33996.583707
HLA A*2501	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.484575	0.920689	-3.563885	30519.316207
HLA A*3201	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.398511	0.834602	-3.563909	25032.879787
HLA A*6802	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.424729	0.860662	-3.564067	26590.635507
HLA A*3301	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.001605	0.437367	-3.564238	10037.030964
HLA A*6801	1:399-407	9	AKELGPDGA	1.258473	-0.142933	-4.679836	1.115540	-3.564296	47844.916225
HLA B*5701	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.398943	0.834602	-3.564341	25057.810413
HLA B*5801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.177065	0.612666	-3.564399	15033.662764
HLA A*0301	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.356274	0.791821	-3.564453	22712.980180
HLA A*2501	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.410998	0.846543	-3.564456	25763.112300
HLA B*0801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.425199	0.860662	-3.564537	26619.421555
HLA B*0802	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.425213	0.860662	-3.564551	26620.285618
HLA B*0801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.411102	0.846543	-3.564559	25769.245556
HLA B*5801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.223260	0.658550	-3.564710	16720.928046
HLA B*5101	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.492345	0.927578	-3.564767	31070.235555
HLA B*0702	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.462219	0.897326	-3.564893	28988.079862
HLA A*2501	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.467212	0.902312	-3.564900	29323.250116
HLA B*1501	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.399747	0.834835	-3.564911	25104.214840
HLA B*1801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.449466	0.884477	-3.564989	28149.225136
HLA B*1517	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.279230	0.714055	-3.565175	19020.845140
HLA B*4801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.408715	0.843357	-3.565358	25627.994798
HLA A*6801	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.565808	1.000328	-3.565480	36796.646692
HLA B*5701	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.400318	0.834835	-3.565482	25137.238619
HLA A*0301	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.335009	0.769461	-3.565548	21627.630099
HLA A*0250	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.582466	1.016861	-3.565606	38235.439936
HLA A*2402	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.556337	0.990658	-3.565680	36002.898726
HLA B*5701	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.412232	0.846543	-3.565689	25836.388490
HLA B*0803	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.353692	0.787998	-3.565695	22578.341521
HLA B*3901	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.334290	0.768573	-3.565717	21591.856775
HLA A*0211	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.446372	0.880484	-3.565888	27949.379639
HLA A*0202	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.334673	0.768573	-3.566100	21610.905129
HLA B*0803	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.472022	0.905846	-3.566176	29649.781726
HLA A*8001	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.178634	0.612321	-3.566313	15088.089789
HLA A*1101	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.438010	0.871584	-3.566426	27416.395450
HLA A*6901	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.357158	0.790719	-3.566439	22759.228090
HLA A*0201	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.231733	0.665274	-3.566458	17050.323403
HLA A*6802	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.243835	0.677348	-3.566486	17532.135486
HLA A*2501	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.439796	0.872828	-3.566968	27529.350440
HLA B*5801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.353361	0.786321	-3.567040	22561.125456
HLA A*0101	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.358873	0.791821	-3.567052	22849.286981
HLA B*1503	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-3.925938	0.358727	-3.567211	8432.138862
HLA A*6801	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.635207	1.067986	-3.567221	43172.513190
HLA A*2402	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.554094	0.986777	-3.567317	35817.371432
HLA B*3901	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.451325	0.883995	-3.567330	28269.940027
HLA A*2902	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.435395	0.867880	-3.567515	27251.811662
HLA A*0250	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.598539	1.031013	-3.567526	39677.008310
HLA A*0202	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.947995	0.380458	-3.567537	8871.452165
HLA A*8001	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.423780	0.856154	-3.567626	26532.582604
HLA A*2403	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.357068	0.789406	-3.567663	22754.549824
HLA B*1801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.284246	0.716494	-3.567752	19241.811694

HLA A*8001	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.435727	0.867880	-3.567846	27272.607121
HLA B*7301	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.584764	1.016861	-3.567903	38438.274852
HLA B*0803	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.439528	0.871584	-3.567944	27512.377571
HLA A*2602	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.535671	0.967578	-3.568093	34329.809916
HLA A*0202	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.483179	0.915076	-3.568103	30421.400582
HLA B*0702	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.413167	0.844865	-3.568302	25892.077677
HLA A*6801	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.554679	0.986192	-3.568486	35865.652178
HLA A*0211	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.356749	0.787998	-3.568751	22737.814437
HLA A*2501	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.453289	0.884477	-3.568812	28398.085122
HLA B*4501	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.324570	0.755651	-3.568919	21113.983183
HLA B*5701	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.413820	0.844865	-3.568955	25931.047343
HLA A*0211	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.242171	0.673165	-3.569006	17465.112312
HLA A*2301	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.503359	0.934152	-3.569207	31868.302543
HLA A*0203	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.346629	0.777400	-3.569229	22214.139048
HLA A*6901	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.291696	0.722436	-3.569260	19574.747882
HLA B*3801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.527075	0.957710	-3.569364	33656.940356
HLA B*0801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.400163	0.830606	-3.569557	25128.264903
HLA A*6801	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.576444	1.006851	-3.569593	37708.943207
HLA B*4402	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.413219	0.843615	-3.569604	25895.159473
HLA A*3001	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.205508	0.635887	-3.569621	16051.206031
HLA B*1509	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.524683	0.955018	-3.569665	33472.092066
HLA B*1801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.508377	0.938712	-3.569665	32238.693361
HLA A*3101	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.400339	0.830606	-3.569733	25138.462556
HLA A*0301	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.368543	0.798809	-3.569734	23363.781316
HLA B*4001	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.400372	0.830606	-3.569766	25140.366576
HLA B*0803	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.483912	0.914083	-3.569829	30472.791780
HLA B*3901	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.361659	0.791821	-3.569838	22996.362266
HLA B*0802	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.360073	0.790220	-3.569854	22912.540159
HLA A*2301	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.524908	0.955018	-3.569890	33489.480290
HLA A*3201	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.357912	0.787998	-3.569914	22798.785520
HLA A*2403	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.437799	0.867880	-3.569919	27403.049929
HLA A*0211	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.430689	0.860662	-3.570027	26958.104992
HLA B*5101	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.453407	0.883265	-3.570142	28405.767685
HLA B*1509	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.527899	0.957710	-3.570189	33720.911264
HLA A*0203	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.243405	0.673165	-3.570239	17514.787091
HLA A*6801	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.559267	0.989026	-3.570241	36246.600121
HLA B*5701	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.391392	0.821048	-3.570344	24625.886543
HLA B*4501	1:43-51	9	FRIEDTDAQ	1.010766	0.051821	-4.633020	1.062587	-3.570433	42955.616886
HLA A*0211	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.250648	0.679867	-3.570781	17809.360484
HLA A*2501	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.345015	0.774156	-3.570860	22131.731349
HLA B*4001	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.346644	0.775701	-3.570943	22214.860116
HLA A*2403	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.308457	0.737370	-3.571088	20344.986366
HLA A*2902	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.431439	0.860349	-3.571089	27004.668233
HLA A*6802	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.237566	0.666384	-3.571182	17280.901398
HLA A*6802	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.417915	0.846543	-3.571372	26176.718967
HLA A*2602	1:191-199	9	SGDPLYTLV	1.035106	0.032880	-4.639389	1.067986	-3.571403	43590.255456
HLA A*0201	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.402075	0.830606	-3.571469	25239.164984
HLA A*0216	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.433629	0.862113	-3.571515	27141.170054
HLA A*3001	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.258084	0.686428	-3.571656	18116.923259
HLA A*2301	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.486074	0.914377	-3.571697	30624.835907
HLA A*3201	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.565024	0.993286	-3.571737	36730.218754
HLA B*3801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.510468	0.938712	-3.571756	32394.290549
HLA B*1509	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.469118	0.897326	-3.571791	29452.186174
HLA A*0219	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.265805	0.693953	-3.571852	18441.865590
HLA A*0211	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.036984	0.464975	-3.572008	10888.894978
HLA B*1801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.455441	0.883265	-3.572176	28539.159909
HLA B*3901	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.487267	0.915076	-3.572191	30709.115563
HLA A*0301	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.361680	0.789406	-3.572275	22997.481963
HLA B*3901	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.360275	0.787998	-3.572278	22923.202709
HLA A*3101	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.364126	0.791821	-3.572305	23127.362137
HLA B*4601	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.407166	0.834835	-3.572331	25536.790673
HLA B*2705	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.418965	0.846543	-3.572423	26240.096643
HLA B*1509	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.417325	0.844865	-3.572461	26141.198189
HLA A*0211	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.511187	0.938712	-3.572475	32447.961315
HLA A*0202	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.233467	0.660945	-3.572522	17118.532861

HLA B*4801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.428819	0.856154	-3.572666	26842.265662
HLA A*0203	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.441713	0.868794	-3.572919	27651.146554
HLA A*0219	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.433476	0.860349	-3.573126	27131.627735
HLA B*0801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.350628	0.777400	-3.573228	22419.623210
HLA B*2705	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.433678	0.860349	-3.573329	27144.253674
HLA B*1509	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.512120	0.938712	-3.573408	32517.725535
HLA A*3101	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.276648	0.703210	-3.573438	18908.092825
HLA B*3501	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.394726	0.821048	-3.573678	24815.657899
HLA B*4501	1:199-207	9	VNPCDDALM	0.975652	0.107530	-4.657121	1.083182	-3.573939	45406.808467
HLA A*0206	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.452354	0.878392	-3.573962	28337.005965
HLA A*2902	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.469425	0.895455	-3.573971	29473.066203
HLA B*1517	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.349853	0.775701	-3.574152	22379.633983
HLA B*2705	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.408827	0.834602	-3.574226	25634.650604
HLA B*1503	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.328550	0.754283	-3.574267	21308.368508
HLA A*3001	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.270001	0.695627	-3.574374	18620.915642
HLA B*5701	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.417864	0.843357	-3.574507	26173.603663
HLA B*4601	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.405148	0.830606	-3.574542	25418.394100
HLA B*4801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.418232	0.843615	-3.574617	26195.843725
HLA B*3801	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.542349	0.967687	-3.574661	34861.705928
HLA B*0803	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.500507	0.925719	-3.574788	31659.689900
HLA A*0101	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.352210	0.777400	-3.574809	22501.398592
HLA A*2301	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.539837	0.965021	-3.574816	34660.676558
HLA B*1509	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.443717	0.868794	-3.574923	27779.041382
HLA A*6901	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.405533	0.830606	-3.574928	25440.955861
HLA B*3801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.522533	0.947523	-3.575010	33306.812992
HLA B*1801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.248433	0.673165	-3.575267	17718.736934
HLA B*3801	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.562056	0.986777	-3.575280	36480.107994
HLA A*6802	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.315854	0.740545	-3.575308	20694.435389
HLA B*4402	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.396511	0.821048	-3.575463	24917.897904
HLA A*0211	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.424287	0.848752	-3.575535	26563.605006
HLA B*2705	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.431697	0.856154	-3.575544	27020.743164
HLA A*2902	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.418909	0.843357	-3.575552	26236.689920
HLA B*1801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.448388	0.872828	-3.575560	28079.413406
HLA B*4801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.435919	0.860349	-3.575570	27284.708230
HLA A*0211	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.345039	0.769461	-3.575578	22132.928683
HLA A*0206	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.345105	0.769461	-3.575644	22136.281565
HLA B*0801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.349801	0.774156	-3.575646	22376.970572
HLA B*0801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.365094	0.789406	-3.575689	23178.967611
HLA A*0216	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.460211	0.884477	-3.575733	28854.306417
HLA B*5801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.353384	0.777400	-3.575984	22562.346021
HLA A*0219	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.421026	0.844865	-3.576161	26364.887868
HLA B*1502	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.490256	0.914083	-3.576173	30921.165386
HLA A*3001	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.256214	0.679867	-3.576347	18039.074603
HLA B*3501	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.449213	0.872828	-3.576385	28132.783248
HLA A*2402	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.510682	0.934152	-3.576530	32410.242182
HLA A*2501	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.459837	0.883265	-3.576572	28829.497411
HLA A*0216	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.419964	0.843357	-3.576607	26300.497360
HLA B*5101	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.420063	0.843357	-3.576706	26306.473915
HLA A*3002	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.199150	0.622434	-3.576716	15817.941422
HLA A*2403	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.407378	0.830606	-3.576772	25549.227309
HLA A*3101	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.411637	0.834835	-3.576802	25801.050364
HLA A*2602	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.604027	1.027215	-3.576813	40181.608269
HLA A*0202	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.593748	1.016861	-3.576888	39241.745650
HLA B*2705	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.472360	0.895455	-3.576905	29672.888618
HLA B*1503	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.354512	0.777400	-3.577112	22621.010856
HLA A*2603	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.544693	0.967578	-3.577115	35050.435720
HLA B*1503	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.412088	0.834835	-3.577253	25827.863805
HLA A*0101	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.351441	0.774156	-3.577285	22461.628047
HLA A*0202	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.200090	0.622434	-3.577656	15852.207808
HLA B*1517	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.257640	0.679867	-3.577773	18098.408732
HLA A*2501	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.398908	0.821048	-3.577860	25055.777096
HLA A*0216	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.446776	0.868794	-3.577982	27975.398666
HLA B*0803	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.505661	0.927578	-3.578084	32037.707116
HLA B*4601	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.353903	0.775701	-3.578203	22589.337366
HLA A*3101	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.412916	0.834602	-3.578314	25877.094174

HLA B*0803	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.462938	0.884477	-3.578461	29036.107227
HLA B*1509	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.456877	0.878392	-3.578485	28633.650535
HLA A*6801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.466416	0.887847	-3.578569	29269.521953
HLA B*1517	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.301122	0.722436	-3.578686	20004.251729
HLA A*0212	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.447507	0.868794	-3.578713	28022.506207
HLA A*2402	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.493230	0.914477	-3.578753	31133.668842
HLA A*0202	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.423852	0.844865	-3.578988	26537.032666
HLA A*0212	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.175054	0.595974	-3.579079	14964.204849
HLA A*2403	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.103033	0.523921	-3.579112	12677.468248
HLA A*1101	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.439632	0.860349	-3.579282	27518.927263
HLA A*0219	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.457680	0.878392	-3.579288	28686.677042
HLA B*1509	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.494398	0.915076	-3.579322	31217.491038
HLA A*2601	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.373825	0.794424	-3.579400	23649.653107
HLA B*1517	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.475066	0.895455	-3.579612	29858.393216
HLA A*0301	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.365973	0.786321	-3.579652	23225.913058
HLA A*6802	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.414266	0.834602	-3.579665	25957.715024
HLA B*0803	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.440014	0.860349	-3.579665	27543.204483
HLA A*0216	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.349557	0.769461	-3.580096	22364.384193
HLA B*7301	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.569220	0.989026	-3.580194	37086.828423
HLA A*2603	1:407-415	9	AAVLDAALA	1.185005	-0.125280	-4.640040	1.059725	-3.580315	43655.626135
HLA B*0802	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.451933	0.871584	-3.580349	28309.578537
HLA A*6802	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.449213	0.868794	-3.580418	28132.783248
HLA B*5801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.368433	0.787998	-3.580435	23357.841484
HLA A*0216	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.458947	0.878392	-3.580555	28770.447466
HLA A*0212	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.436709	0.856154	-3.580555	27334.349369
HLA A*2601	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.276208	0.695627	-3.580581	18888.974139
HLA B*3501	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.476251	0.895455	-3.580796	29939.915725
HLA A*2501	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.368825	0.787998	-3.580828	23378.953696
HLA B*5101	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.459278	0.878392	-3.580886	28792.401774
HLA B*4001	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.371635	0.790719	-3.580917	23530.711267
HLA B*1801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.368964	0.787998	-3.580966	23386.417062
HLA A*8001	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.425871	0.844865	-3.581006	26660.639756
HLA B*5801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.357284	0.776187	-3.581098	22765.877806
HLA A*0301	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.265025	0.683810	-3.581215	18408.772193
HLA A*8001	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.416026	0.834602	-3.581424	26063.109251
HLA A*0206	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.495930	0.914477	-3.581453	31327.797287
HLA A*6801	1:475-483	9	RSMQRLRAA	1.190248	-0.140115	-4.631599	1.050133	-3.581465	42815.253714
HLA A*2501	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.295580	0.714055	-3.581525	19750.581006
HLA B*5301	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.600623	1.019055	-3.581567	39867.858816
HLA A*1101	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.454527	0.872828	-3.581699	28479.163915
HLA B*5801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.350285	0.768573	-3.581712	22401.922201
HLA A*0101	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.357456	0.775701	-3.581755	22774.870325
HLA B*5301	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.575042	0.993286	-3.581756	37587.350948
HLA B*1801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.496242	0.914477	-3.581765	31350.346226
HLA B*1503	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.477277	0.895455	-3.581823	30010.781059
HLA A*2403	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.336163	0.754283	-3.581879	21685.154979
HLA A*2301	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.453700	0.871584	-3.582116	28424.983189
HLA A*2602	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.462602	0.880484	-3.582118	29013.653170
HLA A*0203	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.416783	0.834602	-3.582181	26108.550345
HLA A*0201	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.370228	0.787998	-3.582230	23454.582856
HLA A*3201	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.307501	0.725139	-3.582363	20300.239549
HLA A*6802	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.442799	0.860349	-3.582449	27720.343405
HLA B*0802	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.462964	0.880484	-3.582480	29037.835182
HLA B*1517	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.463046	0.880484	-3.582562	29043.333904
HLA B*1517	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.374391	0.791821	-3.582570	23680.507238
HLA B*1502	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.497659	0.915076	-3.582583	31452.783162
HLA A*0101	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.373303	0.790719	-3.582585	23621.267032
HLA B*1502	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.358579	0.775701	-3.582878	22833.840691
HLA A*2902	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.429512	0.846543	-3.582970	26885.137900
HLA A*0101	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.381787	0.798809	-3.582978	24087.247747
HLA B*0702	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.413592	0.830606	-3.582986	25917.443356
HLA B*1517	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-3.974788	0.391537	-3.583252	9436.006733
HLA B*5301	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.497800	0.914477	-3.583323	31462.994184
HLA A*6801	1:114-122	9	PEEVEARHV	1.295802	-0.190742	-4.688395	1.105060	-3.583335	48797.207819
HLA B*4403	1:138-146	9	HLTDAQRAA	1.287739	-0.220563	-4.650608	1.067176	-3.583432	44730.958569

HLA B*0702	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.357691	0.774156	-3.583535	22787.194611
HLA A*2602	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.547135	0.963515	-3.583619	35248.004566
HLA B*5401	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.430201	0.846543	-3.583658	26927.787258
HLA B*1502	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.378362	0.794424	-3.583937	23898.004052
HLA B*0802	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.432816	0.848752	-3.584064	27090.414142
HLA A*2402	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.573348	0.989026	-3.584322	37441.025914
HLA A*8001	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.378756	0.794424	-3.584332	23919.733898
HLA A*2301	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.542067	0.957710	-3.584356	34839.081516
HLA A*2402	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.542114	0.957710	-3.584403	34842.851232
HLA A*8001	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.427788	0.843357	-3.584431	26778.592496
HLA B*4402	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.445214	0.860662	-3.584552	27874.935855
HLA B*5301	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.510323	0.925719	-3.584604	32383.426901
HLA A*0211	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.518765	0.934152	-3.584612	33019.044736
HLA A*3101	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.180692	0.595974	-3.584718	15159.762893
HLA A*3301	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.574022	0.989026	-3.584996	37499.203433
HLA B*3801	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.548659	0.963515	-3.585144	35371.978457
HLA A*0201	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.384217	0.798809	-3.585407	24222.365164
HLA B*1501	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.251825	0.666384	-3.585441	17857.695637
HLA B*0803	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.463923	0.878392	-3.585531	29101.999288
HLA B*1502	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.602392	1.016861	-3.585531	40030.597626
HLA B*5801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.354987	0.769405	-3.585581	22645.744555
HLA B*0802	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.447782	0.862113	-3.585668	28040.248864
HLA B*5101	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.466249	0.880484	-3.585765	29258.281626
HLA A*2301	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.540676	0.954860	-3.585816	34727.682461
HLA B*5301	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.541099	0.955018	-3.586080	34761.516056
HLA A*6901	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.363527	0.777400	-3.586127	23095.479435
HLA B*1517	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.421066	0.834835	-3.586230	26367.312708
HLA B*4002	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.533775	0.947523	-3.586252	34180.260188
HLA B*2705	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.416900	0.830606	-3.586294	26115.613519
HLA B*4801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.377276	0.790719	-3.586558	23838.348708
HLA B*0702	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.373005	0.786321	-3.586684	23605.043474
HLA B*4801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.421371	0.834602	-3.586769	26385.862982
HLA B*4001	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.421616	0.834835	-3.586780	26400.712597
HLA A*0206	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.247726	0.660945	-3.586781	17689.907636
HLA B*3801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.541867	0.955018	-3.586849	34823.064776
HLA A*3101	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.376426	0.789406	-3.587020	23791.709849
HLA B*0802	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.471091	0.883995	-3.587096	29586.330512
HLA A*6901	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.361302	0.774156	-3.587146	22977.460057
HLA A*0202	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.385972	0.798809	-3.587162	24320.450333
HLA B*0802	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.484575	0.897326	-3.587248	30519.316207
HLA B*5401	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.502393	0.915076	-3.587317	31797.523223
HLA A*3002	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.513039	0.925719	-3.587320	32586.581994
HLA A*2501	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.309853	0.722436	-3.587417	20410.469612
HLA A*2403	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.312607	0.725139	-3.587468	20540.291075
HLA A*0206	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.515135	0.927578	-3.587557	32744.212519
HLA A*2902	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.431176	0.843615	-3.587561	26988.310856
HLA A*0203	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.443828	0.856154	-3.587674	27786.105512
HLA B*3901	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.431103	0.843357	-3.587746	26983.785119
HLA A*0212	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.448435	0.860662	-3.587773	28082.451701
HLA B*3501	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.253122	0.665274	-3.587848	17911.103042
HLA A*2601	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.386691	0.798809	-3.587881	24360.744383
HLA B*2705	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.378622	0.790719	-3.587904	23912.359058
HLA A*3101	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.342318	0.754283	-3.588035	21994.707003
HLA B*5701	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.378834	0.790719	-3.588115	23924.004582
HLA B*3501	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.304637	0.716494	-3.588143	20166.806931
HLA A*0202	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.291433	0.703210	-3.588223	19562.890986
HLA A*6901	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.325595	0.737370	-3.588225	21163.843761
HLA B*1509	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.502323	0.914083	-3.588239	31792.363009
HLA A*6802	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.272104	0.683810	-3.588294	18711.293960
HLA B*5301	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.553382	0.965021	-3.588361	35758.707819
HLA A*3002	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.509066	0.920689	-3.588376	32289.835356
HLA A*2902	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.314514	0.726109	-3.588406	20630.719555
HLA B*3801	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.553429	0.965021	-3.588408	35762.577041
HLA B*4403	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.619449	1.031013	-3.588437	41634.114759
HLA A*2602	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.588803	1.000328	-3.588475	38797.402695

HLA B*4402	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.341472	0.752921	-3.588551	21951.912675
HLA A*2902	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.358116	0.769461	-3.588655	22809.518530
HLA A*3001	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.305187	0.716494	-3.588693	20192.352541
HLA B*1509	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.503246	0.914477	-3.588769	31860.028227
HLA A*0201	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.378376	0.789406	-3.588970	23898.779778
HLA B*4002	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.575770	0.986777	-3.588993	37650.440290
HLA A*0211	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.451144	0.862113	-3.589031	28258.166312
HLA A*2602	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.512538	0.923460	-3.589078	32549.053894
HLA A*2402	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.292460	0.703210	-3.589250	19609.194750
HLA B*0801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.315377	0.726109	-3.589268	20671.721080
HLA A*3001	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.211734	0.622434	-3.589300	16282.976818
HLA A*0301	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.365501	0.776187	-3.589314	23200.671212
HLA B*1517	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-3.878206	0.288865	-3.589340	7554.498036
HLA B*0803	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.450070	0.860662	-3.589408	28188.389392
HLA B*1517	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.449892	0.860349	-3.589542	28176.802074
HLA B*0801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.306122	0.716494	-3.589628	20235.876259
HLA A*2601	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.303697	0.714055	-3.589643	20123.214038
HLA B*1502	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.450376	0.860662	-3.589714	28208.220853
HLA A*3301	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.523919	0.934152	-3.589767	33413.292672
HLA B*3801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.515590	0.925719	-3.589871	32778.596216
HLA A*0202	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.377875	0.787998	-3.589878	23871.256922
HLA A*3001	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.297854	0.707963	-3.589891	19854.281600
HLA A*3301	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.576151	0.986192	-3.589958	37683.451677
HLA A*6901	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.388826	0.798809	-3.590017	24480.835555
HLA B*4501	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.609149	1.019055	-3.590094	40658.297818
HLA B*4002	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.478168	0.887847	-3.590321	30072.376728
HLA B*5101	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.458472	0.867880	-3.590592	28739.024363
HLA A*3001	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.267966	0.677348	-3.590618	18533.881358
HLA A*1101	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.434416	0.843615	-3.590801	27190.402945
HLA B*3501	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.446955	0.856154	-3.590801	27986.903160
HLA A*0206	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.524974	0.934152	-3.590822	33494.553557
HLA B*4601	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.364981	0.774156	-3.590826	23172.949401
HLA B*5101	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.484330	0.893488	-3.590842	30502.150001
HLA B*3901	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.488372	0.897326	-3.591045	30787.297383
HLA B*1509	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.486649	0.895455	-3.591195	30665.453675
HLA B*4801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.385626	0.794424	-3.591202	24301.117093
HLA A*2501	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.459226	0.867880	-3.591346	28788.975176
HLA A*1101	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.437898	0.846543	-3.591355	27409.277030
HLA B*1801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.517162	0.925719	-3.591443	32897.443968
HLA B*4601	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.256719	0.665274	-3.591445	18060.068529
HLA A*3002	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.525639	0.934152	-3.591487	33545.872947
HLA B*0803	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.471982	0.880484	-3.591497	29647.055017
HLA A*1101	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.485035	0.893488	-3.591547	30551.694169
HLA A*0301	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.368966	0.777400	-3.591566	23386.543581
HLA B*1517	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.474902	0.883265	-3.591637	29847.088214
HLA A*2501	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.435271	0.843615	-3.591656	27243.999030
HLA A*2402	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.539184	0.947523	-3.591661	34608.587841
HLA A*6802	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.447836	0.856154	-3.591682	28043.738058
HLA B*4402	1:55-63	9	EESYLALLD	1.112493	-0.915046	-3.789179	0.197447	-3.591732	6154.303744
HLA B*4001	1:55-63	9	EESYLALLD	1.112493	-0.915046	-3.789273	0.197447	-3.591826	6155.635652
HLA A*1101	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.435214	0.843357	-3.591858	27240.461971
HLA B*0802	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.452298	0.860349	-3.591948	28333.327003
HLA B*0803	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.476065	0.883995	-3.592070	29927.122701
HLA B*5401	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.257408	0.665274	-3.592134	18088.718199
HLA A*0301	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.228063	0.635887	-3.592176	16906.851004
HLA B*2705	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.413327	0.821048	-3.592279	25901.604412
HLA A*1101	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.460305	0.867880	-3.592424	28860.551036
HLA B*1501	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.391263	0.798809	-3.592453	24618.560351
HLA B*5101	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.382736	0.790220	-3.592517	24139.950293
HLA A*2603	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.619738	1.027215	-3.592524	41661.828000
HLA B*4002	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.544884	0.952354	-3.592530	35065.798223
HLA B*3501	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.461364	0.868794	-3.592570	28931.052712
HLA A*8001	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.454741	0.862113	-3.592628	28493.187656
HLA A*3201	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.578923	0.986192	-3.592731	37924.779826
HLA B*1502	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.557801	0.965021	-3.592780	36124.446204

HLA A*6801	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.611856	1.019055	-3.592800	40912.479380
HLA B*4801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.437740	0.844865	-3.592876	27399.343993
HLA B*3801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.476302	0.883265	-3.593037	29943.479313
HLA B*4501	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.465908	0.872828	-3.593080	29235.339437
HLA A*0202	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.586385	0.993286	-3.593099	38582.026280
HLA A*3002	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.436728	0.843615	-3.593113	27335.532401
HLA B*1801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.513962	0.920689	-3.593273	32655.937586
HLA A*3201	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.556826	0.963515	-3.593311	36043.434040
HLA A*0212	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.428016	0.834602	-3.593414	26792.648498
HLA B*1517	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.471834	0.878392	-3.593441	29636.952340
HLA A*0201	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.385267	0.791821	-3.593446	24281.011064
HLA A*0211	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.486941	0.893488	-3.593452	30686.031768
HLA A*0250	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.454285	0.860662	-3.593623	28463.299216
HLA A*2301	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.546026	0.952354	-3.593671	35158.114740
HLA B*1509	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.546120	0.952354	-3.593765	35165.723624
HLA A*0301	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.348098	0.754283	-3.593814	22289.376190
HLA A*6901	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-3.975423	0.381582	-3.593841	9449.799697
HLA A*2403	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.388408	0.794424	-3.593984	24457.272830
HLA A*0250	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.587315	0.993286	-3.594029	38664.769776
HLA A*0250	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.583115	0.989026	-3.594089	38292.573038
HLA B*3801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.514792	0.920689	-3.594102	32718.359917
HLA A*2602	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.580382	0.986192	-3.594190	38052.403944
HLA B*3901	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.454891	0.860662	-3.594229	28503.054643
HLA B*4403	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.614753	1.020365	-3.594388	41186.293918
HLA B*3901	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.350090	0.755651	-3.594439	22391.865530
HLA A*3101	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.278304	0.683810	-3.594494	18980.345456
HLA A*3301	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.508986	0.914477	-3.594509	32283.896632
HLA B*1801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.302638	0.707963	-3.594674	20074.176060
HLA B*0803	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.490322	0.895455	-3.594867	30925.849583
HLA A*2602	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.455613	0.860662	-3.594951	28550.432875
HLA A*3001	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.176726	0.581735	-3.594992	15021.955740
HLA A*0219	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.372587	0.777400	-3.595186	23582.323696
HLA B*4801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.425800	0.830606	-3.595194	26656.313174
HLA B*4002	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.615580	1.020365	-3.595215	41264.798919
HLA A*0219	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.425979	0.830606	-3.595373	26667.275213
HLA B*1503	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.302532	0.707098	-3.595434	20069.289697
HLA B*1517	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.492901	0.897326	-3.595575	31110.097612
HLA A*3002	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.440466	0.844865	-3.595601	27571.828438
HLA A*8001	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.385044	0.789406	-3.595638	24268.535300
HLA B*1502	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.622990	1.027215	-3.595775	41974.932735
HLA B*4601	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.386658	0.790719	-3.595939	24358.899408
HLA B*5801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.275814	0.679867	-3.595947	18871.814479
HLA A*8001	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.456296	0.860349	-3.595947	28595.414583
HLA A*2902	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.364666	0.768573	-3.596094	23156.156835
HLA B*1503	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.426886	0.830606	-3.596280	26723.020459
HLA B*4501	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.627311	1.031013	-3.596298	42394.616574
HLA A*0203	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.388143	0.791821	-3.596322	24442.326241
HLA B*0801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.390772	0.794424	-3.596347	24590.740691
HLA A*0211	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.493714	0.897326	-3.596388	31168.384700
HLA A*3201	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.615479	1.019055	-3.596423	41255.200802
HLA A*0250	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.498841	0.902312	-3.596529	31538.488222
HLA A*2601	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.387269	0.790719	-3.596550	24393.186042
HLA B*5101	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.492180	0.895455	-3.596725	31058.471726
HLA A*3301	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.561765	0.965021	-3.596744	36455.644386
HLA A*3201	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.469604	0.872828	-3.596776	29485.186592
HLA B*4402	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.452930	0.856154	-3.596776	28374.589382
HLA A*1101	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.477357	0.880484	-3.596873	30016.301637
HLA B*4403	1:170-178	9	LVRGPVTFA	1.270659	-0.208534	-4.659113	1.062125	-3.596988	45615.594651
HLA A*0202	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.270168	0.673165	-3.597002	18628.069349
HLA B*3801	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.511498	0.914477	-3.597021	32471.140853
HLA A*0216	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.453242	0.856154	-3.597088	28395.012678
HLA B*1501	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.274526	0.677348	-3.597178	18815.949585
HLA B*4001	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.270530	0.673165	-3.597364	18643.595288
HLA A*0216	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.431986	0.834602	-3.597384	27038.729193
HLA B*3501	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.384080	0.786321	-3.597759	24214.766019

HLA B*5701	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.396612	0.798809	-3.597803	24923.695110
HLA A*8001	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.441448	0.843615	-3.597833	27634.248091
HLA B*5801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.264252	0.666384	-3.597868	18376.036416
HLA B*1801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.495404	0.897326	-3.598077	31289.856780
HLA A*3101	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.374382	0.776187	-3.598195	23679.994808
HLA A*3002	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.466143	0.867880	-3.598263	29251.159710
HLA A*1101	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.443135	0.844865	-3.598270	27741.796552
HLA A*0201	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.389139	0.790719	-3.598420	24498.456228
HLA B*3801	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.513539	0.915076	-3.598463	32624.153364
HLA A*0202	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.282373	0.683810	-3.598563	19159.025730
HLA B*5801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.354289	0.755651	-3.598637	22609.388013
HLA B*3501	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-3.896048	0.297408	-3.598640	7871.320602
HLA B*4403	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.486560	0.887847	-3.598713	30659.150249
HLA A*0201	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.393427	0.794424	-3.599002	24741.528613
HLA A*6802	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.393513	0.794424	-3.599089	24746.481519
HLA A*0203	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.282926	0.683810	-3.599115	19183.398547
HLA B*1502	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.479641	0.880484	-3.599157	30174.555442
HLA B*3801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.551545	0.952354	-3.599190	35607.748958
HLA B*5401	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.293338	0.693953	-3.599386	19648.910170
HLA A*3001	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.291814	0.692320	-3.599494	19580.043459
HLA B*5401	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.260540	0.660945	-3.599595	18219.634336
HLA A*0101	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.369022	0.769405	-3.599617	23389.580224
HLA B*4801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.421021	0.821048	-3.599973	26364.602607
HLA B*4402	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.434916	0.834835	-3.600081	27221.752678
HLA A*0301	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.368729	0.768573	-3.600156	23373.768692
HLA B*3901	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.488014	0.887847	-3.600168	30761.991297
HLA A*2301	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.521100	0.920689	-3.600410	33197.080590
HLA B*2705	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.273626	0.673165	-3.600461	18777.003533
HLA A*2501	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.462635	0.862113	-3.600522	29015.850702
HLA B*5801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.362355	0.761813	-3.600541	23033.216466
HLA B*4001	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.394998	0.794424	-3.600574	24831.235782
HLA A*0219	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.435207	0.834602	-3.600606	27240.019871
HLA A*0201	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.370169	0.769461	-3.600708	23451.410903
HLA B*0802	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.469517	0.868794	-3.600723	29479.285254
HLA B*5701	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.374934	0.774156	-3.600778	23710.118897
HLA A*2301	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.526499	0.925719	-3.600780	33612.360229
HLA A*0212	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.435684	0.834835	-3.600849	27269.951498
HLA A*0216	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.327068	0.726109	-3.600959	21235.753420
HLA A*0101	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.362794	0.761813	-3.600981	23056.529793
HLA A*0250	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.539858	0.938712	-3.601146	34662.364193
HLA B*3501	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.435753	0.834602	-3.601151	27274.230128
HLA B*3901	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.496780	0.895455	-3.601326	31389.209128
HLA A*6802	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.436222	0.834835	-3.601387	27303.756211
HLA B*3501	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.461982	0.860349	-3.601633	28972.245136
HLA A*2403	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.436236	0.834602	-3.601635	27304.642487
HLA A*0211	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.445026	0.843357	-3.601669	27862.874441
HLA B*0702	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.392484	0.790719	-3.601766	24687.913370
HLA A*0219	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.389827	0.787998	-3.601830	24537.319463
HLA B*4501	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.618759	1.016861	-3.601898	41567.948024
HLA A*0202	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.525414	0.923460	-3.601953	33528.455443
HLA B*1502	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.540688	0.938712	-3.601975	34728.621839
HLA B*1502	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.595268	0.993286	-3.601982	39379.340204
HLA A*3201	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.328097	0.726109	-3.601988	21286.131868
HLA B*3501	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.309108	0.707098	-3.602010	20375.496983
HLA A*6901	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.371503	0.769405	-3.602098	23523.583628
HLA B*1517	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.489974	0.887847	-3.602127	30901.098291
HLA A*0101	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.388570	0.786321	-3.602249	24466.404002
HLA A*3001	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.267666	0.665274	-3.602391	18521.051722
HLA B*5301	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.554841	0.952354	-3.602487	35879.042692
HLA B*1801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.504867	0.902312	-3.602555	31979.178334
HLA B*3501	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.433342	0.830606	-3.602736	27123.262616
HLA B*7301	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.596234	0.993286	-3.602948	39466.996180
HLA B*1801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.297032	0.693953	-3.603079	19816.723857
HLA B*3901	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.449680	0.846543	-3.603137	28163.086409
HLA B*3501	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.471077	0.867880	-3.603197	29585.370175

HLA A*0219	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.372671	0.769405	-3.603266	23586.916942
HLA B*3901	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.209492	0.606197	-3.603296	16199.156304
HLA B*7301	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.590109	0.986777	-3.603332	38914.277024
HLA A*0301	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.328585	0.725139	-3.603447	21310.097717
HLA B*0802	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.447281	0.843615	-3.603666	28007.956515
HLA B*5401	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.561379	0.957710	-3.603669	36423.314487
HLA A*3301	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.630920	1.027215	-3.603705	42748.366166
HLA A*6802	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.283656	0.679867	-3.603789	19215.701313
HLA B*1509	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.381259	0.777400	-3.603858	24057.945983
HLA A*2601	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.372441	0.768573	-3.603868	23574.415201
HLA B*4403	1:380-388	9	WELLKFFND	0.942251	-0.784797	-3.761333	0.157454	-3.603879	5772.086499
HLA A*0301	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.307149	0.703210	-3.603939	20283.772925
HLA A*2301	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.542750	0.938712	-3.604038	34893.971101
HLA A*0211	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.499532	0.895455	-3.604077	31588.690334
HLA A*2301	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.510029	0.905846	-3.604183	32361.535460
HLA B*0802	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.447552	0.843357	-3.604195	28025.386730
HLA A*8001	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.425307	0.821048	-3.604259	26626.046753
HLA B*5701	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.394491	0.790220	-3.604271	24802.236534
HLA A*0202	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.284164	0.679867	-3.604297	19238.168677
HLA A*3201	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.621235	1.016861	-3.604374	41805.646464
HLA A*0219	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.460563	0.856154	-3.604409	28877.730709
HLA B*1517	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.477242	0.872828	-3.604414	30008.345833
HLA A*3001	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.200405	0.595974	-3.604430	15863.703639
HLA A*0212	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.057556	0.452989	-3.604567	11417.102492
HLA A*0203	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.330773	0.726109	-3.604664	21417.699045
HLA A*2402	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.569741	0.965021	-3.604720	37131.396291
HLA B*1801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.217429	0.612666	-3.604763	16497.910993
HLA A*0301	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.366584	0.761813	-3.604770	23258.604945
HLA B*1501	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.284784	0.679867	-3.604917	19265.664466
HLA A*0201	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.374365	0.769405	-3.604960	23679.098082
HLA A*6901	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.374494	0.769461	-3.605033	23686.144702
HLA B*4801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.439895	0.834835	-3.605059	27535.606242
HLA A*2902	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.396880	0.791821	-3.605059	24939.070976
HLA A*0219	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.473861	0.868794	-3.605067	29775.642900
HLA B*7301	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.557477	0.952354	-3.605123	36097.487032
HLA A*2501	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.448679	0.843357	-3.605322	28098.256134
HLA A*3002	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.312560	0.707098	-3.605461	20538.068782
HLA A*0216	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.473354	0.867880	-3.605473	29740.869308
HLA B*1517	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.374948	0.769461	-3.605487	23710.888525
HLA A*2403	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.379666	0.774156	-3.605510	23969.865361
HLA B*0803	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.502964	0.897326	-3.605638	31839.351832
HLA B*4501	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.592083	0.986192	-3.605890	39091.517855
HLA B*1801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.108826	0.502859	-3.605967	12847.728826
HLA A*0206	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.309195	0.703210	-3.605986	20379.575871
HLA A*0202	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.332136	0.726109	-3.606027	21485.007667
HLA B*4403	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.454941	0.848752	-3.606189	28506.292993
HLA A*6801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.499687	0.893488	-3.606198	31599.971174
HLA A*2501	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.503535	0.897326	-3.606209	31881.235466
HLA B*1801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-3.965794	0.359537	-3.606257	9242.605436
HLA A*3301	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.573947	0.967687	-3.606259	37492.712266
HLA A*3201	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.613127	1.006851	-3.606276	41032.395376
HLA A*0219	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.405094	0.798809	-3.606285	25415.231550
HLA B*1502	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.593135	0.986777	-3.606359	39186.376147
HLA A*2601	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.392750	0.786321	-3.606429	24703.010136
HLA A*3301	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.613289	1.006851	-3.606438	41047.714904
HLA A*0201	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.229317	0.622672	-3.606646	16955.763499
HLA A*0206	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.467353	0.860662	-3.606691	29332.769793
HLA B*0801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.300650	0.693953	-3.606697	19982.511174
HLA A*2403	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.376163	0.769405	-3.606757	23777.298638
HLA B*3501	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.361086	0.754283	-3.606802	22966.026796
HLA A*2301	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.490138	0.883265	-3.606873	30912.802513
HLA A*2402	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.561755	0.954860	-3.606895	36454.855510
HLA A*0202	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.595943	0.989026	-3.606917	39440.529561
HLA A*0201	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.987377	0.380458	-3.606919	9713.523222
HLA B*5401	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.521405	0.914477	-3.606928	33220.435830

HLA A*0201	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.393471	0.786321	-3.607150	24744.071873
HLA A*0201	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.285670	0.678487	-3.607183	19304.997429
HLA A*2601	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.396598	0.789406	-3.607193	24922.886117
HLA A*2902	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.463371	0.856154	-3.607217	29065.024727
HLA A*0301	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.313819	0.706599	-3.607220	20597.709460
HLA B*2705	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.485721	0.878392	-3.607329	30599.994442
HLA A*0206	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.522411	0.915076	-3.607335	33297.444629
HLA A*0250	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.513297	0.905846	-3.607451	32605.979643
HLA A*6802	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.438097	0.830606	-3.607491	27421.883826
HLA A*6802	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.381677	0.774156	-3.607521	24081.123987
HLA B*1517	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.454109	0.846543	-3.607566	28451.752811
HLA B*5801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.360496	0.752921	-3.607575	22934.862801
HLA B*1517	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.463798	0.856154	-3.607645	29093.656239
HLA B*3501	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.377260	0.769461	-3.607799	23837.445985
HLA B*1501	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.273079	0.665274	-3.607805	18753.349953
HLA A*1101	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.505278	0.897326	-3.607952	32009.468336
HLA B*0803	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.495824	0.887847	-3.607977	31320.171619
HLA A*3301	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.476824	0.868794	-3.608030	29979.462897
HLA B*4001	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.397470	0.789406	-3.608064	24972.958298
HLA A*0216	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.468436	0.860349	-3.608087	29406.015813
HLA B*1517	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.453047	0.844865	-3.608182	28382.265589
HLA B*5401	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.476131	0.867880	-3.608250	29931.656312
HLA B*5101	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.505593	0.897326	-3.608267	32032.681218
HLA B*7301	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.615180	1.006851	-3.608329	41226.865907
HLA A*3101	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.134962	0.526478	-3.608484	13644.638458
HLA B*5801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.292314	0.683810	-3.608504	19602.618672
HLA B*0702	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.457271	0.848752	-3.608520	28659.686384
HLA A*8001	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.443384	0.834835	-3.608548	27757.709599
HLA B*5301	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.489210	0.880484	-3.608726	30846.815283
HLA B*1502	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.487194	0.878392	-3.608802	30703.965874
HLA B*1502	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.595038	0.986192	-3.608846	39358.468026
HLA B*0803	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.477663	0.868794	-3.608868	30037.419094
HLA A*2403	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.292704	0.683810	-3.608894	19620.230546
HLA A*3301	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.572504	0.963515	-3.608989	37368.380385
HLA B*4501	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.599657	0.990658	-3.608999	39779.312526
HLA A*2501	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.453867	0.844865	-3.609002	28435.903382
HLA B*3801	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.502548	0.893488	-3.609060	31808.878641
HLA B*2705	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.453989	0.844865	-3.609125	28443.903932
HLA B*2705	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.407993	0.798809	-3.609184	25585.466229
HLA B*0702	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.443788	0.834602	-3.609186	27783.550194
HLA A*2902	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.430243	0.821048	-3.609195	26930.409560
HLA A*1101	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.497060	0.887847	-3.609213	31409.423279
HLA B*5701	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.401039	0.791821	-3.609218	25179.022137
HLA A*2403	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.400224	0.790719	-3.609505	25131.799621
HLA A*0201	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.371435	0.761813	-3.609622	23519.893378
HLA B*5401	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.548474	0.938712	-3.609762	35356.864367
HLA A*0212	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.404204	0.794424	-3.609779	25363.174867
HLA B*4001	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.324042	0.714055	-3.609987	21088.298348
HLA A*0101	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.386188	0.776187	-3.610001	24332.557872
HLA A*2902	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.222701	0.612666	-3.610036	16699.412808
HLA A*0216	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.371851	0.761813	-3.610038	23542.425647
HLA B*5101	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.472174	0.862113	-3.610061	29660.209692
HLA B*3801	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.524511	0.914377	-3.610135	33458.875813
HLA A*1101	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.458972	0.848752	-3.610221	28772.159611
HLA A*3001	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.289055	0.678719	-3.610336	19456.080568
HLA B*3501	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.058796	0.448098	-3.610698	11449.761170
HLA B*0702	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.386446	0.775701	-3.610745	24347.042190
HLA A*0206	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.441398	0.830606	-3.610792	27631.108806
HLA A*3002	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.335984	0.725139	-3.610845	21676.240926
HLA B*1502	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.494917	0.883995	-3.610923	31254.836538
HLA A*0250	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.568722	0.957710	-3.611011	37044.318052
HLA B*5701	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.405444	0.794424	-3.611020	25435.726354
HLA B*3801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.538653	0.927578	-3.611075	34566.300028
HLA A*6801	1:242-250	9	PKFAHLPTV	1.053234	0.000789	-4.665126	1.054023	-3.611103	46251.484111
HLA B*7301	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.325169	0.714055	-3.611115	21143.130481

HLA A*3001	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.214342	0.603125	-3.611217	16381.049887
HLA A*2403	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.446071	0.834835	-3.611236	27930.032349
HLA B*5401	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.405832	0.794424	-3.611407	25458.441226
HLA B*7301	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.535112	0.923460	-3.611652	34285.636889
HLA B*5101	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.472019	0.860349	-3.611670	29649.621325
HLA B*4002	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.525829	0.914083	-3.611746	33560.576004
HLA A*6901	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.388020	0.776187	-3.611834	24435.451233
HLA B*0702	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.446689	0.834835	-3.611854	27969.799506
HLA A*3201	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.569565	0.957710	-3.611855	37116.333591
HLA A*0206	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.479751	0.867880	-3.611871	30182.228745
HLA A*0101	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.381437	0.769461	-3.611976	24067.839479
HLA A*2602	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.386190	0.774156	-3.612034	24332.689509
HLA B*4002	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.579614	0.967578	-3.612036	37985.147464
HLA A*0201	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.388323	0.776187	-3.612137	24452.510093
HLA A*3101	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.398483	0.786321	-3.612161	25031.254739
HLA A*2603	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.580105	0.967687	-3.612417	38028.120300
HLA A*0201	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.389860	0.777400	-3.612460	24539.177952
HLA A*0301	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.368311	0.755651	-3.612659	23351.271515
HLA A*3002	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.518609	0.905846	-3.612764	33007.257302
HLA A*0206	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.510137	0.897326	-3.612811	32369.589789
HLA B*5101	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.407286	0.794424	-3.612862	25543.837356
HLA A*2902	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.447700	0.834835	-3.612864	28034.940055
HLA B*7301	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.599058	0.986192	-3.612866	39724.473935
HLA B*4601	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.411760	0.798809	-3.612950	25808.309588
HLA B*0803	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.461738	0.848752	-3.612986	28955.949111
HLA A*6901	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.338195	0.725139	-3.613056	21786.869639
HLA A*0216	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.402498	0.789406	-3.613092	25263.754350
HLA A*6901	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.008052	0.394899	-3.613153	10187.139441
HLA B*1501	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.274131	0.660945	-3.613187	18798.856264
HLA B*1517	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.481128	0.867880	-3.613248	30278.064125
HLA B*4501	1:469-477	9	ELLGRDRSM	0.939519	0.080846	-4.633617	1.020365	-3.613252	43014.683281
HLA A*2403	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.390762	0.777400	-3.613362	24590.208564
HLA B*4402	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.367650	0.754283	-3.613367	23315.800374
HLA B*0802	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.459950	0.846543	-3.613407	28836.984673
HLA A*2501	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.473774	0.860349	-3.613425	29769.683428
HLA A*3001	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.286610	0.673165	-3.613444	19346.817820
HLA B*3901	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.458538	0.844865	-3.613673	28743.377991
HLA A*0206	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.448414	0.834602	-3.613812	28081.084428
HLA B*4402	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.448477	0.834602	-3.613875	28085.186447
HLA A*0202	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.236678	0.622672	-3.614007	17245.599132
HLA B*0803	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.497438	0.883265	-3.614173	31436.792558
HLA A*2301	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.541780	0.927578	-3.614202	34816.095083
HLA B*1801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.340345	0.726109	-3.614236	21894.983064
HLA A*3001	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.220441	0.606197	-3.614244	16612.729590
HLA A*2601	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.389968	0.775701	-3.614267	24545.285407
HLA A*0301	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.367258	0.752921	-3.614337	23294.745192
HLA B*1801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.458007	0.843615	-3.614392	28708.256807
HLA A*0203	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.224022	0.609548	-3.614474	16750.262258
HLA A*1101	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.406379	0.791821	-3.614558	25490.551931
HLA B*4801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.413404	0.798809	-3.614595	25906.228943
HLA A*2603	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.621493	1.006851	-3.614642	41830.531898
HLA A*0219	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.449516	0.834835	-3.614680	28152.423286
HLA B*0801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.275659	0.660945	-3.614714	18865.077450
HLA B*4402	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.406537	0.791821	-3.614716	25499.792977
HLA B*4001	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.384369	0.769461	-3.614908	24230.884282
HLA A*0212	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.370571	0.755651	-3.614919	23473.115631
HLA B*0702	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.293681	0.678719	-3.614962	19664.435871
HLA B*4002	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.631833	1.016861	-3.614973	42838.422558
HLA B*4601	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.403034	0.787998	-3.615036	25294.935273
HLA A*3301	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.322141	0.707098	-3.615043	20996.204970
HLA B*4002	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.605714	0.990658	-3.615056	40337.989225
HLA B*4002	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.634171	1.019055	-3.615116	43069.636655
HLA A*2603	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.615476	1.000328	-3.615148	41254.977616
HLA B*5801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.355832	0.740545	-3.615287	22689.891478
HLA B*0802	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.471465	0.856154	-3.615311	29611.790805

HLA A*2602	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.562923	0.947523	-3.615400	36553.004111
HLA B*0801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.407225	0.791821	-3.615404	25540.244687
HLA A*0201	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.288571	0.673165	-3.615406	19434.410066
HLA B*4501	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.500030	0.884477	-3.615553	31624.940076
HLA B*1517	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.458970	0.843357	-3.615613	28772.003957
HLA A*3301	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.646642	1.031013	-3.615630	44324.339673
HLA B*3901	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.294379	0.678719	-3.615660	19696.056846
HLA B*4001	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.414558	0.798809	-3.615748	25975.133982
HLA A*0203	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.319079	0.703210	-3.615870	20848.721348
HLA A*0206	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.410336	0.794424	-3.615911	25723.838352
HLA A*0202	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.521906	0.905846	-3.616060	33258.738014
HLA B*2705	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.265908	0.649772	-3.616136	18446.255924
HLA A*3002	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.555010	0.938712	-3.616298	35893.020732
HLA A*0211	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.543979	0.927578	-3.616402	34992.838928
HLA B*5801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.353840	0.737370	-3.616470	22586.038051
HLA A*3002	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.497201	0.880484	-3.616717	31419.620224
HLA B*7301	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.584407	0.967687	-3.616719	38406.679930
HLA B*5101	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.385344	0.768573	-3.616771	24285.346251
HLA A*1101	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.495298	0.878392	-3.616906	31282.240347
HLA A*3201	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.617241	1.000328	-3.616913	41422.930393
HLA A*0250	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.479432	0.862113	-3.617318	30160.030490
HLA A*2403	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.438367	0.821048	-3.617319	27438.949310
HLA A*3002	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.463881	0.846543	-3.617338	29099.165531
HLA B*4001	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.391559	0.774156	-3.617403	24635.347215
HLA B*4801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.409307	0.791821	-3.617486	25662.957067
HLA B*4601	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.406906	0.789406	-3.617500	25521.460492
HLA B*1801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.416313	0.798809	-3.617503	26080.316749
HLA B*1801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.486316	0.868794	-3.617521	30641.905389
HLA A*0216	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.290796	0.673165	-3.617631	19534.231237
HLA A*6802	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.407199	0.789406	-3.617794	25538.724863
HLA B*4501	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.511387	0.893488	-3.617899	32462.885635
HLA B*0801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.408639	0.790719	-3.617921	25623.558555
HLA B*1503	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-3.886805	0.268538	-3.618267	7705.569249
HLA B*1502	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.570643	0.952354	-3.618289	37208.613135
HLA A*0201	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.279455	0.660945	-3.618511	19030.726169
HLA A*3201	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.503307	0.884477	-3.618830	31864.509881
HLA A*2601	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.396415	0.777400	-3.619015	24912.371591
HLA B*0801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.296365	0.677348	-3.619016	19786.300651
HLA A*6901	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.284455	0.665274	-3.619181	19251.078475
HLA A*6901	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.372138	0.752921	-3.619217	23557.968929
HLA A*1101	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.409643	0.790220	-3.619423	25682.817975
HLA A*0206	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-3.999984	0.380458	-3.619526	9999.634340
HLA B*0702	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.389000	0.769461	-3.619539	24490.637974
HLA B*4801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.407695	0.787998	-3.619697	25567.893620
HLA B*7301	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-3.978566	0.358727	-3.619839	9518.449585
HLA A*0212	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.418768	0.798809	-3.619959	26228.175047
HLA A*2402	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.492819	0.872828	-3.619991	31104.207593
HLA B*5101	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.454936	0.834835	-3.620101	28505.984563
HLA A*2603	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.572516	0.952354	-3.620162	37369.391192
HLA B*1501	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.396436	0.776187	-3.620250	24913.584579
HLA B*1801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.411043	0.790719	-3.620324	25765.760572
HLA A*6901	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.376036	0.755651	-3.620384	23770.353495
HLA B*0802	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.488285	0.867880	-3.620404	30781.135433
HLA A*3001	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.146042	0.525631	-3.620411	13997.233385
HLA B*5401	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.410667	0.790220	-3.620448	25743.467837
HLA A*2902	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.299205	0.678719	-3.620486	19916.138200
HLA A*2403	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.343018	0.722436	-3.620582	22030.194301
HLA B*0801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.294046	0.673165	-3.620880	19680.932061
HLA B*1509	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.389543	0.768573	-3.620970	24521.262674
HLA B*0801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.390609	0.769461	-3.621149	24581.563115
HLA B*1502	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.535599	0.914377	-3.621222	34324.053064
HLA A*3201	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.467811	0.846543	-3.621268	29363.730092
HLA B*3501	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.456181	0.834835	-3.621346	28587.835385
HLA B*2705	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.464740	0.843357	-3.621384	29156.839523
HLA A*3001	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.215418	0.594015	-3.621403	16421.688018

HLA A*3101	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.389987	0.768573	-3.621414	24546.347728
HLA A*3201	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.301360	0.679867	-3.621493	20015.185015
HLA B*1501	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.328130	0.706599	-3.621531	21287.744108
HLA B*1509	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.483654	0.862113	-3.621540	30454.663188
HLA B*0803	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.464905	0.843357	-3.621548	29167.883083
HLA A*2403	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.347663	0.726109	-3.621554	22267.079485
HLA A*3201	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.610599	0.989026	-3.621573	40794.237966
HLA B*3901	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.420615	0.798809	-3.621805	26339.939233
HLA A*6802	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.412551	0.790719	-3.621833	25855.404477
HLA A*2301	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.470628	0.848752	-3.621876	29554.815731
HLA A*0211	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.383756	0.761813	-3.621943	24196.694875
HLA A*3002	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.147710	0.525631	-3.622079	14051.100442
HLA A*0250	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.542802	0.920689	-3.622113	34898.124344
HLA A*6801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.305997	0.683810	-3.622187	20230.074977
HLA B*1509	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.396455	0.774156	-3.622299	24914.662841
HLA A*1101	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.456957	0.834602	-3.622355	28638.917785
HLA B*5301	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.484523	0.862113	-3.622410	30515.684089
HLA B*5701	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.306324	0.683810	-3.622514	20245.293200
HLA B*1503	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.330510	0.707963	-3.622546	21404.725830
HLA A*6801	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.577570	0.955018	-3.622551	37806.786501
HLA B*2705	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.396728	0.774156	-3.622572	24930.302873
HLA B*4002	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.629458	1.006851	-3.622607	42604.761753
HLA A*2501	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.478910	0.856154	-3.622757	30123.830175
HLA B*4601	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.377065	0.754283	-3.622781	23826.744879
HLA B*5801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.348911	0.726109	-3.622802	22331.136999
HLA A*1101	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.302680	0.679867	-3.622813	20076.130939
HLA A*2601	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.392296	0.769405	-3.622891	24677.230971
HLA A*3101	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.348225	0.725139	-3.623086	22295.888627
HLA A*3201	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.506378	0.883265	-3.623113	32090.613488
HLA A*2902	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.411132	0.787998	-3.623135	25771.057933
HLA A*0203	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.417685	0.794424	-3.623261	26162.844556
HLA B*0801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.377577	0.754283	-3.623293	23854.861666
HLA B*5801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.348471	0.725139	-3.623333	22308.557144
HLA A*2301	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.511199	0.887847	-3.623352	32448.839026
HLA B*5301	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.302133	0.678719	-3.623413	20050.840834
HLA A*2501	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.415256	0.791821	-3.623435	26016.902740
HLA B*0801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.259358	0.635887	-3.623471	18170.122932
HLA B*1502	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.307318	0.683810	-3.623508	20291.675237
HLA A*6802	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.422353	0.798809	-3.623544	26445.597737
HLA A*0101	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.349656	0.726109	-3.623547	22369.466301
HLA B*5101	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.484227	0.860662	-3.623565	30494.890282
HLA B*7301	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.578458	0.954860	-3.623598	37884.178142
HLA A*0202	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.538218	0.914477	-3.623741	34531.722362
HLA B*4601	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.393192	0.769405	-3.623786	24728.147340
HLA B*4601	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.410113	0.786321	-3.623791	25710.621253
HLA B*4403	1:284-292	9	LALLGWSIA	1.221511	-0.221183	-4.624360	1.000328	-3.624032	42107.529212
HLA B*4801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.398238	0.774156	-3.624083	25017.175403
HLA A*3002	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.454783	0.830606	-3.624178	28495.962401
HLA B*3801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.508840	0.884477	-3.624363	32273.070005
HLA A*3201	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.592200	0.967687	-3.624513	39102.093324
HLA B*4001	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.410949	0.786321	-3.624628	25760.185579
HLA A*0202	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.527032	0.902312	-3.624720	33653.663070
HLA A*0301	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.365395	0.740545	-3.624850	23195.023812
HLA A*2301	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.497697	0.872828	-3.624869	31455.505777
HLA B*7301	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.485251	0.860349	-3.624902	30566.903831
HLA A*3201	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.589959	0.965021	-3.624937	38900.805953
HLA A*6802	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.386761	0.761813	-3.624948	24364.698372
HLA B*3801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.527310	0.902312	-3.624998	33675.153314
HLA A*2402	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.485728	0.860662	-3.625066	30600.491074
HLA A*0203	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.319115	0.693953	-3.625162	20850.413256
HLA B*4601	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.401351	0.776187	-3.625165	25197.145347
HLA B*5801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.347644	0.722436	-3.625208	22266.115806
HLA B*0803	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.468951	0.843615	-3.625336	29440.875699
HLA A*0250	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.379630	0.754283	-3.625347	23967.920325
HLA A*3301	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.513222	0.887847	-3.625375	32600.335500

HLA A*0202	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.020331	0.394899	-3.625432	10479.261054
HLA B*0801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.424268	0.798809	-3.625459	26562.455381
HLA B*1501	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.381120	0.755651	-3.625468	24050.268310
HLA B*4501	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.632381	1.006851	-3.625530	42892.454615
HLA B*0802	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.416249	0.790719	-3.625531	26076.507554
HLA B*0801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.401812	0.776187	-3.625625	25223.877015
HLA A*3001	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.286642	0.660945	-3.625698	19348.283173
HLA B*3501	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.415166	0.789406	-3.625761	26011.554844
HLA A*8001	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.416538	0.790719	-3.625820	26093.865063
HLA B*2705	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.494715	0.868794	-3.625921	31240.298593
HLA A*8001	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.395417	0.769461	-3.625956	24855.158792
HLA A*0203	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.416776	0.790719	-3.626057	26108.126616
HLA A*0211	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.470967	0.844865	-3.626102	29577.848613
HLA B*3901	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.401932	0.775701	-3.626231	25230.837352
HLA A*0301	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.333465	0.707098	-3.626367	21550.895525
HLA B*0803	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.447481	0.821048	-3.626433	28020.838672
HLA B*1503	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.306350	0.679867	-3.626483	20246.498009
HLA A*6901	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.306392	0.679867	-3.626525	20248.469668
HLA B*0801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.402432	0.775701	-3.626731	25259.927764
HLA A*8001	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.418599	0.791821	-3.626778	26217.960847
HLA B*0803	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.352919	0.726109	-3.626810	22538.191121
HLA A*6801	1:95-103	9	RDVLARLLA	1.274825	-0.247610	-4.654031	1.027215	-3.626817	45084.930517
HLA A*3301	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.400975	0.774156	-3.626820	25175.344582
HLA A*2301	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.529243	0.902312	-3.626931	33825.420777
HLA B*1501	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.413287	0.786321	-3.626966	25899.222400
HLA A*3002	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.554547	0.927578	-3.626970	35854.788188
HLA B*3901	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.483193	0.856154	-3.627040	30422.388057
HLA A*2601	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.389000	0.761813	-3.627187	24490.637974
HLA B*5701	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.396697	0.769461	-3.627236	24928.549622
HLA B*4403	1:438-446	9	EGLALKPRK	1.007012	0.009849	-4.644119	1.016861	-3.627258	44067.552185
HLA B*4601	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.364810	0.737370	-3.627440	23163.799703
HLA B*1502	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.553161	0.925719	-3.627442	35740.528081
HLA B*3801	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.533651	0.905846	-3.627805	34170.461288
HLA A*1101	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.458484	0.830606	-3.627878	28739.801748
HLA B*1502	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.591434	0.963515	-3.627919	39033.192714
HLA A*3002	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.476690	0.848752	-3.627938	29970.219745
HLA A*0250	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.496851	0.868794	-3.628057	31394.303906
HLA B*1501	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.405458	0.777400	-3.628058	25436.551994
HLA A*8001	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.397493	0.769405	-3.628088	24974.309344
HLA A*2402	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.499689	0.871584	-3.628105	31600.142127
HLA B*0801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.323856	0.695627	-3.628228	21079.287531
HLA A*3101	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.381158	0.752921	-3.628236	24052.350149
HLA A*2902	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.231582	0.603125	-3.628457	17044.421042
HLA B*5701	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.416553	0.787998	-3.628555	26094.712066
HLA A*3101	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.264607	0.635887	-3.628720	18391.053810
HLA B*5301	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.576475	0.947523	-3.628952	37711.595316
HLA B*4402	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.459604	0.830606	-3.628999	28814.061071
HLA A*2601	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.405242	0.776187	-3.629055	25423.895122
HLA B*5301	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.343115	0.714055	-3.629060	22035.081260
HLA A*1101	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.485336	0.856154	-3.629182	30572.857499
HLA A*6802	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.238931	0.609548	-3.629384	17335.303238
HLA A*1101	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.417509	0.787998	-3.629511	26152.231353
HLA B*1801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.489906	0.860349	-3.629556	30896.250697
HLA B*4601	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.399086	0.769461	-3.629626	25066.080936
HLA A*0301	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.367072	0.737370	-3.629703	23284.791582
HLA B*4001	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.391697	0.761813	-3.629884	24643.211666
HLA A*0206	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.490322	0.860349	-3.629972	30925.849583
HLA A*0216	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.464994	0.834835	-3.630159	29173.879910
HLA B*5301	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.585074	0.954860	-3.630214	38465.733633
HLA A*8001	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.384607	0.754283	-3.630323	24244.127626
HLA A*2402	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.582696	0.952354	-3.630342	38255.716561
HLA A*2603	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.420678	0.790220	-3.630459	26343.786911
HLA A*2902	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.429402	0.798809	-3.630592	26878.302825
HLA B*7301	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.585697	0.955018	-3.630678	38520.918450
HLA B*1801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.465380	0.834602	-3.630778	29199.775098

HLA A*3101	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.371325	0.740545	-3.630780	23513.913858
HLA B*0802	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.475696	0.844865	-3.630832	29901.714813
HLA A*0203	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.407058	0.776187	-3.630872	25530.436508
HLA A*0250	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.465483	0.834602	-3.630881	29206.726498
HLA A*2402	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.514152	0.883265	-3.630888	32670.250587
HLA B*4402	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.408463	0.777400	-3.631063	25613.164118
HLA B*3901	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.384280	0.752921	-3.631359	24225.903511
HLA A*2603	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.504191	0.872828	-3.631363	31929.392031
HLA A*0250	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.475038	0.843615	-3.631423	29856.454911
HLA B*4501	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.596514	0.965021	-3.631492	39492.412297
HLA A*6901	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.308937	0.677348	-3.631588	20367.451841
HLA B*3801	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.519467	0.887847	-3.631620	33072.498139
HLA B*4001	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.401088	0.769405	-3.631683	25181.882830
HLA A*0203	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.208867	0.577123	-3.631744	16175.861988
HLA A*0216	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.271841	0.639976	-3.631865	18699.960079
HLA B*0702	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.430722	0.798809	-3.631913	26960.146834
HLA A*2602	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.586904	0.954860	-3.632044	38628.181978
HLA A*2402	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.422295	0.790220	-3.632075	26442.021285
HLA B*1801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.499990	0.867880	-3.632110	31622.031723
HLA B*5701	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.421533	0.789406	-3.632128	26395.714197
HLA B*1509	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.426606	0.794424	-3.632182	26705.822335
HLA A*2603	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.587062	0.954860	-3.632202	38642.185786
HLA B*4402	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.426688	0.794424	-3.632264	26710.879458
HLA A*0206	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.272275	0.639976	-3.632299	18718.684919
HLA A*0211	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.466907	0.834602	-3.632305	29302.634747
HLA B*3901	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.475926	0.843615	-3.632311	29917.571982
HLA A*0101	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.354848	0.722436	-3.632412	22638.517561
HLA B*4801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.408625	0.776187	-3.632439	25622.726844
HLA B*5401	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.560108	0.927578	-3.632531	36316.868397
HLA B*4402	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.420580	0.787998	-3.632582	26337.801878
HLA A*0206	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-3.901024	0.268381	-3.632643	7962.030025
HLA A*2601	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.402214	0.769461	-3.632753	25247.222194
HLA B*0803	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.500669	0.867880	-3.632789	31671.510109
HLA A*2501	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.463460	0.830606	-3.632854	29071.000407
HLA A*3101	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.394688	0.761813	-3.632875	24813.509993
HLA B*0802	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.359039	0.726109	-3.632931	22858.065127
HLA A*3201	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.504616	0.871584	-3.633032	31960.672283
HLA B*3901	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.501907	0.868794	-3.633113	31761.934791
HLA A*0250	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.548220	0.915076	-3.633144	35336.212515
HLA A*3301	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.619938	0.986777	-3.633161	41680.990204
HLA B*4001	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.401744	0.768573	-3.633171	25219.920032
HLA A*0201	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.388824	0.755651	-3.633172	24480.703117
HLA A*0212	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.422579	0.789406	-3.633173	26459.335808
HLA A*0301	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.347323	0.714055	-3.633268	22249.619281
HLA B*4601	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.317106	0.683810	-3.633296	20754.193305
HLA A*0212	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.311798	0.678487	-3.633311	20502.101102
HLA B*4402	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.325736	0.692320	-3.633415	21170.714519
HLA A*1101	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.422823	0.789406	-3.633418	26474.226772
HLA A*3001	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.288933	0.655319	-3.633614	19450.608065
HLA A*2902	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.256372	0.622672	-3.633700	18045.614277
HLA A*2301	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.514399	0.880484	-3.633915	32688.813814
HLA B*0802	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.428366	0.794424	-3.633941	26814.254048
HLA A*0216	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.410282	0.776187	-3.634095	25720.637799
HLA A*0219	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.428542	0.794424	-3.634118	26825.135916
HLA A*0212	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.109334	0.475212	-3.634122	12862.750636
HLA A*0219	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.256820	0.622672	-3.634149	18064.270246
HLA B*4403	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.581695	0.947523	-3.634172	38167.653462
HLA A*0212	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.411590	0.777400	-3.634190	25798.258899
HLA B*4001	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.411722	0.777400	-3.634322	25806.075763
HLA B*0801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.387247	0.752921	-3.634326	24391.998391
HLA A*8001	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.402923	0.768573	-3.634350	25288.504479
HLA A*3002	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.507191	0.872828	-3.634363	32150.737646
HLA A*2301	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.527937	0.893488	-3.634449	33723.830213
HLA A*2601	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.390137	0.755651	-3.634486	24554.847953
HLA A*0216	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.422504	0.787998	-3.634506	26454.755658

HLA A*0206	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-3.813064	0.178488	-3.634575	6502.251919
HLA A*2403	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.433436	0.798809	-3.634626	27129.132605
HLA A*0301	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.257387	0.622672	-3.634715	18087.837499
HLA A*0212	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.016304	0.381582	-3.634722	10382.540697
HLA B*4801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.403363	0.768573	-3.634790	25314.100521
HLA B*5101	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.519375	0.884477	-3.634898	33065.521051
HLA B*1517	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.503744	0.868794	-3.634950	31896.589343
HLA B*5701	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.412363	0.777400	-3.634963	25844.216908
HLA B*4403	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.621244	0.986192	-3.635052	41806.551129
HLA B*5801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.349150	0.714055	-3.635096	22343.462915
HLA B*4501	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.592809	0.957710	-3.635098	39156.920065
HLA A*6901	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.313969	0.678719	-3.635250	20604.842299
HLA B*4601	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.412690	0.777400	-3.635290	25863.658411
HLA A*0203	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.290679	0.655319	-3.635360	19528.948051
HLA A*0212	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.397202	0.761813	-3.635389	24957.561540
HLA A*0216	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.427252	0.791821	-3.635431	26745.582677
HLA B*7301	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.530897	0.895455	-3.635443	33954.492621
HLA A*0219	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.397296	0.761813	-3.635483	24962.962830
HLA A*3002	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.533078	0.897326	-3.635751	34125.385593
HLA A*0211	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.434651	0.798809	-3.635841	27205.116631
HLA B*4001	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.390175	0.754283	-3.635891	24556.973469
HLA B*1801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.466545	0.830606	-3.635939	29278.232216
HLA B*4402	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.426249	0.790220	-3.636029	26683.871080
HLA B*1801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.498221	0.862113	-3.636107	31493.476765
HLA B*4801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.389111	0.752921	-3.636189	24496.865873
HLA A*2402	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.529732	0.893488	-3.636244	33863.504489
HLA B*5701	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.398248	0.761813	-3.636434	25017.716770
HLA A*6802	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.358910	0.722436	-3.636474	22851.264861
HLA A*0211	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.514911	0.878392	-3.636519	32727.388300
HLA B*4002	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.604293	0.967687	-3.636605	40206.179498
HLA B*5301	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.575495	0.938712	-3.636783	37626.616720
HLA B*4403	1:16-24	9	TGTPHVGLV	1.075466	-0.068615	-4.643642	1.006851	-3.636791	44019.183433
HLA B*5401	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-3.889850	0.252948	-3.636902	7759.784497
HLA B*0702	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.458059	0.821048	-3.637010	28711.673797
HLA B*1501	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.362326	0.725139	-3.637188	23031.721228
HLA B*5701	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.423530	0.786321	-3.637209	26517.371903
HLA B*1501	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.374605	0.737370	-3.637235	23692.168020
HLA A*0250	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.482108	0.844865	-3.637243	30346.446233
HLA A*0212	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.467872	0.830606	-3.637266	29367.860600
HLA B*5301	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.429108	0.791821	-3.637287	26860.132889
HLA A*8001	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.345370	0.707963	-3.637407	22149.817997
HLA A*0250	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.551895	0.914477	-3.637418	35636.462992
HLA A*2402	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.563182	0.925719	-3.637462	36574.762832
HLA A*0250	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.525421	0.887847	-3.637574	33528.999603
HLA B*5701	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.391949	0.754283	-3.637665	24657.480719
HLA B*1509	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.425685	0.787998	-3.637687	26649.247933
HLA A*0212	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.424071	0.786321	-3.637750	26550.387329
HLA B*5401	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.498244	0.860349	-3.637895	31495.180573
HLA B*5301	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.459149	0.821048	-3.638101	28783.836044
HLA B*5701	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.407613	0.769405	-3.638207	25563.052897
HLA A*3101	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.415624	0.777400	-3.638224	26039.009651
HLA A*0219	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.407725	0.769461	-3.638265	25569.691837
HLA A*3101	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.437146	0.798809	-3.638336	27361.868110
HLA B*4801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.364537	0.726109	-3.638428	23149.267887
HLA B*4601	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.251116	0.612666	-3.638450	17828.543795
HLA B*5101	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.507306	0.868794	-3.638512	32159.261440
HLA B*3901	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.429266	0.790719	-3.638547	26869.870447
HLA A*0101	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.376022	0.737370	-3.638652	23769.581937
HLA B*0702	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.416120	0.777400	-3.638720	26068.749802
HLA A*2403	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.425069	0.786321	-3.638748	26611.502287
HLA A*3301	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.591183	0.952354	-3.638829	39010.604571
HLA A*6901	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.261519	0.622672	-3.638848	18260.782839
HLA A*0206	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.305267	0.666384	-3.638883	20196.066988
HLA B*0702	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.408409	0.769405	-3.639004	25609.977335
HLA B*4501	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.541463	0.902312	-3.639151	34790.676952

HLA A*2601	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.346449	0.707098	-3.639350	22204.887421
HLA A*3201	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.495505	0.856154	-3.639351	31297.136437
HLA B*4403	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.628406	0.989026	-3.639380	42501.628589
HLA A*2403	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.319289	0.679867	-3.639422	20858.762010
HLA A*0250	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.562925	0.923460	-3.639465	36553.201860
HLA A*3101	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.289342	0.649772	-3.639570	19468.925945
HLA B*1501	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.262093	0.622434	-3.639659	18284.903225
HLA A*3001	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.276993	0.637330	-3.639663	18923.135537
HLA B*4601	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.401589	0.761813	-3.639775	25210.916799
HLA B*0803	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.165566	0.525631	-3.639935	14640.854488
HLA B*3801	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.500603	0.860662	-3.639941	31666.712970
HLA A*0101	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.365129	0.725139	-3.639991	23180.848622
HLA B*1501	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.343375	0.703210	-3.640166	22048.317249
HLA B*4001	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.416616	0.776187	-3.640429	26098.523921
HLA A*0206	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.320327	0.679867	-3.640460	20908.698557
HLA B*1517	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.431312	0.790719	-3.640593	26996.780403
HLA A*0219	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.430125	0.789406	-3.640720	26923.126018
HLA B*1501	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.319218	0.678487	-3.640731	20855.376977
HLA B*4801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.410211	0.769461	-3.640750	25716.463764
HLA A*0101	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.393802	0.752921	-3.640881	24762.953712
HLA B*4001	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.378263	0.737370	-3.640893	23892.574675
HLA B*4001	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.367075	0.726109	-3.640966	23284.917550
HLA A*2301	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.485841	0.844865	-3.640977	30608.438278
HLA A*0203	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.166760	0.525631	-3.641129	14681.146171
HLA B*1502	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.588723	0.947523	-3.641200	38790.267104
HLA A*3201	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.529105	0.887847	-3.641258	33814.625985
HLA B*5801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.357754	0.716494	-3.641261	22790.523311
HLA B*4002	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.630426	0.989026	-3.641400	42699.828319
HLA A*0101	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.397132	0.755651	-3.641480	24953.511339
HLA A*6802	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.427931	0.786321	-3.641610	26787.430977
HLA A*2501	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.431079	0.789406	-3.641674	26982.325365
HLA B*1517	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.403588	0.761813	-3.641775	25327.250798
HLA B*7301	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.513473	0.871584	-3.641889	32619.211932
HLA A*2602	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.219031	0.577123	-3.641908	16558.893197
HLA A*2602	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.557019	0.915076	-3.641942	36059.426847
HLA B*7301	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.599681	0.957710	-3.641970	39781.464601
HLA B*0803	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.504195	0.862113	-3.642082	31929.737502
HLA A*8001	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.440950	0.798809	-3.642140	27602.572636
HLA B*4402	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.428478	0.786321	-3.642157	26821.217935
HLA B*4601	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.410742	0.768573	-3.642169	25747.924840
HLA B*1509	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.315363	0.673165	-3.642197	20671.050100
HLA A*6801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.526243	0.883995	-3.642248	33592.545605
HLA A*2603	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.597411	0.955018	-3.642393	39574.110823
HLA B*1517	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.430391	0.787998	-3.642393	26939.589627
HLA B*1509	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.477395	0.834835	-3.642559	30018.899907
HLA A*6801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.463777	0.821048	-3.642729	29092.239732
HLA A*0212	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.433565	0.790719	-3.642847	27137.205914
HLA B*1801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.434669	0.791821	-3.642849	27206.294070
HLA B*5801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.346103	0.703210	-3.642894	22187.235922
HLA A*0101	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.336893	0.693953	-3.642940	21721.670431
HLA B*0802	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.477550	0.834602	-3.642948	30029.620150
HLA A*2603	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.523550	0.880484	-3.643066	33384.925054
HLA A*6901	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.326915	0.683810	-3.643105	21228.287333
HLA B*4002	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.629604	0.986192	-3.643411	42619.054346
HLA B*5101	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.478050	0.834602	-3.643448	30064.243417
HLA A*2403	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.058801	0.415126	-3.643675	11449.885055
HLA A*6901	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.322272	0.678487	-3.643785	21002.566814
HLA A*2602	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.369039	0.725139	-3.643900	23390.465986
HLA A*2403	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.431904	0.787998	-3.643907	27033.609999
HLA B*3801	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.558050	0.914083	-3.643967	36145.167645
HLA A*0101	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.347269	0.703210	-3.644059	22246.850990
HLA B*5801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.351242	0.707098	-3.644143	22451.301653
HLA A*3002	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.500321	0.856154	-3.644167	31646.162033
HLA B*3801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.492953	0.848752	-3.644201	31113.800480
HLA B*4403	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.631025	0.986777	-3.644249	42758.774309

HLA B*4801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.433791	0.789406	-3.644385	27151.303265
HLA A*2601	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.381775	0.737370	-3.644406	24086.596210
HLA B*5801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.352383	0.707963	-3.644420	22510.408421
HLA A*2902	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.435304	0.790719	-3.644585	27246.062526
HLA A*2403	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.385234	0.740545	-3.644689	24279.172127
HLA B*4601	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.397613	0.752921	-3.644692	24981.200815
HLA B*4403	1:422-430	9	DWTAPLIEA	1.292489	-0.273434	-4.663855	1.019055	-3.644799	46116.315478
HLA B*4801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.431166	0.786321	-3.644845	26987.726847
HLA B*1501	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.413439	0.768573	-3.644867	25908.331276
HLA A*0212	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.436866	0.791821	-3.645045	27344.258843
HLA A*2501	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.479664	0.834602	-3.645063	30176.187896
HLA B*0801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.352202	0.707098	-3.645104	22501.033405
HLA A*2601	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.399530	0.754283	-3.645247	25091.723335
HLA B*0802	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.480407	0.834835	-3.645571	30227.818963
HLA B*1509	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.529572	0.883995	-3.645578	33851.049330
HLA A*3001	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.110593	0.464975	-3.645618	12900.102890
HLA B*3501	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.444429	0.798809	-3.645620	27824.614028
HLA A*0216	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-3.825845	0.180214	-3.645631	6696.455542
HLA B*3501	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.281612	0.635887	-3.645725	19125.473125
HLA B*2705	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.480571	0.834835	-3.645736	30239.268171
HLA A*3001	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.295768	0.650029	-3.645739	19759.130732
HLA B*4001	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.368210	0.722436	-3.645773	23345.840051
HLA B*2705	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.433781	0.787998	-3.645784	27150.715729
HLA B*0801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.324530	0.678719	-3.645811	21112.041459
HLA A*0206	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.530352	0.884477	-3.645875	33911.903263
HLA A*2603	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.610914	0.965021	-3.645892	40823.821457
HLA B*5301	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.603616	0.957710	-3.645906	40143.585113
HLA B*0803	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.476563	0.830606	-3.645957	29961.465703
HLA A*3201	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.543352	0.897326	-3.646026	34942.330345
HLA A*0216	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.268810	0.622672	-3.646138	18569.911917
HLA B*1509	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.467243	0.821048	-3.646194	29325.312450
HLA B*5301	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.561290	0.915076	-3.646214	36415.827505
HLA A*3301	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.340206	0.693953	-3.646253	21887.995663
HLA A*0211	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.435663	0.789406	-3.646258	27268.623783
HLA A*0201	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.399225	0.752921	-3.646304	25074.082891
HLA B*3801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.543688	0.897326	-3.646361	34969.372685
HLA A*2902	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.400663	0.754283	-3.646380	25157.237052
HLA A*0250	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.539870	0.893488	-3.646382	34663.301803
HLA B*0702	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.438271	0.791821	-3.646450	27432.863876
HLA B*5801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.342116	0.695627	-3.646489	21984.476335
HLA A*3101	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.353615	0.707098	-3.646516	22574.311052
HLA B*4501	1:222-230	9	TPRQLALHQ	1.133197	-0.144171	-4.635604	0.989026	-3.646578	43212.002628
HLA A*8001	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.434613	0.787998	-3.646615	27202.761906
HLA A*6801	1:120-128	9	RHVAAGRNP	0.777242	0.253771	-4.677651	1.031013	-3.646638	47604.803564
HLA A*2602	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.360710	0.714055	-3.646655	22946.156411
HLA B*4402	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.422440	0.775701	-3.646740	26450.891773
HLA A*3301	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.602195	0.954860	-3.647335	40012.410627
HLA A*0101	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.387912	0.740545	-3.647367	24429.371108
HLA B*0702	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.436857	0.789406	-3.647451	27343.667132
HLA B*3501	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.042359	0.394899	-3.647461	11024.513428
HLA B*0702	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.400496	0.752921	-3.647575	25147.575960
HLA A*0212	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.423956	0.776187	-3.647769	26543.350164
HLA A*0250	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.575352	0.927578	-3.647774	37614.201863
HLA B*4403	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.602636	0.954860	-3.647776	40053.126317
HLA A*2403	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.424240	0.776187	-3.648053	26560.731038
HLA B*4402	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.438819	0.790719	-3.648100	27467.464918
HLA A*0202	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.582323	0.934152	-3.648170	38222.824199
HLA A*2301	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.532269	0.883995	-3.648275	34061.937244
HLA B*0702	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.442726	0.794424	-3.648301	27715.694911
HLA B*5101	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.494858	0.846543	-3.648316	31250.609694
HLA A*2301	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.543993	0.895455	-3.648539	34993.974791
HLA A*2403	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.417185	0.768573	-3.648612	26132.714307
HLA B*5701	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.424874	0.776187	-3.648688	26599.555851
HLA A*2301	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.516807	0.867880	-3.648927	32870.581242
HLA A*0206	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.097055	0.448098	-3.648957	12504.186473

HLA A*2403	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.441076	0.791821	-3.649256	27610.637464
HLA B*2705	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.418801	0.769461	-3.649340	26230.161604
HLA A*2602	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.588100	0.938712	-3.649388	38734.696420
HLA B*7301	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.070469	0.421060	-3.649409	11761.661312
HLA A*2501	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.443882	0.794424	-3.649457	27789.563081
HLA B*5701	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.271902	0.622434	-3.649468	18702.590546
HLA B*1501	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.175143	0.525631	-3.649512	14967.281443
HLA B*1501	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.356805	0.707098	-3.649707	22740.766846
HLA B*1502	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.522557	0.872828	-3.649728	33308.614902
HLA B*4501	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.575516	0.925719	-3.649797	37628.448767
HLA A*2402	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.570601	0.920689	-3.649912	37204.990011
HLA A*8001	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.372361	0.722436	-3.649925	23570.079411
HLA B*0803	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.425704	0.775701	-3.650003	26650.401314
HLA B*5801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.272440	0.622434	-3.650006	18725.774882
HLA A*2601	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.315346	0.665274	-3.650072	20670.267318
HLA A*0250	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.584231	0.934152	-3.650078	38391.099899
HLA B*4403	1:417-425	9	LTSVTDWTA	1.141259	-0.173681	-4.617690	0.967578	-3.650111	41465.754365
HLA A*3201	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.602524	0.952354	-3.650170	40042.726885
HLA B*4501	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.510591	0.860349	-3.650241	32403.404806
HLA A*0203	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.357451	0.707098	-3.650353	22774.623907
HLA A*2402	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.589179	0.938712	-3.650466	38830.999577
HLA A*3301	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.522160	0.871584	-3.650575	33278.175710
HLA A*2301	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.373195	0.722436	-3.650759	23615.389495
HLA B*5801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.344769	0.693953	-3.650816	22119.163246
HLA B*1503	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.316124	0.665274	-3.650850	20707.314174
HLA B*0801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.306209	0.655319	-3.650890	20239.927197
HLA B*3901	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.485552	0.834602	-3.650950	30588.077697
HLA B*5401	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.523816	0.872828	-3.650988	33405.340081
HLA A*2601	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.403971	0.752921	-3.651050	25349.594519
HLA A*0211	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.445620	0.794424	-3.651196	27901.036522
HLA A*6802	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.354432	0.703210	-3.651223	22616.850415
HLA A*3001	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.263953	0.612666	-3.651288	18363.415388
HLA B*3801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.507456	0.856154	-3.651303	32170.397962
HLA B*4801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.406995	0.755651	-3.651343	25526.707626
HLA A*1101	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.520202	0.868794	-3.651408	33128.547085
HLA A*1101	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.347092	0.695627	-3.651465	22237.826346
HLA A*0206	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.442225	0.790719	-3.651507	27683.776332
HLA A*2602	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.539424	0.887847	-3.651577	34627.690430
HLA A*2601	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.392146	0.740545	-3.651601	24668.688381
HLA B*5801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.358208	0.706599	-3.651609	22814.331520
HLA A*0301	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.368127	0.716494	-3.651634	23341.420026
HLA B*0801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.245672	0.594015	-3.651657	17606.462881
HLA B*1502	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.482343	0.830606	-3.651737	30362.867765
HLA A*6802	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.427983	0.776187	-3.651796	26790.619341
HLA B*1501	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.404737	0.752921	-3.651816	25394.341116
HLA A*1101	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.335693	0.683810	-3.651882	21661.704811
HLA A*3101	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.407634	0.755651	-3.651982	25564.297567
HLA B*1502	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.557872	0.905846	-3.652026	36130.309557
HLA A*0216	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.429545	0.777400	-3.652145	26887.174215
HLA B*0803	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.497046	0.844865	-3.652181	31408.403767
HLA A*3301	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.607230	0.955018	-3.652211	40478.989596
HLA B*3501	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.274907	0.622672	-3.652235	18832.447150
HLA A*2301	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.442463	0.790220	-3.652243	27698.906848
HLA A*0201	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.392867	0.740545	-3.652322	24709.693068
HLA A*2902	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.441772	0.789406	-3.652366	27654.886548
HLA A*0206	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.049727	0.397240	-3.652487	11213.144421
HLA A*2301	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.443304	0.790719	-3.652585	27752.604420
HLA B*1501	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.307922	0.655319	-3.652603	20319.907217
HLA A*6802	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.422043	0.769405	-3.652638	26426.719535
HLA B*4801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.430057	0.777400	-3.652657	26918.902467
HLA B*1503	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.440658	0.787998	-3.652661	27584.062315
HLA A*2603	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.473753	0.821048	-3.652705	29768.234007
HLA A*3201	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.600256	0.947523	-3.652733	39834.226822
HLA A*0202	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.447399	0.794424	-3.652974	28015.533537
HLA B*5701	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.421552	0.768573	-3.652979	26396.856605

HLA A*0203	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.390504	0.737370	-3.653134	24575.579584
HLA A*0206	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.379250	0.726109	-3.653141	23946.923993
HLA A*2902	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.347360	0.693953	-3.653407	22251.545252
HLA A*2301	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.531844	0.878392	-3.653452	34028.600462
HLA A*0203	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.439796	0.786321	-3.653475	27529.350440
HLA B*0801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.303697	0.650029	-3.653668	20123.214038
HLA A*6802	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.431270	0.777400	-3.653869	26994.151639
HLA B*0803	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.500617	0.846543	-3.654074	31667.740867
HLA A*3201	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.592790	0.938712	-3.654078	39155.225425
HLA B*5101	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.452972	0.798809	-3.654162	28377.352577
HLA A*0201	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.391585	0.737370	-3.654215	24636.813278
HLA A*0211	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.538700	0.884477	-3.654223	34570.040228
HLA B*0702	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.266907	0.612666	-3.654241	18488.716403
HLA A*0201	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.361340	0.707098	-3.654241	22979.449032
HLA B*2705	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.260457	0.606197	-3.654261	18216.184846
HLA B*4002	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.611973	0.957710	-3.654263	40923.547475
HLA A*0203	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.368433	0.714055	-3.654378	23357.841484
HLA B*4402	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.423848	0.769461	-3.654387	26536.745543
HLA B*0801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.357611	0.703210	-3.654401	22783.003605
HLA B*7301	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.499381	0.844865	-3.654517	31577.755183
HLA A*0101	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.361131	0.706599	-3.654532	22968.387547
HLA A*3301	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.333301	0.678719	-3.654582	21542.735913
HLA A*2902	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.432080	0.777400	-3.654680	27044.580887
HLA B*3801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.516944	0.862113	-3.654830	32880.896780
HLA B*1501	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.416649	0.761813	-3.654835	26100.500658
HLA A*0211	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.522721	0.867880	-3.654841	33321.231005
HLA A*3301	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.251264	0.596390	-3.654873	17834.621209
HLA B*3801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.453902	0.798809	-3.655093	28438.211002
HLA B*0802	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.485862	0.830606	-3.655256	30609.928609
HLA A*0203	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.316338	0.660945	-3.655393	20717.510893
HLA B*4601	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.395948	0.740545	-3.655402	24885.566162
HLA A*3002	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.517569	0.862113	-3.655455	32928.247455
HLA B*4801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.328637	0.673165	-3.655472	21312.634144
HLA A*2902	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.417368	0.761813	-3.655554	26143.743890
HLA B*4002	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.648891	0.993286	-3.655605	44554.413540
HLA B*4801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.378059	0.722436	-3.655622	23881.332034
HLA A*2603	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.351256	0.695627	-3.655628	22452.030419
HLA A*0211	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.524457	0.868794	-3.655663	33454.712870
HLA B*4002	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.594500	0.938712	-3.655788	39309.738404
HLA A*0202	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.583389	0.927578	-3.655812	38316.818264
HLA A*6801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.425417	0.769405	-3.656012	26632.817680
HLA B*4501	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.579560	0.923460	-3.656100	37980.421363
HLA A*3201	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.340086	0.683810	-3.656276	21881.957503
HLA A*8001	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.382574	0.726109	-3.656465	24130.940957
HLA B*3501	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.340316	0.683810	-3.656506	21893.561717
HLA B*4403	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.608935	0.952354	-3.656581	40638.286668
HLA A*0250	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.121622	0.464975	-3.656646	13231.883144
HLA B*4402	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.294532	0.637857	-3.656675	19702.984040
HLA A*0216	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.455610	0.798809	-3.656801	28550.278420
HLA A*2602	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.614572	0.957710	-3.656861	41169.140868
HLA B*4403	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.541341	0.884477	-3.656864	34780.891216
HLA B*4002	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.622104	0.965021	-3.657083	41889.410917
HLA A*6802	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.021660	0.364577	-3.657083	10511.397698
HLA B*4601	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.379626	0.722436	-3.657189	23967.660999
HLA B*3901	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.478255	0.821048	-3.657207	30078.396795
HLA B*5401	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.394599	0.737370	-3.657229	24808.409460
HLA B*4001	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.341122	0.683810	-3.657312	21934.224950
HLA B*1801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.513530	0.856154	-3.657376	32623.447399
HLA A*2602	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.585055	0.927578	-3.657478	38464.068907
HLA B*1502	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.615434	0.957710	-3.657724	41250.960484
HLA A*0301	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.365703	0.707963	-3.657739	23211.467847
HLA A*1101	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.360971	0.703210	-3.657761	22959.939663
HLA A*2402	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.427231	0.769461	-3.657770	26744.280493
HLA A*2301	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.542297	0.884477	-3.657820	34857.557019
HLA B*3801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.448047	0.790220	-3.657828	28057.395599

HLA B*1502	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.380410	0.722436	-3.657974	24011.007386
HLA A*6901	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.293862	0.635887	-3.657975	19672.629023
HLA B*5701	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.413653	0.755651	-3.658002	25921.089085
HLA A*0212	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.824327	0.166266	-3.658062	6673.093693
HLA A*0203	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.398760	0.740545	-3.658215	25047.238965
HLA A*0211	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.342083	0.683810	-3.658273	21982.811328
HLA B*4001	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.383615	0.725139	-3.658476	24188.842064
HLA B*5301	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.586094	0.927578	-3.658516	38556.153123
HLA B*2705	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.453129	0.794424	-3.658705	28387.640170
HLA A*2603	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.552212	0.893488	-3.658723	35662.499055
HLA A*3002	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.542764	0.883995	-3.658770	34895.103755
HLA B*2705	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.365416	0.706599	-3.658817	23196.153182
HLA A*0202	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.428291	0.769461	-3.658830	26809.612461
HLA B*4601	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.385022	0.726109	-3.658914	24267.353718
HLA A*2603	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.574043	0.915076	-3.658967	37501.029276
HLA A*3301	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.606574	0.947523	-3.659051	40417.938352
HLA B*7301	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.573500	0.914377	-3.659124	37454.194096
HLA B*3801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.527260	0.867880	-3.659380	33671.327775
HLA B*0802	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.433730	0.774156	-3.659574	27147.484509
HLA B*1801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.421444	0.761813	-3.659631	26390.288435
HLA B*1501	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.355283	0.695627	-3.659655	22661.186199
HLA A*3101	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.338540	0.678719	-3.659821	21804.202619
HLA B*0803	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.494537	0.834602	-3.659935	31227.456735
HLA B*1502	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.557343	0.897326	-3.660017	36086.357594
HLA A*8001	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.363301	0.703210	-3.660092	23083.487927
HLA B*1801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.071770	0.411532	-3.660238	11796.964813
HLA A*2501	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.495100	0.834835	-3.660265	31268.027967
HLA B*4001	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.400858	0.740545	-3.660313	25168.535711
HLA A*2601	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.385504	0.725139	-3.660365	24294.281804
HLA A*0101	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.374565	0.714055	-3.660510	23689.989196
HLA A*0201	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.386627	0.726109	-3.660518	24357.186342
HLA A*0211	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.520879	0.860349	-3.660530	33180.203185
HLA A*2402	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.588208	0.927578	-3.660631	38744.336939
HLA B*4601	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.385788	0.725139	-3.660650	24310.189964
HLA A*0202	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.315971	0.655319	-3.660652	20700.033876
HLA B*4501	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.522768	0.862113	-3.660655	33324.836483
HLA B*1509	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.374964	0.714055	-3.660910	23711.786454
HLA B*4501	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.628601	0.967687	-3.660913	42520.716989
HLA A*3301	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.451799	0.790719	-3.661081	28300.850236
HLA B*4403	1:391-399	9	YVIDPKAAA	1.161744	-0.171086	-4.651757	0.990658	-3.661099	44849.448107
HLA B*5401	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.558431	0.897326	-3.661105	36176.859229
HLA B*1517	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.368235	0.707098	-3.661137	23347.229375
HLA A*2601	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.369105	0.707963	-3.661141	23394.009370
HLA B*1501	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.243050	0.581735	-3.661315	17500.485222
HLA B*7301	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.460133	0.798809	-3.661324	28849.155623
HLA B*1517	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.450773	0.789406	-3.661367	28234.022612
HLA A*0202	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.507976	0.846543	-3.661433	32208.883425
HLA B*4601	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.417093	0.755651	-3.661441	26127.201260
HLA A*6901	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.364777	0.703210	-3.661567	23162.045379
HLA B*4402	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.435734	0.774156	-3.661578	27273.049749
HLA A*6802	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.431070	0.769461	-3.661609	26981.741486
HLA A*0203	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-3.755201	0.093574	-3.661627	5691.158420
HLA A*2403	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.274329	0.612666	-3.661663	18807.400982
HLA B*3801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.530627	0.868794	-3.661833	33933.374836
HLA A*2602	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.546322	0.884477	-3.661844	35182.088300
HLA B*4403	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.619858	0.957710	-3.662148	41673.324265
HLA A*1101	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.483229	0.821048	-3.662180	30424.856883
HLA A*2601	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.365392	0.703210	-3.662183	23194.898330
HLA B*4501	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.655474	0.993286	-3.662188	45234.936864
HLA B*0802	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.402817	0.740545	-3.662272	25282.348868
HLA A*2501	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.448646	0.786321	-3.662325	28096.128096
HLA B*1502	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.431780	0.769405	-3.662374	27025.859922
HLA A*3301	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.590053	0.927578	-3.662475	38909.224826
HLA A*3002	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.522853	0.860349	-3.662503	33331.327327
HLA A*0211	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.044220	0.381582	-3.662638	11071.850752

HLA A*0101	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.379353	0.716494	-3.662859	23952.624880
HLA B*1509	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.530752	0.867880	-3.662871	33943.105748
HLA A*0212	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.356831	0.693953	-3.662878	22742.120162
HLA B*1503	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.379395	0.716494	-3.662902	23954.957453
HLA B*1503	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.449243	0.786321	-3.662922	28134.761856
HLA A*2403	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.424762	0.761813	-3.662948	26592.649517
HLA A*3001	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.225694	0.562720	-3.662974	16814.906025
HLA A*0216	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.457523	0.794424	-3.663098	28676.281079
HLA B*5401	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.511881	0.848752	-3.663129	32499.786921
HLA B*5101	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.519357	0.856154	-3.663203	33064.090036
HLA B*4801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.318619	0.655319	-3.663300	20826.626367
HLA A*0219	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.303390	0.639976	-3.663414	20108.957860
HLA B*0802	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.432830	0.769405	-3.663424	27091.293493
HLA A*0301	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.359054	0.695627	-3.663426	22858.807097
HLA B*4601	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.377535	0.714055	-3.663480	23852.538840
HLA B*1801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.419170	0.755651	-3.663518	26252.449723
HLA B*1501	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.269738	0.606197	-3.663541	18609.636506
HLA B*7301	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.343418	0.679867	-3.663551	22050.464375
HLA A*2603	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.602272	0.938712	-3.663560	40019.554534
HLA B*0802	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.439267	0.775701	-3.663567	27495.861411
HLA B*4403	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.602286	0.938712	-3.663574	40020.853563
HLA A*0101	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.341089	0.677348	-3.663741	21932.563749
HLA A*0301	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.259783	0.595974	-3.663809	18187.923647
HLA B*5801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.356175	0.692320	-3.663855	22707.820028
HLA A*0202	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.561194	0.897326	-3.663868	36407.751171
HLA B*3501	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.324885	0.660945	-3.663940	21129.294789
HLA B*3901	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.214647	0.550534	-3.664113	16392.574496
HLA A*3001	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.027962	0.363771	-3.664190	10665.022762
HLA A*2403	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.276702	0.612321	-3.664381	18910.445657
HLA B*5101	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.495100	0.830606	-3.664495	31268.027967
HLA B*1503	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.331052	0.666384	-3.664668	21431.491702
HLA A*3201	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.579785	0.915076	-3.664709	38000.151594
HLA A*2902	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.260685	0.595974	-3.664711	18225.746466
HLA B*5801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.351190	0.686428	-3.664762	22448.629713
HLA B*3501	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.387203	0.722436	-3.664766	24389.491317
HLA B*5101	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.419076	0.754283	-3.664792	26246.769424
HLA A*3301	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.570639	0.905846	-3.664793	37208.210548
HLA A*2501	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.343580	0.678719	-3.664861	22058.696961
HLA A*0216	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.455681	0.790719	-3.664962	28554.912412
HLA A*0212	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.434564	0.769461	-3.665103	27199.671639
HLA A*0101	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.348932	0.683810	-3.665122	22332.224307
HLA A*0201	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.140516	0.475212	-3.665304	13820.260055
HLA A*6901	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.373270	0.707963	-3.665307	23619.478061
HLA A*3001	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.305295	0.639976	-3.665319	20197.378132
HLA B*0802	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.453374	0.787998	-3.665376	28403.616358
HLA A*0202	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.549876	0.884477	-3.665399	35471.241169
HLA A*6801	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.455620	0.790220	-3.665400	28550.896242
HLA A*6901	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.049948	0.384545	-3.665404	11218.848087
HLA A*2403	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.330836	0.665274	-3.665562	21420.827693
HLA B*4402	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.441802	0.776187	-3.665616	27656.831545
HLA A*2603	1:363-371	9	AAAAELVQT	1.246349	-0.259572	-4.652431	0.986777	-3.665655	44919.137159
HLA B*5401	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.561210	0.895455	-3.665756	36409.129931
HLA A*0201	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.303617	0.637857	-3.665761	20119.512990
HLA B*1502	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.550257	0.884477	-3.665780	35502.341863
HLA B*3901	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.496400	0.830606	-3.665794	31361.711613
HLA B*7301	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.549869	0.883995	-3.665875	35470.665487
HLA A*0219	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.456630	0.790719	-3.665912	28617.390142
HLA A*0206	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.073857	0.407915	-3.665942	11853.773559
HLA B*5301	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.586806	0.920689	-3.666116	38619.406059
HLA B*0801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.434747	0.768573	-3.666174	27211.151543
HLA B*1502	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.600353	0.934152	-3.666200	39843.063250
HLA B*4002	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.537910	0.871584	-3.666326	34507.258556
HLA B*4403	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.629851	0.963515	-3.666335	42643.270481
HLA B*4402	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.435839	0.769405	-3.666434	27279.690046
HLA A*2601	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.345185	0.678719	-3.666465	22140.353603

HLA B*1517	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.407065	0.740545	-3.666520	25530.850862
HLA B*0803	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.501416	0.834835	-3.666580	31726.042919
HLA A*0216	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.350504	0.683810	-3.666694	22413.195885
HLA B*4801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.436206	0.769405	-3.666801	27302.722259
HLA B*1801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.461280	0.794424	-3.666855	28925.418765
HLA A*2603	1:237-245	9	VAERIPKFA	1.243567	-0.257375	-4.653085	0.986192	-3.666892	44986.744085
HLA A*2402	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.569257	0.902312	-3.666945	37090.038732
HLA B*4403	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.582104	0.915076	-3.667028	38203.598380
HLA A*1101	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.502015	0.834835	-3.667180	31769.839887
HLA B*3801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.545600	0.878392	-3.667208	35123.705118
HLA B*0803	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.523409	0.856154	-3.667256	33374.090288
HLA A*6901	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.333707	0.666384	-3.667323	21562.907430
HLA A*3101	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.381428	0.714055	-3.667373	24067.318667
HLA A*0206	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.536184	0.868794	-3.667389	34370.320861
HLA A*6801	1:356-364	9	ALDEAAFAA	1.187140	-0.232280	-4.622424	0.954860	-3.667564	41920.242179
HLA A*8001	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.429522	0.761813	-3.667708	26885.719688
HLA A*0301	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.360076	0.692320	-3.667756	22912.664114
HLA B*7301	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.502647	0.834835	-3.667812	31816.106927
HLA B*2705	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.459701	0.791821	-3.667880	28820.452896
HLA A*3001	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.277442	0.609548	-3.667894	18942.698707
HLA A*3101	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.334330	0.666384	-3.667946	21593.842629
HLA A*0211	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.524321	0.856154	-3.668167	33444.217312
HLA B*4403	1:145-153	9	AAYLAEGRQ	0.787901	0.177120	-4.633213	0.965021	-3.668191	42974.676694
HLA B*1509	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.514855	0.846543	-3.668312	32723.139339
HLA B*3901	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.442498	0.774156	-3.668342	27701.154659
HLA A*0203	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.424057	0.755651	-3.668405	26549.525535
HLA A*2403	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.424071	0.755651	-3.668419	26550.387329
HLA A*0216	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.133425	0.464975	-3.668450	13596.448107
HLA A*8001	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.454875	0.786321	-3.668554	28501.975275
HLA A*3002	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.245724	0.577123	-3.668601	17608.558484
HLA A*6901	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.360968	0.692320	-3.668648	22959.815453
HLA B*3901	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.376668	0.707963	-3.668704	23804.970726
HLA B*3901	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.458209	0.789406	-3.668803	28721.616444
HLA A*2601	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.362756	0.693953	-3.668804	23054.534147
HLA B*3901	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.391317	0.722436	-3.668880	24621.623766
HLA A*8001	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.394214	0.725139	-3.669075	24786.408659
HLA A*2403	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.422032	0.752921	-3.669110	26426.004716
HLA A*0219	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.460972	0.791821	-3.669151	28904.926713
HLA B*0802	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.455535	0.786321	-3.669214	28545.336325
HLA B*1509	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.525446	0.856154	-3.669293	33530.994932
HLA B*5701	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.409859	0.740545	-3.669314	25695.603746
HLA A*2402	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.553405	0.883995	-3.669411	35760.642378
HLA A*2603	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.627149	0.957710	-3.669438	42378.794365
HLA A*0203	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.051109	0.381582	-3.669527	11248.870392
HLA B*7301	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.603689	0.934152	-3.669537	40150.318020
HLA A*2602	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.563283	0.893488	-3.669794	36583.272034
HLA B*4402	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.394961	0.725139	-3.669822	24829.086527
HLA A*0211	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.348331	0.678487	-3.669844	22301.317110
HLA A*8001	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.054544	0.384545	-3.669999	11338.193383
HLA B*3801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.565554	0.895455	-3.670100	36775.153867
HLA B*5301	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.456501	0.786321	-3.670180	28608.876479
HLA A*0301	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.347581	0.677348	-3.670233	22262.863699
HLA A*2402	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.576083	0.905846	-3.670237	37677.540105
HLA A*2902	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.395682	0.725139	-3.670543	24870.357830
HLA B*7301	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.567888	0.897326	-3.670561	36973.242317
HLA B*0801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.337004	0.666384	-3.670620	21727.194189
HLA A*0203	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.357160	0.686428	-3.670732	22759.351215
HLA A*2902	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.408108	0.737370	-3.670739	25592.249440
HLA A*0301	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.364713	0.693953	-3.670761	23158.662415
HLA A*3101	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.351000	0.679867	-3.671133	22438.794856
HLA A*3002	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.573597	0.902312	-3.671285	37462.502562
HLA A*0101	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.367061	0.695627	-3.671433	23284.161750
HLA B*5301	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.577342	0.905846	-3.671496	37786.952244
HLA A*8001	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.448919	0.777400	-3.671519	28113.765274
HLA B*4001	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.424637	0.752921	-3.671716	26585.025856

HLA B*4403	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.585835	0.914083	-3.671752	38533.215652
HLA A*0301	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.330315	0.658550	-3.671765	21395.116820
HLA B*5701	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.398034	0.726109	-3.671925	25005.403581
HLA B*4501	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.606109	0.934152	-3.671957	40374.667531
HLA A*2902	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.458507	0.786321	-3.672186	28741.356581
HLA B*0802	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.441664	0.769461	-3.672203	27648.005350
HLA B*4002	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.635720	0.963515	-3.672204	43223.458981
HLA A*6901	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.378864	0.706599	-3.672266	23925.687182
HLA B*1502	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.593046	0.920689	-3.672356	39178.321205
HLA A*2402	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.567819	0.895455	-3.672365	36967.442159
HLA A*0101	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.337751	0.665274	-3.672477	21764.604624
HLA B*5701	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.425427	0.752921	-3.672505	26633.394009
HLA A*3301	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.630292	0.957710	-3.672582	42686.663273
HLA B*0801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.395081	0.722436	-3.672644	24835.937925
HLA A*2501	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.448475	0.775701	-3.672774	28085.034510
HLA B*4403	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.553278	0.880484	-3.672794	35750.197004
HLA B*1509	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.428455	0.755651	-3.672804	26819.766976
HLA A*0101	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.359242	0.686428	-3.672813	22868.702327
HLA A*2602	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.607023	0.934152	-3.672871	40459.723340
HLA B*0801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.398013	0.725139	-3.672874	25004.186123
HLA A*3301	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.587402	0.914377	-3.673026	38672.509919
HLA B*5801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.350405	0.677348	-3.673057	22408.103841
HLA B*5401	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.450526	0.777400	-3.673126	28217.989158
HLA A*3101	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.276446	0.603125	-3.673321	18899.297872
HLA B*2705	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.441988	0.768573	-3.673415	27668.654082
HLA B*4501	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.462896	0.789406	-3.673491	29033.279886
HLA A*8001	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.449685	0.776187	-3.673498	28163.391129
HLA A*2501	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.380901	0.707098	-3.673803	24038.171190
HLA A*2403	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.274672	0.600860	-3.673812	18822.261760
HLA A*2601	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.366142	0.692320	-3.673822	23234.961593
HLA A*3201	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.567335	0.893488	-3.673847	36926.267215
HLA A*2402	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.534459	0.860349	-3.674110	34234.111788
HLA B*5701	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.377410	0.703210	-3.674201	23845.700722
HLA B*4002	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.557489	0.883265	-3.674224	36098.463462
HLA B*5801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.347391	0.673165	-3.674225	22253.110226
HLA A*0206	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.329586	0.655319	-3.674267	21359.265876
HLA A*0212	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.390833	0.716494	-3.674339	24594.199797
HLA B*3801	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.558396	0.883995	-3.674401	36173.923656
HLA A*0212	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.427428	0.752921	-3.674507	26756.436677
HLA A*2603	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.388725	0.714055	-3.674671	24475.141357
HLA A*0301	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.354714	0.679867	-3.674847	22631.537741
HLA A*0219	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.451088	0.776187	-3.674901	28254.497585
HLA A*0202	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.140009	0.464975	-3.675033	13804.120015
HLA A*0203	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.428027	0.752921	-3.675106	26793.373234
HLA B*1503	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.069407	0.394299	-3.675108	11732.936011
HLA B*7301	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.590217	0.915076	-3.675141	38923.962238
HLA B*7301	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.465539	0.790220	-3.675320	29210.518868
HLA A*0216	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.353807	0.678487	-3.675320	22584.327484
HLA A*0301	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.361866	0.686428	-3.675438	23007.312756
HLA B*3501	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.400623	0.725139	-3.675484	25154.923495
HLA B*1509	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.238248	0.562720	-3.675528	17308.034127
HLA B*0702	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.400795	0.725139	-3.675656	25164.859687
HLA A*0206	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.474517	0.798809	-3.675707	29820.618970
HLA A*0201	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.369739	0.693953	-3.675786	23428.205267
HLA B*2705	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.462125	0.786321	-3.675804	28981.807648
HLA B*4002	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.601535	0.925719	-3.675815	39951.630816
HLA B*4001	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.371466	0.695627	-3.675838	23521.547557
HLA A*0202	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.571315	0.895455	-3.675861	37266.227914
HLA A*0212	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.402059	0.726109	-3.675950	25238.209215
HLA B*4801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.390067	0.714055	-3.676012	24550.863106
HLA B*3901	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.510901	0.834835	-3.676065	32426.552516
HLA B*4403	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.569574	0.893488	-3.676086	37117.136781
HLA A*2902	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.379393	0.703210	-3.676184	23954.827859
HLA A*0216	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.431876	0.755651	-3.676224	27031.855070
HLA B*1501	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.416799	0.740545	-3.676254	26109.539075

HLA A*6801	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.538397	0.862113	-3.676283	34545.923053
HLA B*4001	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.356157	0.679867	-3.676290	22706.837275
HLA A*0301	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.355142	0.678719	-3.676422	22653.831722
HLA A*2501	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.475250	0.798809	-3.676440	29870.995261
HLA A*2301	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.536797	0.860349	-3.676447	34418.885382
HLA A*8001	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.383617	0.707098	-3.676519	24188.972923
HLA B*5401	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.497666	0.821048	-3.676618	31453.293635
HLA A*3101	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.370817	0.693953	-3.676865	23486.453049
HLA A*0301	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.355506	0.678487	-3.677019	22672.835670
HLA B*7301	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.468892	0.791821	-3.677071	29436.894171
HLA A*6901	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.280494	0.603125	-3.677369	19076.286339
HLA B*4403	1:248-256	9	PTVLGEGTK	0.954110	0.039176	-4.670833	0.993286	-3.677546	46863.268129
HLA B*5801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.356269	0.678719	-3.677550	22712.734432
HLA A*2402	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.545612	0.867880	-3.677732	35124.655207
HLA B*5401	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.512374	0.834602	-3.677772	32536.730153
HLA A*1101	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.476598	0.798809	-3.677789	29963.897125
HLA A*2301	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.472240	0.794424	-3.677816	29664.702868
HLA A*0201	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.381042	0.703210	-3.677833	24045.975087
HLA A*3101	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.384484	0.706599	-3.677886	24237.308367
HLA A*2301	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.540030	0.862113	-3.677916	34676.055823
HLA A*2601	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.394430	0.716494	-3.677936	24798.748168
HLA A*3301	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.601398	0.923460	-3.677938	39939.097017
HLA A*3001	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.278805	0.600860	-3.677944	19002.229235
HLA A*2301	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.499109	0.821048	-3.678061	31557.944870
HLA B*1503	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.381348	0.703210	-3.678138	24062.892223
HLA A*3101	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.394660	0.716494	-3.678166	24811.899185
HLA A*0250	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.558694	0.880484	-3.678210	36198.785704
HLA A*3002	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.538942	0.860662	-3.678280	34589.308664
HLA A*3101	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.364876	0.686428	-3.678447	23167.308749
HLA A*0219	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.356941	0.678487	-3.678454	22747.903417
HLA A*0211	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.381853	0.703210	-3.678643	24090.896685
HLA A*2301	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.522002	0.843357	-3.678645	33266.115802
HLA B*5701	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.372772	0.693953	-3.678819	23592.404493
HLA B*0803	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.452993	0.774156	-3.678837	28378.734276
HLA A*3201	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.613160	0.934152	-3.679007	41035.503224
HLA B*4801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.440844	0.761813	-3.679030	27595.853745
HLA A*2402	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.566981	0.887847	-3.679134	36896.114714
HLA B*2705	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.301963	0.622672	-3.679292	20043.032312
HLA B*2705	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.441114	0.761813	-3.679301	27613.027496
HLA B*3501	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.416679	0.737370	-3.679310	26102.336333
HLA B*1509	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.523008	0.843615	-3.679393	33343.230492
HLA B*3501	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.076685	0.397240	-3.679445	11931.235190
HLA A*3201	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.528268	0.848752	-3.679516	33749.564374
HLA A*6802	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.340471	0.660945	-3.679527	21901.380268
HLA B*0702	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.435179	0.755651	-3.679528	27238.251543
HLA A*0250	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.522886	0.843357	-3.679529	33333.851886
HLA B*3501	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.455827	0.776187	-3.679640	28564.491710
HLA B*5401	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.564150	0.884477	-3.679672	36656.374299
HLA B*1517	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.478485	0.798809	-3.679675	30094.347661
HLA B*1503	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.335086	0.655319	-3.679768	21631.491546
HLA A*0201	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.396309	0.716494	-3.679816	24906.307537
HLA B*4002	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.607519	0.927578	-3.679941	40505.933942
HLA B*3501	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.276335	0.596390	-3.679945	18894.493057
HLA B*0801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.275962	0.595974	-3.679987	18878.247524
HLA B*1509	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.523388	0.843357	-3.680031	33372.465376
HLA A*3201	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.594145	0.914083	-3.680062	39277.639656
HLA B*5701	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.359989	0.679867	-3.680122	22908.078239
HLA B*1502	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.563463	0.883265	-3.680199	36598.514390
HLA B*1501	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.338756	0.658550	-3.680206	21815.057485
HLA A*2602	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.276194	0.595974	-3.680220	18888.361026
HLA B*2705	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.449694	0.769405	-3.680289	28164.000579
HLA B*1801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.454600	0.774156	-3.680444	28483.940458
HLA A*6801	1:482-490	9	AARQLVGHA	1.019716	-0.067362	-4.632818	0.952354	-3.680464	42935.636414
HLA B*5301	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.541127	0.860662	-3.680465	34763.772801
HLA B*7301	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.558891	0.878392	-3.680499	36215.239282

HLA A*0206	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.515431	0.834835	-3.680595	32766.540091
HLA A*0206	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.536832	0.856154	-3.680678	34421.678530
HLA A*1101	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.456975	0.776187	-3.680789	28640.157279
HLA B*4403	1:362-370	9	FAAAAELVQ	0.958698	0.008989	-4.648602	0.967687	-3.680914	44524.776165
HLA B*0801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.436763	0.755651	-3.681111	27337.750724
HLA B*3501	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.450538	0.769405	-3.681133	28218.752449
HLA B*4501	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.595548	0.914377	-3.681171	39404.699872
HLA B*4403	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.601878	0.920689	-3.681188	39983.198830
HLA B*2705	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.319075	0.637857	-3.681218	20848.495771
HLA B*0803	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.472181	0.790719	-3.681463	29660.691071
HLA B*2705	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.435774	0.754283	-3.681490	27275.558116
HLA A*0201	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.395642	0.714055	-3.681587	24868.070655
HLA B*5801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.360165	0.678487	-3.681678	22917.374887
HLA A*2301	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.451156	0.769461	-3.681695	28258.930690
HLA B*4402	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.361629	0.679867	-3.681762	22994.745022
HLA B*0802	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.473593	0.791821	-3.681772	29757.285107
HLA A*0212	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.419414	0.737370	-3.682044	26267.224255
HLA B*2705	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.458261	0.776187	-3.682074	28725.035024
HLA B*0702	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.458265	0.776187	-3.682079	28725.345824
HLA A*6801	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.607843	0.925719	-3.682124	40536.185533
HLA A*0101	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.079397	0.397240	-3.682156	12005.955031
HLA B*4403	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.555113	0.872828	-3.682285	35901.565549
HLA B*0801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.332074	0.649772	-3.682303	21481.985861
HLA B*3901	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.459745	0.777400	-3.682345	28823.415441
HLA B*0803	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.476857	0.794424	-3.682432	29981.733581
HLA A*0212	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.320329	0.637857	-3.682472	20908.811671
HLA A*2501	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.473264	0.790719	-3.682546	29734.755934
HLA A*3201	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.069689	0.387024	-3.682665	11740.555350
HLA B*5401	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.408853	0.726109	-3.682744	25636.176136
HLA A*0301	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.349360	0.666384	-3.682975	22354.223439
HLA B*1501	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.323043	0.639976	-3.683067	21039.867769
HLA B*5701	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.397143	0.714055	-3.683089	24954.186327
HLA A*0211	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-3.862267	0.178924	-3.683343	7282.268817
HLA B*5101	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.475344	0.791821	-3.683523	29877.459911
HLA A*2603	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.611106	0.927578	-3.683529	40841.935367
HLA B*4801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.386740	0.703210	-3.683530	24363.512108
HLA B*5101	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.349966	0.666384	-3.683582	22385.446162
HLA B*4801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.438039	0.754283	-3.683755	27418.175343
HLA B*1503	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.421146	0.737370	-3.683776	26372.163059
HLA A*0203	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.290000	0.606197	-3.683803	19498.439217
HLA B*2705	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-3.790208	0.106226	-3.683982	6168.903851
HLA A*0101	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.391972	0.707963	-3.684009	24658.814697
HLA B*3501	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.287141	0.603125	-3.684016	19370.486381
HLA A*0216	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.159242	0.475212	-3.684029	14429.178655
HLA A*0212	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.424696	0.740545	-3.684151	26588.621650
HLA A*0202	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.544917	0.860662	-3.684255	35068.454152
HLA A*2501	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.379950	0.695627	-3.684322	23985.561090
HLA A*2601	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.391035	0.706599	-3.684436	24605.644922
HLA B*0802	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.406917	0.722436	-3.684481	25522.150843
HLA B*1502	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.391580	0.707098	-3.684482	24636.546715
HLA A*0202	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.473903	0.789406	-3.684498	29778.542533
HLA B*0702	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.406981	0.722436	-3.684544	25525.879059
HLA A*2301	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.540753	0.856154	-3.684600	34733.882821
HLA A*1101	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.454125	0.769405	-3.684720	28452.830278
HLA B*4403	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.618911	0.934152	-3.684759	41582.567664
HLA A*6802	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.437773	0.752921	-3.684852	27401.419256
HLA B*5701	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.407347	0.722436	-3.684911	25547.430532
HLA A*2402	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.565402	0.880484	-3.684918	36762.224422
HLA B*0801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-3.910018	0.225072	-3.684946	8128.635313
HLA A*0211	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.422325	0.737370	-3.684955	26443.880979
HLA A*2601	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.358133	0.673165	-3.684967	22810.382325
HLA A*2601	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.364861	0.679867	-3.684995	23166.556766
HLA A*0212	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.399098	0.714055	-3.685044	25066.758969
HLA B*4601	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.393060	0.707963	-3.685097	24720.656989
HLA A*3002	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.563503	0.878392	-3.685111	36601.880441

HLA A*6802	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.391815	0.706599	-3.685216	24649.878419
HLA A*0250	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.582903	0.897326	-3.685577	38273.933305
HLA B*0803	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.408073	0.722436	-3.685637	25590.172756
HLA B*5301	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.573500	0.887847	-3.685654	37454.194096
HLA B*5701	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.423039	0.737370	-3.685670	26487.406534
HLA A*2602	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.587987	0.902312	-3.685675	38724.639306
HLA B*1801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.520618	0.834835	-3.685783	33160.284530
HLA B*4403	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.611675	0.925719	-3.685956	40895.440366
HLA A*2902	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.392614	0.706599	-3.686015	24695.260201
HLA A*0250	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.581665	0.895455	-3.686210	38164.969280
HLA A*3101	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.351533	0.665274	-3.686259	22466.367628
HLA A*2601	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.370270	0.683810	-3.686460	23456.866928
HLA B*4002	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.641511	0.955018	-3.686493	43803.720494
HLA B*3901	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.448357	0.761813	-3.686544	28077.438691
HLA A*2902	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.442277	0.755651	-3.686626	27687.071384
HLA B*3801	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.558285	0.871584	-3.686701	36164.727070
HLA A*2301	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.517381	0.830606	-3.686775	32913.999485
HLA B*1503	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.309254	0.622434	-3.686820	20382.332338
HLA B*4402	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.448684	0.761813	-3.686871	28098.560152
HLA B*4002	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.477096	0.790220	-3.686877	29998.282328
HLA B*5701	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.412138	0.725139	-3.686999	25830.798215
HLA A*0101	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.394101	0.707098	-3.687003	24779.973092
HLA A*6802	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.442947	0.755651	-3.687295	27729.792746
HLA B*1801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.464698	0.777400	-3.687298	29154.000426
HLA A*2603	1:102-110	9	LAAGEAYHA	1.141966	-0.178451	-4.651038	0.963515	-3.687523	44775.264580
HLA B*4801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.424999	0.737370	-3.687629	26607.183679
HLA B*5801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.348587	0.660945	-3.687642	22314.471582
HLA B*5101	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.478508	0.790719	-3.687790	30095.975776
HLA B*4402	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.395804	0.707963	-3.687841	24877.355200
HLA B*0802	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.477538	0.789406	-3.688133	30028.807876
HLA B*1801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.464014	0.775701	-3.688314	29108.140041
HLA B*1503	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.326215	0.637857	-3.688358	21194.091785
HLA B*5701	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.354759	0.666384	-3.688375	22633.864108
HLA A*2501	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.457079	0.768573	-3.688506	28646.975454
HLA A*1101	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.450465	0.761813	-3.688652	28214.020376
HLA B*3901	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.483132	0.794424	-3.688708	30418.109232
HLA A*3101	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.366116	0.677348	-3.688768	23233.578950
HLA A*1101	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.311526	0.622672	-3.688854	20489.239103
HLA B*4001	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.396819	0.707963	-3.688856	24935.563365
HLA B*5101	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.476970	0.787998	-3.688972	29989.520089
HLA A*0216	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.392261	0.703210	-3.689052	24675.228536
HLA A*0201	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.397122	0.707963	-3.689159	24952.971362
HLA B*1502	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.616759	0.927578	-3.689182	41377.016698
HLA B*0702	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.395816	0.706599	-3.689217	24878.028128
HLA B*1517	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.475557	0.786321	-3.689236	29892.172203
HLA A*2501	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.458716	0.769405	-3.689311	28755.198305
HLA B*4601	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.396471	0.707098	-3.689373	24915.606357
HLA B*4403	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.567789	0.878392	-3.689397	36964.842384
HLA B*3901	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.475720	0.786321	-3.689398	29903.332506
HLA B*4001	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.392686	0.703210	-3.689477	24699.402105
HLA A*6901	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.329528	0.639976	-3.689552	21356.377289
HLA A*3101	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.397571	0.707963	-3.689608	24978.768314
HLA A*0211	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.329603	0.639976	-3.689627	21360.074750
HLA B*0802	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.488473	0.798809	-3.689663	30794.460118
HLA A*0219	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.475985	0.786321	-3.689664	29921.618525
HLA A*6801	1:24-32	9	VRTALFNWA	1.057189	-0.109666	-4.637263	0.947523	-3.689740	43377.361344
HLA A*3101	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.312210	0.622434	-3.689776	20521.520260
HLA A*0211	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.524699	0.834835	-3.689864	33473.359652
HLA B*3501	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.339955	0.650029	-3.689925	21875.329285
HLA A*1101	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.415516	0.725139	-3.690378	26032.530522
HLA B*1503	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.525169	0.834602	-3.690567	33509.596685
HLA B*3501	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-3.708014	0.017415	-3.690599	5105.210080
HLA A*0212	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.374440	0.683810	-3.690630	23683.197678
HLA B*0803	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.489624	0.798809	-3.690814	30876.199772
HLA A*2602	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.616606	0.925719	-3.690887	41362.469326

HLA A*6801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.482862	0.791821	-3.691041	30399.190879
HLA B*3901	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.460509	0.769461	-3.691048	28874.137750
HLA A*0301	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.156032	0.464975	-3.691057	14322.941369
HLA B*1501	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.313880	0.622672	-3.691208	20600.606878
HLA B*1502	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.586686	0.895455	-3.691231	38608.752267
HLA B*2705	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.446915	0.755651	-3.691263	27984.329376
HLA B*4501	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.646349	0.955018	-3.691330	44294.376085
HLA B*3501	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.468857	0.777400	-3.691456	29434.505513
HLA B*1801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.375345	0.683810	-3.691535	23732.576621
HLA A*2601	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.369123	0.677348	-3.691775	23395.021864
HLA B*5301	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.575805	0.883995	-3.691811	37653.495685
HLA A*3201	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.617572	0.925719	-3.691853	41454.539625
HLA B*4001	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.398492	0.706599	-3.691893	25031.796410
HLA B*7301	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.375852	0.683810	-3.692042	23760.325202
HLA B*5401	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.552773	0.860662	-3.692111	35708.639187
HLA B*4601	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.398748	0.706599	-3.692149	25046.561460
HLA B*0801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.429545	0.737370	-3.692175	26887.174215
HLA A*1101	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.461665	0.769461	-3.692204	28951.093415
HLA A*1101	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.469703	0.777400	-3.692302	29491.886840
HLA B*4501	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.619903	0.927578	-3.692325	41677.607998
HLA A*0101	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.370827	0.678487	-3.692340	23486.961291
HLA A*3201	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.619994	0.927578	-3.692417	41686.402304
HLA A*3101	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.384884	0.692320	-3.692564	24259.609216
HLA A*3002	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.536000	0.843357	-3.692643	34355.820630
HLA A*3001	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-3.907339	0.214632	-3.692707	8078.658065
HLA A*0219	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.409220	0.716494	-3.692726	25657.820732
HLA B*5301	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.536477	0.843615	-3.692862	34393.571175
HLA B*4501	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.607977	0.915076	-3.692900	40548.687348
HLA A*6901	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.315419	0.622434	-3.692985	20673.734149
HLA B*1501	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.379518	0.686428	-3.693089	23961.697271
HLA B*4601	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.370561	0.677348	-3.693213	23472.607689
HLA B*1502	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.538206	0.844865	-3.693342	34530.788311
HLA A*0202	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.562197	0.868794	-3.693403	36491.951116
HLA B*5401	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.562199	0.868794	-3.693405	36492.148534
HLA B*3901	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.469691	0.776187	-3.693504	29491.089112
HLA B*0802	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.407723	0.714055	-3.693669	25569.553508
HLA A*6802	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.372410	0.678487	-3.693923	23572.757305
HLA B*4601	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.410500	0.716494	-3.694007	25733.581615
HLA B*5301	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.591375	0.897326	-3.694049	39027.913940
HLA B*5301	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.577424	0.883265	-3.694159	37794.107734
HLA B*1501	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.388175	0.693953	-3.694223	24444.177535
HLA A*0219	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.349559	0.655319	-3.694240	22364.505182
HLA A*2603	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.540791	0.846543	-3.694248	34736.889454
HLA B*4001	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.410745	0.716494	-3.694251	25748.064134
HLA A*2403	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.408430	0.714055	-3.694376	25611.224290
HLA A*3201	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.463873	0.769461	-3.694413	29098.693265
HLA A*0219	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.450171	0.755651	-3.694520	28194.947486
HLA B*1502	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.609126	0.914477	-3.694649	40656.098308
HLA A*1101	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.450326	0.755651	-3.694675	28205.016365
HLA A*0212	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.334750	0.639976	-3.694775	21614.763589
HLA B*4601	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.368022	0.673165	-3.694856	23335.738365
HLA B*4402	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.344982	0.650029	-3.694953	22130.055189
HLA B*4402	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.435532	0.740545	-3.694987	27260.363902
HLA A*6802	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.317681	0.622672	-3.695010	20781.719625
HLA A*1101	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.481333	0.786321	-3.695011	30292.318163
HLA B*0801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.378824	0.683810	-3.695014	23923.486882
HLA B*7301	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.543775	0.848752	-3.695023	34976.373061
HLA A*8001	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.448104	0.752921	-3.695183	28061.038733
HLA B*1501	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.368402	0.673165	-3.695237	23356.198818
HLA A*3001	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.291699	0.596390	-3.695308	19574.853779
HLA B*5101	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.484793	0.789406	-3.695388	30534.674940
HLA B*4801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.333291	0.637857	-3.695435	21542.269743
HLA B*4002	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.597780	0.902312	-3.695468	39607.737475
HLA A*0301	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.368668	0.673165	-3.695502	23370.481236
HLA A*0301	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.360823	0.665274	-3.695548	22952.115721

HLA B*4501	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.544524	0.848752	-3.695772	35036.785813
HLA B*3801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.539518	0.843615	-3.695902	34635.184520
HLA A*3201	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.598257	0.902312	-3.695945	39651.258883
HLA A*8001	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.433483	0.737370	-3.696113	27132.068076
HLA A*6802	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.333978	0.637857	-3.696121	21576.326692
HLA A*0216	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.357078	0.660945	-3.696133	22755.042228
HLA A*0219	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.375023	0.678719	-3.696304	23714.993625
HLA A*3201	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.418745	0.722436	-3.696308	26226.756170
HLA A*8001	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.452131	0.755651	-3.696479	28322.446201
HLA A*8001	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.332427	0.635887	-3.696540	21499.425210
HLA A*0101	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.388890	0.692320	-3.696570	24484.411659
HLA A*8001	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.437120	0.740545	-3.696575	27360.239887
HLA B*5301	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.568235	0.871584	-3.696651	37002.857300
HLA B*5301	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.575147	0.878392	-3.696755	37596.502515
HLA A*0219	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.437317	0.740545	-3.696772	27372.676045
HLA A*2301	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.543335	0.846543	-3.696793	34941.007131
HLA B*5101	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.062495	0.365377	-3.697118	11547.674062
HLA A*2301	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.540901	0.843615	-3.697286	34745.722945
HLA B*5801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.337279	0.639976	-3.697303	21740.950923
HLA B*1509	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.437996	0.740545	-3.697451	27415.505546
HLA A*2402	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.581975	0.884477	-3.697498	38192.232823
HLA A*0211	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.335488	0.637857	-3.697631	21651.511904
HLA B*4402	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.411720	0.714055	-3.697665	25805.936156
HLA B*5701	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.404269	0.706599	-3.697671	25367.017093
HLA B*1801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.483992	0.786321	-3.697671	30478.397346
HLA B*5101	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.473384	0.775701	-3.697683	29742.961014
HLA A*0101	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.376529	0.678719	-3.697810	23797.373785
HLA A*0250	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.576209	0.878392	-3.697817	37688.548604
HLA B*1501	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.335693	0.637857	-3.697836	21661.704811
HLA B*3801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.532450	0.834602	-3.697848	34076.129090
HLA B*0802	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.475374	0.777400	-3.697974	29879.561224
HLA A*0202	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.405132	0.707098	-3.698033	25417.431543
HLA B*0702	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.412135	0.714055	-3.698081	25830.658474
HLA A*2902	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.334060	0.635887	-3.698173	21580.412473
HLA A*3001	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.260450	0.562255	-3.698195	18215.889206
HLA A*0216	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.363579	0.665274	-3.698304	23098.228366
HLA B*5301	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.593861	0.895455	-3.698406	39251.937061
HLA A*2602	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.619109	0.920689	-3.698419	41601.468353
HLA B*1501	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.406485	0.707963	-3.698522	25496.758234
HLA A*3101	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.321199	0.622672	-3.698527	20950.705896
HLA A*0202	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.558880	0.860349	-3.698530	36214.259693
HLA B*5701	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.394237	0.695627	-3.698610	24787.749613
HLA A*2501	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.460429	0.761813	-3.698616	28868.827239
HLA B*4001	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.405837	0.707098	-3.698738	25458.716682
HLA A*2602	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.596135	0.897326	-3.698809	39458.029692
HLA A*2902	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.276030	0.577123	-3.698907	18881.209504
HLA B*5801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.348728	0.649772	-3.698956	22321.715887
HLA A*3301	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.624754	0.925719	-3.699035	42145.816515
HLA B*1509	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.468706	0.769461	-3.699245	29424.316083
HLA A*3101	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.436624	0.737370	-3.699254	27329.026358
HLA B*0702	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.467830	0.768573	-3.699257	29365.000955
HLA A*0206	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.406375	0.707098	-3.699276	25490.276130
HLA A*2402	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.548048	0.848752	-3.699297	35322.260226
HLA A*3201	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.620098	0.920689	-3.699408	41696.326313
HLA A*0201	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.322129	0.622434	-3.699695	20995.637042
HLA A*6802	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.416212	0.716494	-3.699718	26074.250515
HLA A*1101	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.468328	0.768573	-3.699755	29398.698892
HLA B*1503	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.425053	0.725139	-3.699914	26610.494549
HLA A*2902	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.452913	0.752921	-3.699992	28373.514878
HLA A*0101	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.366452	0.666384	-3.700068	23251.559729
HLA A*0101	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.312395	0.612321	-3.700074	20530.292647
HLA B*1503	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.378923	0.678719	-3.700204	23928.923283
HLA A*3201	1:115-123	9	EEVEARHVA	1.314318	-0.408472	-4.606118	0.905846	-3.700273	40375.541230
HLA B*3501	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.453202	0.752921	-3.700281	28392.401362
HLA A*6801	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.580803	0.880484	-3.700318	38089.270604

HLA B*4801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.350095	0.649772	-3.700323	22392.107806
HLA B*2705	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.394348	0.693953	-3.700395	24794.053066
HLA B*0803	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.489856	0.789406	-3.700451	30892.740846
HLA A*6901	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.338315	0.637857	-3.700458	21792.881560
HLA B*1502	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.544144	0.843615	-3.700529	35006.092954
HLA B*5801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.350572	0.650029	-3.700543	22416.712495
HLA B*7301	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.396173	0.695627	-3.700546	24898.493822
HLA B*4402	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.361570	0.660945	-3.700625	22991.635256
HLA A*0203	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.092225	0.391537	-3.700688	12365.876376
HLA A*2602	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.297168	0.596390	-3.700778	19822.942797
HLA B*5701	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.359467	0.658550	-3.700917	22880.582257
HLA B*4801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.441523	0.740545	-3.700978	27639.032448
HLA A*2601	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.387438	0.686428	-3.701009	24402.689331
HLA A*3301	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.639732	0.938712	-3.701020	43624.698551
HLA A*6801	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.579597	0.878392	-3.701205	37983.709023
HLA B*5301	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.594799	0.893488	-3.701310	39336.755673
HLA B*5401	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.455667	0.754283	-3.701383	28553.985553
HLA A*1101	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.338839	0.637330	-3.701508	21819.188473
HLA B*0802	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.463394	0.761813	-3.701581	29066.597156
HLA A*0201	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.397458	0.695627	-3.701831	24972.282803
HLA A*0202	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.569720	0.867880	-3.701840	37129.588444
HLA A*0201	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.394228	0.692320	-3.701908	24787.213223
HLA A*0216	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.439371	0.737370	-3.702001	27502.407171
HLA A*0202	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.368442	0.666384	-3.702058	23358.346943
HLA A*6802	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.409290	0.707098	-3.702192	25661.985249
HLA A*3001	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.252852	0.550534	-3.702318	17899.963343
HLA A*3201	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.616886	0.914477	-3.702409	41389.106098
HLA A*3001	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.228932	0.526478	-3.702454	16940.726647
HLA B*3901	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.382433	0.679867	-3.702566	24123.109485
HLA B*3801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.546054	0.843357	-3.702697	35160.397233
HLA B*1503	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.305983	0.603125	-3.702859	20229.418333
HLA A*2902	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.380349	0.677348	-3.703001	24007.630305
HLA A*2902	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.443727	0.740545	-3.703182	27779.642515
HLA B*2705	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.315969	0.612666	-3.703303	20699.921892
HLA A*3101	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.361875	0.658550	-3.703325	23007.810629
HLA B*3801	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.491400	0.787998	-3.703403	31002.738193
HLA B*5801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.368790	0.665274	-3.703516	23377.056610
HLA B*1517	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.429728	0.726109	-3.703620	26898.522227
HLA B*4002	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.637862	0.934152	-3.703710	43437.242651
HLA B*4601	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.406967	0.703210	-3.703757	25525.050520
HLA A*0250	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.550410	0.846543	-3.703867	35514.828201
HLA A*2603	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.618352	0.914477	-3.703875	41529.062332
HLA B*3901	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.341893	0.637857	-3.704036	21973.180548
HLA A*0101	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.365005	0.660945	-3.704060	23174.203066
HLA B*5301	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.326741	0.622672	-3.704069	21219.790675
HLA A*2602	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.582501	0.878392	-3.704109	38238.542804
HLA A*0101	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.342001	0.637857	-3.704144	21978.649362
HLA A*2902	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.387966	0.683810	-3.704156	24432.410982
HLA B*4801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.365122	0.660945	-3.704178	23180.472407
HLA B*1503	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.326922	0.622672	-3.704250	21228.631864
HLA B*1501	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.420793	0.716494	-3.704300	26350.771168
HLA B*4002	1:477-485	9	MQRLRAARQ	0.843210	0.050278	-4.597937	0.893488	-3.704449	39622.096400
HLA A*2602	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.566577	0.862113	-3.704463	36861.798813
HLA A*0216	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.445035	0.740545	-3.704490	27863.477387
HLA A*0206	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.163222	0.458535	-3.704687	14562.020505
HLA A*2402	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.560856	0.856154	-3.704702	36379.399703
HLA A*2601	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.360040	0.655319	-3.704721	22910.804865
HLA A*3301	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.548488	0.843615	-3.704873	35358.012046
HLA B*1517	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.459160	0.754283	-3.704877	28784.614642
HLA A*0219	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.342734	0.637857	-3.704877	22015.778130
HLA B*4601	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.340871	0.635887	-3.704984	21921.531820
HLA A*2501	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.482399	0.777400	-3.704999	30366.810255
HLA A*2402	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.480705	0.775701	-3.705004	30248.594301
HLA B*5401	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.086619	0.381582	-3.705037	12207.283460
HLA A*2301	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.473614	0.768573	-3.705042	29758.733995

HLA B*4402	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.427574	0.722436	-3.705138	26765.412642
HLA B*1801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.419210	0.714055	-3.705155	26254.864223
HLA A*2402	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.504057	0.798809	-3.705247	31919.547684
HLA B*5401	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.497081	0.791821	-3.705260	31410.952610
HLA B*0802	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.481452	0.776187	-3.705266	30300.677099
HLA A*3201	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.583770	0.878392	-3.705378	38350.413921
HLA A*0212	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.384191	0.678719	-3.705472	24220.923764
HLA B*5801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.343350	0.637857	-3.705493	22047.005220
HLA B*5401	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.561666	0.856154	-3.705512	36447.362045
HLA A*2301	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.540570	0.834835	-3.705735	34719.229209
HLA A*0201	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.385795	0.679867	-3.705929	24310.584514
HLA A*0301	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.366887	0.660945	-3.705942	23274.842225
HLA A*0250	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.475407	0.769461	-3.705946	29881.824341
HLA B*5801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.341956	0.635887	-3.706069	21976.390339
HLA B*3801	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.496874	0.790719	-3.706156	31396.002349
HLA A*0206	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.412854	0.706599	-3.706256	25873.454633
HLA B*0702	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.460568	0.754283	-3.706284	28878.043162
HLA A*0201	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.390170	0.683810	-3.706360	24556.707769
HLA B*3501	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.379623	0.673165	-3.706458	23967.531337
HLA B*4403	1:174-182	9	PVTFAAGSV	0.996948	-0.041930	-4.661482	0.955018	-3.706463	45865.023635
HLA B*5701	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.413634	0.707098	-3.706536	25919.967268
HLA B*4801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.414548	0.707963	-3.706585	25974.571898
HLA B*3501	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-3.995591	0.288865	-3.706725	9898.983089
HLA A*1101	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.173602	0.466843	-3.706758	14914.258391
HLA A*3101	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.379992	0.673165	-3.706827	23987.896869
HLA B*5401	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.497645	0.790719	-3.706926	31451.762242
HLA A*0212	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.386982	0.679867	-3.707115	24377.091693
HLA A*0250	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.575396	0.867880	-3.707516	37618.068347
HLA A*0201	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.394094	0.686428	-3.707666	24779.570925
HLA B*5701	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.310812	0.603125	-3.707687	20455.570066
HLA B*0802	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.476323	0.768573	-3.707751	29944.937266
HLA A*3002	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.528938	0.821048	-3.707890	33801.640209
HLA B*1801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.448494	0.740545	-3.707949	28086.250032
HLA A*0206	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.448632	0.740545	-3.708087	28095.216129
HLA B*4402	1:380-388	9	WELLKFFND	0.942251	-0.784797	-3.865683	0.157454	-3.708229	7339.776871
HLA B*4402	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.394667	0.686428	-3.708239	24812.301877
HLA A*0202	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.116603	0.408334	-3.708269	13079.861846
HLA B*5701	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.424780	0.716494	-3.708287	26593.800448
HLA A*2902	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.400656	0.692320	-3.708336	25156.828762
HLA A*2603	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.415486	0.707098	-3.708388	26030.699756
HLA A*2601	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.369678	0.660945	-3.708733	23424.910155
HLA A*0250	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.569194	0.860349	-3.708844	37084.621497
HLA B*1517	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.478266	0.769405	-3.708861	30079.210410
HLA B*5301	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.552329	0.843357	-3.708972	35672.146868
HLA A*6802	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.321387	0.612321	-3.709066	20959.775139
HLA A*2402	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.571203	0.862113	-3.709089	37256.552075
HLA A*2602	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.604577	0.895455	-3.709122	40232.506942
HLA A*2501	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.478656	0.769461	-3.709196	30106.234925
HLA B*0702	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.393022	0.683810	-3.709212	24718.517305
HLA A*0219	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.370270	0.660945	-3.709325	23456.866928
HLA B*0802	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.463634	0.754283	-3.709350	29082.640783
HLA A*0219	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.446727	0.737370	-3.709357	27972.220627
HLA A*6901	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.359484	0.650029	-3.709454	22881.448743
HLA B*5801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.364861	0.655319	-3.709543	23166.556766
HLA A*2501	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.485750	0.776187	-3.709563	30601.981017
HLA A*2301	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.544188	0.834602	-3.709586	35009.691341
HLA B*1517	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.462570	0.752921	-3.709648	29011.455804
HLA B*4402	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.403607	0.693953	-3.709654	25328.346962
HLA A*2301	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.487079	0.777400	-3.709679	30695.827805
HLA B*5701	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.417643	0.707963	-3.709679	26160.296995
HLA B*5101	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.487091	0.777400	-3.709691	30696.658122
HLA B*1801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.117712	0.407915	-3.709797	13113.303528
HLA B*1503	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.057293	0.347179	-3.710114	11410.186879
HLA B*4601	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.388866	0.678719	-3.710147	24483.087115
HLA B*4601	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.388662	0.678487	-3.710175	24471.566608

HLA B*3901	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.424350	0.714055	-3.710296	26567.485355
HLA B*5101	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.484554	0.774156	-3.710398	30517.830288
HLA B*3801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.496743	0.786321	-3.710422	31386.492252
HLA A*3002	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.605947	0.895455	-3.710492	40359.599192
HLA B*4001	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.404537	0.693953	-3.710584	25382.666452
HLA A*0250	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.595104	0.884477	-3.710627	39364.430377
HLA A*0101	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.390520	0.679867	-3.710653	24576.510260
HLA A*0203	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.390539	0.679867	-3.710672	24577.573933
HLA B*5301	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.583622	0.872828	-3.710794	38337.345445
HLA A*2603	1:26-34	9	TALFNWAYA	1.066638	-0.152555	-4.624910	0.914083	-3.710826	42160.867479
HLA A*3002	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.333573	0.622672	-3.710902	21556.259238
HLA A*2402	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.433375	0.722436	-3.710938	27125.316968
HLA A*3301	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.606438	0.895455	-3.710983	40405.258260
HLA B*1517	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.479596	0.768573	-3.711023	30171.454023
HLA B*1509	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.261559	0.550534	-3.711025	18262.462326
HLA A*2402	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.555924	0.844865	-3.711059	35968.635223
HLA B*4402	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.448466	0.737370	-3.711096	28084.426769
HLA B*2705	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.451710	0.740545	-3.711165	28295.032865
HLA A*0301	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.366530	0.655319	-3.711211	23255.711116
HLA A*3301	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.594528	0.883265	-3.711263	39312.290423
HLA B*0702	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.419245	0.707963	-3.711282	26256.994848
HLA A*2402	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.288470	0.577123	-3.711347	19429.889657
HLA A*0219	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.464353	0.752921	-3.711432	29130.824816
HLA B*3801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.558090	0.846543	-3.711547	36148.492001
HLA B*1502	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.499553	0.787998	-3.711555	31590.228393
HLA B*4001	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.388979	0.677348	-3.711631	24489.445578
HLA B*3501	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.389350	0.677348	-3.712002	24510.387186
HLA A*0212	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.385281	0.673165	-3.712115	24281.799222
HLA A*2402	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.590647	0.878392	-3.712255	38962.516420
HLA B*4501	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.596408	0.883995	-3.712413	39482.799237
HLA B*0702	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.335230	0.622672	-3.712558	21638.631186
HLA B*0702	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.419666	0.707098	-3.712567	26282.433653
HLA B*3801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.557458	0.844865	-3.712594	36095.924799
HLA B*0801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.371207	0.658550	-3.712657	23507.554334
HLA A*3201	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.543281	0.830606	-3.712676	34936.659781
HLA B*1502	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.573049	0.860349	-3.712700	37415.310670
HLA A*3001	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-3.729629	0.016864	-3.712765	5365.730798
HLA A*2603	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.581611	0.868794	-3.712817	38160.220806
HLA B*1509	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.543425	0.830606	-3.712819	34948.190894
HLA A*2602	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.556645	0.843615	-3.713030	36028.422861
HLA B*1801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.435651	0.722436	-3.713215	27267.886192
HLA A*8001	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.419832	0.706599	-3.713234	26292.530731
HLA B*0803	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.490676	0.777400	-3.713276	30951.123022
HLA B*1501	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.405602	0.692320	-3.713282	25444.947523
HLA A*0101	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.368684	0.655319	-3.713365	23371.366275
HLA B*5801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.316709	0.603125	-3.713584	20735.227014
HLA B*5401	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.397439	0.683810	-3.713629	24971.202048
HLA A*2402	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.544261	0.830606	-3.713655	35015.563189
HLA A*2602	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.586488	0.872828	-3.713660	38591.211251
HLA A*2601	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.392188	0.678487	-3.713701	24671.090686
HLA A*0216	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.500030	0.786321	-3.713709	31624.940076
HLA B*4402	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.409344	0.695627	-3.713717	25665.178503
HLA A*0101	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.349625	0.635887	-3.713738	22367.893144
HLA A*3002	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.548577	0.834835	-3.713742	35365.281544
HLA B*4801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.420866	0.707098	-3.713768	26355.190735
HLA A*0301	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.363574	0.649772	-3.713802	23097.978450
HLA A*0202	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.569974	0.856154	-3.713820	37151.288414
HLA A*0101	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.372561	0.658550	-3.714011	23580.920382
HLA B*5101	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.451421	0.737370	-3.714051	28276.211150
HLA A*6801	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.557695	0.843615	-3.714080	36115.652958
HLA B*1503	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.482801	0.768573	-3.714228	30394.915317
HLA B*4601	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.406579	0.692320	-3.714259	25502.276216
HLA B*0801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.406642	0.692320	-3.714322	25506.001530
HLA B*3901	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.276603	0.562255	-3.714348	18906.149402
HLA B*0801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.152921	0.438531	-3.714390	14220.717072

HLA B*4801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.406821	0.692320	-3.714501	25516.490518
HLA B*1509	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.505248	0.790719	-3.714529	32007.217236
HLA B*4601	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.408578	0.693953	-3.714626	25619.954672
HLA B*5801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.352010	0.637330	-3.714679	22491.053915
HLA B*1501	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-3.808355	0.093574	-3.714782	6432.139037
HLA B*1517	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.350769	0.635887	-3.714882	22426.901652
HLA B*4501	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.593361	0.878392	-3.714969	39206.732852
HLA A*2902	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.388150	0.673165	-3.714984	24442.722935
HLA B*4501	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.582877	0.867880	-3.714997	38271.655737
HLA B*1509	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.507003	0.791821	-3.715182	32136.826102
HLA A*6802	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.311258	0.595974	-3.715284	20476.606725
HLA A*6801	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.642947	0.927578	-3.715369	43948.750726
HLA B*5301	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.560285	0.844865	-3.715420	36331.606654
HLA B*4601	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.411062	0.695627	-3.715434	25766.875716
HLA B*4001	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.393976	0.678487	-3.715489	24772.869095
HLA A*6801	1:166-174	9	AWNDLVRGP	0.764003	0.193707	-4.673262	0.957710	-3.715552	47126.147633
HLA A*2402	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.559206	0.843615	-3.715591	36241.502137
HLA B*3501	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.423643	0.707963	-3.715680	26524.258687
HLA A*2403	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.388866	0.673165	-3.715701	24483.087115
HLA B*0801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.328379	0.612666	-3.715713	21299.955028
HLA B*3501	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.471375	0.755651	-3.715724	29605.703963
HLA A*0212	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.419024	0.703210	-3.715815	26243.645784
HLA A*3002	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.485475	0.769461	-3.716014	30582.617407
HLA A*2603	1:389-397	9	DQYVIDPKA	1.202969	-0.315122	-4.603882	0.887847	-3.716035	40168.133090
HLA B*5401	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.484864	0.768573	-3.716291	30539.631018
HLA B*4001	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.402785	0.686428	-3.716356	25280.434095
HLA A*0301	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.366499	0.650029	-3.716470	23254.075633
HLA A*3201	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.611983	0.895455	-3.716528	40924.433052
HLA A*0216	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.430619	0.714055	-3.716564	26953.730136
HLA B*4601	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.382974	0.666384	-3.716590	24153.143937
HLA B*1509	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.492326	0.775701	-3.716625	31068.890892
HLA B*5701	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.403125	0.686428	-3.716697	25300.272705
HLA B*4002	1:28-36	9	LFNWAYARH	1.045344	-0.130268	-4.631824	0.915076	-3.716748	42837.495563
HLA A*0206	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.503173	0.786321	-3.716852	31854.685539
HLA A*0216	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.312896	0.595974	-3.716921	20553.963470
HLA A*0201	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.395651	0.678719	-3.716932	24868.608795
HLA B*5101	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.396880	0.679867	-3.717013	24939.070976
HLA B*4002	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.631411	0.914377	-3.717034	42796.727661
HLA A*6901	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.375610	0.658550	-3.717060	23747.089196
HLA B*4002	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.585015	0.867880	-3.717135	38460.531601
HLA B*0802	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.472820	0.755651	-3.717169	29704.368604
HLA B*0803	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.486579	0.769405	-3.717174	30660.477178
HLA A*2603	1:425-433	9	APLIEAALK	0.788948	0.145204	-4.651384	0.934152	-3.717231	44810.886438
HLA A*0212	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.425255	0.707963	-3.717292	26622.877974
HLA A*2902	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.243774	0.526478	-3.717296	17529.669640
HLA A*3101	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.354712	0.637330	-3.717381	22631.415307
HLA A*2403	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.411362	0.693953	-3.717410	25784.724575
HLA A*6801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.442597	0.725139	-3.717458	27707.449502
HLA B*4801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.433965	0.716494	-3.717471	27162.174971
HLA B*4002	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.614856	0.897326	-3.717530	41196.098870
HLA B*3801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.506951	0.789406	-3.717546	32133.001483
HLA B*7301	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.561234	0.843615	-3.717619	36411.099678
HLA A*6901	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.355064	0.637330	-3.717734	22649.787777
HLA B*5701	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.330061	0.612321	-3.717740	21382.619989
HLA B*4001	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.396655	0.678719	-3.717936	24926.122248
HLA B*1509	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.378883	0.660945	-3.717939	23926.722686
HLA B*4801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-3.914035	0.196045	-3.717990	8204.181487
HLA A*0203	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.384466	0.666384	-3.718081	24236.259421
HLA B*0803	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.486680	0.768573	-3.718107	30667.610408
HLA A*2403	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.404756	0.686428	-3.718328	25395.440184
HLA B*1509	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.504653	0.786321	-3.718332	31963.438862
HLA A*2603	1:158-166	9	LRMPDDDLA	0.980169	-0.054450	-4.644070	0.925719	-3.718351	44062.546057
HLA A*0201	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.384783	0.666384	-3.718399	24253.966475
HLA A*2402	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.539468	0.821048	-3.718420	34631.249921
HLA A*2902	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.432543	0.714055	-3.718489	27073.418963

HLA B*1517	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.321760	0.603125	-3.718635	20977.811914
HLA B*0803	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.505062	0.786321	-3.718741	31993.540874
HLA B*1502	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.562134	0.843357	-3.718777	36486.621235
HLA A*2403	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.354684	0.635887	-3.718797	22629.946153
HLA B*1502	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.580937	0.862113	-3.718823	38101.017762
HLA B*4002	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.591653	0.872828	-3.718824	39052.836023
HLA B*4801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.444027	0.725139	-3.718889	27798.885629
HLA B*4402	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.435511	0.716494	-3.719017	27259.036654
HLA A*0301	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.356916	0.637857	-3.719059	22746.549757
HLA B*4402	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.385459	0.666384	-3.719075	24291.784775
HLA A*0250	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.567866	0.848752	-3.719114	36971.442171
HLA B*3901	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.405555	0.686428	-3.719126	25442.194585
HLA B*3901	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.488602	0.769405	-3.719197	30803.624185
HLA A*0206	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.377925	0.658550	-3.719374	23873.969034
HLA A*0219	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.433443	0.714055	-3.719388	27129.572905
HLA B*7301	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.633981	0.914477	-3.719504	43050.767631
HLA A*3201	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.587402	0.867880	-3.719522	38672.509919
HLA A*2603	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.509005	0.789406	-3.719599	32285.293880
HLA A*0250	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.342278	0.622672	-3.719606	21992.684284
HLA A*2601	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.386094	0.666384	-3.719710	24327.292984
HLA A*6801	1:321-329	9	QKKADALNA	1.204390	-0.265678	-4.658470	0.938712	-3.719757	45548.028306
HLA B*4601	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.380760	0.660945	-3.719816	24030.369825
HLA A*3001	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.104400	0.384545	-3.719855	12717.446864
HLA B*0803	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.511707	0.791821	-3.719886	32486.778827
HLA B*5701	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.393166	0.673165	-3.720000	24726.675842
HLA B*0801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.427966	0.707963	-3.720003	26789.604820
HLA A*0202	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.481826	0.761813	-3.720013	30326.752117
HLA A*2403	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.427285	0.707098	-3.720187	26747.608423
HLA B*1517	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.496433	0.776187	-3.720246	31364.086990
HLA B*0702	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.457629	0.737370	-3.720259	28683.263027
HLA B*1801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.406699	0.686428	-3.720271	25509.313376
HLA A*3301	1:135-143	9	FDRHLTDAQ	1.017574	-0.139182	-4.598741	0.878392	-3.720349	39695.472351
HLA A*0211	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.497755	0.777400	-3.720355	31459.760335
HLA A*0301	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.357705	0.637330	-3.720375	22787.934280
HLA A*0206	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.370155	0.649772	-3.720383	23450.649698
HLA A*3002	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.509923	0.789406	-3.720518	32353.658165
HLA B*5301	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.555146	0.834602	-3.720544	35904.284780
HLA B*5301	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.605035	0.884477	-3.720558	40274.971750
HLA A*2501	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.412939	0.692320	-3.720619	25878.494134
HLA A*0250	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.489229	0.768573	-3.720656	30848.150335
HLA A*0202	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.498077	0.777400	-3.720677	31483.085530
HLA B*7301	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.605202	0.884477	-3.720725	40290.444424
HLA B*4001	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.358837	0.637857	-3.720981	22847.432875
HLA B*4601	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.407505	0.686428	-3.721076	25556.692198
HLA B*0702	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.437609	0.716494	-3.721115	27391.044516
HLA B*4403	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.635548	0.914377	-3.721171	43206.392460
HLA B*1509	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.555851	0.834602	-3.721249	35962.603552
HLA A*3201	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.590050	0.868794	-3.721256	38909.014332
HLA A*0101	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.361248	0.639976	-3.721272	22974.601208
HLA A*0301	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.343775	0.622434	-3.721341	22068.603998
HLA A*3002	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.371121	0.649772	-3.721349	23502.849395
HLA B*1801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.474371	0.752921	-3.721450	29810.618421
HLA B*7301	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.583758	0.862113	-3.721645	38349.376578
HLA A*0101	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.344409	0.622672	-3.721737	22100.862501
HLA A*3101	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.400294	0.678487	-3.721807	25135.878759
HLA A*2403	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.359679	0.637857	-3.721822	22891.725297
HLA A*2603	1:304-312	9	VAAFDVADV	0.706341	0.208036	-4.636265	0.914377	-3.721888	43277.742556
HLA A*3301	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.642594	0.920689	-3.721905	43913.101512
HLA B*4501	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.619240	0.897326	-3.721914	41614.073585
HLA B*1801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.429181	0.707098	-3.722083	26864.637887
HLA B*5701	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.414429	0.692320	-3.722109	25967.406389
HLA A*2501	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.477815	0.755651	-3.722164	30047.983394
HLA B*4001	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.383190	0.660945	-3.722245	24165.168186
HLA A*0216	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.475186	0.752921	-3.722265	29866.632413
HLA B*4402	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.429388	0.707098	-3.722290	26877.430387

HLA A*3301	1:353-361	9	HHIALDEAA	1.131588	-0.251104	-4.602829	0.880484	-3.722345	40070.898263
HLA A*3301	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.624717	0.902312	-3.722405	42142.168606
HLA A*0206	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.491837	0.769405	-3.722432	31033.950069
HLA A*0250	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.578596	0.856154	-3.722443	37896.272075
HLA A*0250	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.557331	0.834835	-3.722496	36085.381491
HLA A*0203	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.439051	0.716494	-3.722558	27482.179856
HLA B*4403	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.646071	0.923460	-3.722611	44266.109044
HLA B*3501	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.345121	0.622434	-3.722687	22137.119864
HLA B*1503	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.498893	0.776187	-3.722706	31542.242079
HLA B*4402	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.429383	0.706599	-3.722784	26877.139581
HLA B*0802	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.475720	0.752921	-3.722798	29903.332506
HLA B*4403	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.606069	0.883265	-3.722804	40370.954519
HLA A*3001	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.165646	0.442758	-3.722888	14643.547719
HLA B*0802	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.448064	0.725139	-3.722925	28058.458131
HLA A*6802	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.431018	0.707963	-3.723055	26978.530376
HLA A*2602	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.637719	0.914477	-3.723242	43422.910585
HLA B*0803	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.492713	0.769461	-3.723252	31096.636351
HLA B*1509	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.477728	0.754283	-3.723445	30041.969414
HLA A*3201	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.544618	0.821048	-3.723570	35044.368438
HLA B*1509	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.430187	0.706599	-3.723588	26926.913214
HLA B*4801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.407573	0.683810	-3.723763	25560.702019
HLA B*3801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.558619	0.834835	-3.723783	36192.519641
HLA A*2602	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.592783	0.868794	-3.723988	39154.589954
HLA A*0219	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.450218	0.726109	-3.724109	28197.998281
HLA A*1101	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.362035	0.637857	-3.724178	23016.276126
HLA A*3001	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.248181	0.523921	-3.724261	17708.483267
HLA B*0702	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.390725	0.666384	-3.724341	24588.080172
HLA B*5401	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.397524	0.673165	-3.724359	24976.065813
HLA A*6802	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.403205	0.678719	-3.724486	25304.926770
HLA A*8001	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.397947	0.673165	-3.724782	25000.398853
HLA A*3002	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.559394	0.834602	-3.724792	36257.190533
HLA B*2705	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.450016	0.725139	-3.724878	28184.882201
HLA B*5101	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.501193	0.776187	-3.725006	31709.741843
HLA A*0211	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.501240	0.776187	-3.725053	31713.172952
HLA B*3801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.555720	0.830606	-3.725114	35951.710196
HLA A*2301	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.524081	0.798809	-3.725272	33425.767593
HLA A*0216	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.363132	0.637857	-3.725275	23074.498382
HLA B*3901	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.479610	0.754283	-3.725327	30172.433384
HLA A*2301	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.501533	0.776187	-3.725347	31734.625799
HLA B*1801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.494795	0.769405	-3.725390	31246.045344
HLA A*2501	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.466012	0.740545	-3.725466	29242.299303
HLA A*2902	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.405348	0.679867	-3.725481	25430.085196
HLA A*2501	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.463072	0.737370	-3.725702	29045.062289
HLA B*1509	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.418028	0.692320	-3.725708	26183.517280
HLA B*4001	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.418148	0.692320	-3.725828	26190.742423
HLA B*4402	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.452091	0.726109	-3.725982	28319.841559
HLA A*6802	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.418423	0.692320	-3.726103	26207.325285
HLA A*0212	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.387078	0.660945	-3.726134	24382.499264
HLA A*0201	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.381491	0.655319	-3.726172	24070.834365
HLA B*7301	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.556798	0.830606	-3.726192	36041.094224
HLA A*3201	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.502398	0.776187	-3.726211	31797.867267
HLA B*0702	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.421865	0.695627	-3.726237	26415.856381
HLA A*0212	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.391523	0.665274	-3.726249	24633.348179
HLA A*2902	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.332535	0.606197	-3.726338	21504.776113
HLA B*4002	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.640949	0.914477	-3.726472	43747.120481
HLA B*5401	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.557219	0.830606	-3.726613	36076.012248
HLA B*1502	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.405374	0.678719	-3.726654	25431.598555
HLA A*2403	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.320670	0.594015	-3.726655	20925.219687
HLA A*8001	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.385372	0.658550	-3.726822	24286.922874
HLA A*2403	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.434925	0.707963	-3.726962	27222.341752
HLA B*5101	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.496440	0.769405	-3.727034	31364.596023
HLA A*1101	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.479982	0.752921	-3.727060	30198.234673
HLA B*1509	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.405834	0.678719	-3.727115	25458.578954
HLA B*5301	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.250897	0.523691	-3.727206	17819.576160
HLA A*3002	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.323287	0.595974	-3.727313	21051.708729

HLA A*0216	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.421270	0.693953	-3.727317	26379.725678
HLA B*1517	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.482989	0.755651	-3.727337	30408.072814
HLA A*2403	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.404706	0.677348	-3.727358	25392.555231
HLA B*3501	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.365470	0.637857	-3.727613	23199.039600
HLA B*1517	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.505053	0.777400	-3.727653	31992.848556
HLA A*0203	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.386218	0.658550	-3.727668	24334.269206
HLA B*1501	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.340065	0.612321	-3.727744	21880.892118
HLA B*5301	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.595628	0.867880	-3.727748	39411.948490
HLA B*1501	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.406494	0.678719	-3.727775	25497.309979
HLA A*0201	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.386352	0.658550	-3.727802	24341.774168
HLA A*0219	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.414320	0.686428	-3.727892	25960.945077
HLA A*2601	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.363849	0.635887	-3.727962	23112.603106
HLA B*4403	1:474-482	9	DRSMQRLRA	1.151128	-0.223550	-4.655540	0.927578	-3.727962	45241.789431
HLA A*2902	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.414433	0.686428	-3.728005	25967.687352
HLA A*2403	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.350711	0.622672	-3.728039	22423.868681
HLA A*0301	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.368212	0.639976	-3.728236	23345.966350
HLA B*1502	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.453409	0.725139	-3.728270	28405.921358
HLA B*1501	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.378094	0.649772	-3.728322	23883.270043
HLA B*0702	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.389310	0.660945	-3.728366	24508.133116
HLA A*3002	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.407133	0.678719	-3.728414	25534.856629
HLA A*2301	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.504132	0.775701	-3.728431	31925.073962
HLA B*0802	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.393967	0.665274	-3.728693	24772.333027
HLA B*1501	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.331823	0.603125	-3.728698	21469.554437
HLA B*4403	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.573660	0.844865	-3.728796	37467.974997
HLA A*2403	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.445376	0.716494	-3.728882	27885.343019
HLA B*4403	1:302-310	9	EMVAAFDVA	1.165830	-0.294246	-4.600567	0.871584	-3.728982	39862.682816
HLA A*2603	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.612253	0.883265	-3.728988	40949.901588
HLA A*0202	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.520888	0.791821	-3.729068	33180.921197
HLA A*2603	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.624569	0.895455	-3.729114	42127.808032
HLA A*2602	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.575685	0.846543	-3.729143	37643.108355
HLA B*4801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.407958	0.678719	-3.729239	25583.390095
HLA B*4403	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.572652	0.843357	-3.729295	37381.118559
HLA A*0212	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.424971	0.695627	-3.729343	26605.456432
HLA B*5701	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.407866	0.678487	-3.729380	25577.992936
HLA A*6802	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.113976	0.384545	-3.729432	13000.990251
HLA B*2705	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.466914	0.737370	-3.729544	29303.110323
HLA A*0219	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.402813	0.673165	-3.729647	25282.075320
HLA A*2601	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.388204	0.658550	-3.729653	24445.764470
HLA B*4402	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.408527	0.678719	-3.729807	25616.905629
HLA B*1501	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.326459	0.596390	-3.730069	21206.019540
HLA B*1502	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.499635	0.769461	-3.730174	31596.210447
HLA A*0202	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.506402	0.776187	-3.730215	32092.349601
HLA B*0802	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.408940	0.678719	-3.730221	25641.308138
HLA B*5701	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.391272	0.660945	-3.730327	24619.093091
HLA A*0203	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.438365	0.707963	-3.730402	27438.800868
HLA A*0212	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.385859	0.655319	-3.730540	24314.135748
HLA A*2603	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.651311	0.920689	-3.730621	44803.371988
HLA A*2403	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.397071	0.666384	-3.730686	24950.001697
HLA B*7301	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.591432	0.860662	-3.730770	39032.981550
HLA B*4002	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.591145	0.860349	-3.730796	39007.228029
HLA A*2402	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.520209	0.789406	-3.730804	33129.084754
HLA A*2902	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.368698	0.637857	-3.730841	23372.124906
HLA A*3201	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.110011	0.379131	-3.730880	12882.807040
HLA A*3001	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.286290	0.555221	-3.731069	19332.588732
HLA A*0206	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.508570	0.777400	-3.731170	32252.997970
HLA B*3501	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.426944	0.695627	-3.731317	26726.634918
HLA B*4001	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.389966	0.658550	-3.731416	24545.152620
HLA B*1502	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.313260	0.581735	-3.731525	20571.205871
HLA B*7301	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.600421	0.868794	-3.731627	39849.314591
HLA A*2501	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.484556	0.752921	-3.731635	30517.995387
HLA A*0219	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.411534	0.679867	-3.731667	25794.909539
HLA A*0202	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.566522	0.834835	-3.731687	36857.212478
HLA A*0203	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.293954	0.562255	-3.731699	19676.780104
HLA A*2501	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.486013	0.754283	-3.731729	30620.528608
HLA A*3301	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.629061	0.897326	-3.731735	42565.827245

HLA B*1801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.521147	0.789406	-3.731741	33200.672635
HLA A*1101	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.110880	0.379131	-3.731749	12908.619852
HLA A*0211	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.523630	0.791821	-3.731809	33391.066316
HLA A*0216	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.354322	0.622434	-3.731888	22611.100478
HLA B*4801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.438511	0.706599	-3.731912	27448.005746
HLA A*2403	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.258446	0.526478	-3.731968	18132.023172
HLA B*1517	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.438802	0.706599	-3.732203	27466.424766
HLA B*0803	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.487899	0.755651	-3.732248	30753.837849
HLA A*0216	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.412213	0.679867	-3.732346	25835.270339
HLA A*1101	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.473135	0.740545	-3.732590	29725.909855
HLA A*2902	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.428396	0.695627	-3.732769	26816.139922
HLA B*4801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.426738	0.693953	-3.732785	26713.914191
HLA A*3101	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.393798	0.660945	-3.732853	24762.685784
HLA B*5301	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.567765	0.834835	-3.732930	36962.842681
HLA A*0219	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.436199	0.703210	-3.732989	27302.279148
HLA A*0101	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.370427	0.637330	-3.733097	23465.370705
HLA B*1517	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.458258	0.725139	-3.733120	28724.879625
HLA A*0206	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.486043	0.752921	-3.733122	30622.682182
HLA A*2402	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.567866	0.834602	-3.733265	36971.442171
HLA B*3901	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.394326	0.660945	-3.733382	24792.845898
HLA A*8001	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.394392	0.660945	-3.733447	24796.601726
HLA B*1502	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.470840	0.737370	-3.733470	29569.209180
HLA A*3002	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.127791	0.394299	-3.733493	13421.201738
HLA A*3001	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.200353	0.466843	-3.733509	15861.815692
HLA A*2602	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.601473	0.867880	-3.733593	39946.011730
HLA A*2601	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.356105	0.622434	-3.733671	22704.134924
HLA B*5301	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.528195	0.794424	-3.733771	33743.904825
HLA A*3301	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.441777	0.707963	-3.733813	27655.185769
HLA B*0702	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.426289	0.692320	-3.733969	26686.325258
HLA A*8001	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.426326	0.692320	-3.734006	26688.635279
HLA A*0212	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.328120	0.594015	-3.734105	21287.283455
HLA A*3002	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.526053	0.791821	-3.734232	33577.828542
HLA B*4002	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-3.961955	0.227561	-3.734395	9161.263086
HLA B*5701	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.411832	0.677348	-3.734484	25812.638174
HLA A*8001	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.451001	0.716494	-3.734507	28248.842564
HLA B*5301	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.595132	0.860349	-3.734783	39366.985946
HLA B*3901	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.418606	0.683810	-3.734796	26218.386360
HLA A*8001	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.418622	0.683810	-3.734812	26219.379248
HLA B*5301	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.603809	0.868794	-3.735015	40161.397195
HLA A*0101	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.338197	0.603125	-3.735072	21786.987504
HLA B*5301	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.401495	0.666384	-3.735111	25205.461859
HLA A*6901	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.344787	0.609548	-3.735240	22120.120565
HLA A*1101	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.441859	0.706599	-3.735260	27660.422667
HLA B*7301	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.529767	0.794424	-3.735343	33866.252568
HLA A*0212	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.421775	0.686428	-3.735347	26410.426478
HLA B*1502	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.604147	0.868794	-3.735353	40192.696079
HLA B*4801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.421921	0.686428	-3.735493	26419.286368
HLA A*2501	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.460636	0.725139	-3.735497	28882.574100
HLA A*2902	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.452041	0.716494	-3.735548	28316.624391
HLA A*2603	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.578972	0.843357	-3.735616	37929.088617
HLA A*0101	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.385678	0.650029	-3.735649	24304.009525
HLA B*5101	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.429721	0.693953	-3.735769	26898.085676
HLA B*3801	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.509928	0.774156	-3.735772	32354.008226
HLA B*7301	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.579271	0.843357	-3.735914	37955.156976
HLA A*1101	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.422659	0.686428	-3.736231	26464.203086
HLA B*1503	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.431913	0.695627	-3.736286	27034.195000
HLA A*0219	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.431956	0.695627	-3.736328	27036.827665
HLA A*0201	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.386493	0.650029	-3.736464	24349.676628
HLA A*2602	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.619797	0.883265	-3.736532	41667.463028
HLA B*5401	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.006201	0.269593	-3.736608	10143.804175
HLA B*3801	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.462743	0.726109	-3.736635	29023.072338
HLA B*4001	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.359117	0.622434	-3.736683	22862.146258
HLA B*0801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.416731	0.679867	-3.736864	26105.443154
HLA B*1801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.403412	0.666384	-3.737028	25316.976561
HLA B*3501	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.377039	0.639976	-3.737063	23825.327020

HLA B*4002	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.621176	0.883995	-3.737182	41799.992748
HLA A*6801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.491506	0.754283	-3.737222	31010.286573
HLA B*0802	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.444335	0.707098	-3.737237	27818.593556
HLA A*3201	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.580977	0.843615	-3.737362	38104.522002
HLA A*0219	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.445334	0.707963	-3.737370	27882.627732
HLA A*8001	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.433055	0.695627	-3.737428	27105.366993
HLA B*3801	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.531879	0.794424	-3.737455	34031.361938
HLA A*6801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.403858	0.666384	-3.737474	25343.012726
HLA B*1801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.387628	0.650029	-3.737599	24413.384958
HLA A*2501	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.445703	0.707963	-3.737739	27906.319975
HLA B*1509	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.507172	0.769405	-3.737767	32149.346221
HLA A*2301	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.507219	0.769405	-3.737814	32152.824897
HLA B*0802	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.433445	0.695627	-3.737818	27129.719674
HLA B*5701	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.350527	0.612666	-3.737862	22414.408447
HLA B*5101	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.507424	0.769461	-3.737963	32167.961519
HLA B*5401	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.393283	0.655319	-3.737964	24733.365175
HLA B*0803	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.499804	0.761813	-3.737991	31608.519947
HLA B*4402	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.375324	0.637330	-3.737993	23731.421134
HLA B*3801	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.559253	0.821048	-3.738205	36245.423600
HLA B*4403	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.640668	0.902312	-3.738356	43718.729649
HLA A*2402	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.581757	0.843357	-3.738400	38173.022392
HLA B*5801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.350823	0.612321	-3.738503	22429.692348
HLA B*5301	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.537424	0.798809	-3.738615	34468.637333
HLA A*6802	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.397174	0.658550	-3.738624	24955.941381
HLA A*0211	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.529431	0.790719	-3.738713	33840.063287
HLA A*3101	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.332838	0.594015	-3.738823	21519.789012
HLA B*1801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.508415	0.769461	-3.738954	32241.484006
HLA A*0219	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.422765	0.683810	-3.738954	26470.646448
HLA A*2301	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.528437	0.789406	-3.739032	33762.712796
HLA A*2403	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.397665	0.658550	-3.739115	24984.174194
HLA A*2601	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.376456	0.637330	-3.739126	23793.383144
HLA B*7301	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.595377	0.856154	-3.739223	39389.141165
HLA A*3101	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.377203	0.637857	-3.739346	23834.351196
HLA B*4501	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.653832	0.914477	-3.739355	45064.203403
HLA B*3501	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.417995	0.678487	-3.739508	26181.534257
HLA B*4001	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.362484	0.622672	-3.739812	23040.070879
HLA B*4402	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.423683	0.683810	-3.739873	26526.698186
HLA B*1801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.336348	0.596390	-3.739958	21694.424788
HLA B*4403	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.529542	0.789406	-3.740136	33848.668718
HLA B*4403	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.508798	0.768573	-3.740225	32269.927471
HLA B*4801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.417633	0.677348	-3.740285	26159.730904
HLA A*3101	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.395684	0.655319	-3.740365	24870.492376
HLA B*4801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.406762	0.666384	-3.740378	25513.039717
HLA A*6801	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.625069	0.884477	-3.740592	42176.380154
HLA A*0301	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.343824	0.603125	-3.740699	22071.111304
HLA B*2705	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.376686	0.635887	-3.740799	23806.001006
HLA A*2403	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.390666	0.649772	-3.740894	24584.754927
HLA A*3001	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.281293	0.540290	-3.741002	19111.406831
HLA A*0212	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.433323	0.692320	-3.741003	27122.088771
HLA A*3301	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.516716	0.775701	-3.741015	32863.646751
HLA B*1517	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.138322	0.397240	-3.741082	13750.604668
HLA A*0201	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.390922	0.649772	-3.741150	24599.256289
HLA A*8001	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.455411	0.714055	-3.741356	28537.152862
HLA A*2301	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.533190	0.791821	-3.741370	34134.248242
HLA A*3001	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.121894	0.380458	-3.741436	13240.189381
HLA A*1101	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.455519	0.714055	-3.741464	28544.255356
HLA B*3901	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.458162	0.716494	-3.741668	28718.508997
HLA B*4801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.407089	0.665274	-3.741815	25532.232090
HLA B*4403	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.639194	0.897326	-3.741868	43570.686919
HLA B*5401	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.517658	0.775701	-3.741957	32935.017401
HLA A*3001	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.252150	0.510101	-3.742049	17871.032540
HLA A*3101	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.392174	0.650029	-3.742145	24670.289891
HLA B*2705	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.407465	0.665274	-3.742190	25554.341905
HLA B*0702	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.392207	0.649772	-3.742435	24672.158452
HLA B*2705	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.010825	0.268381	-3.742444	10252.378780

HLA B*5801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.351998	0.609548	-3.742450	22490.445552
HLA A*2403	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.449370	0.706599	-3.742771	28142.982177
HLA A*2902	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.421381	0.678487	-3.742894	26386.433966
HLA B*0801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.380765	0.637857	-3.742908	24030.629830
HLA A*0203	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.438544	0.695627	-3.742916	27450.084694
HLA A*0206	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-3.995938	0.252948	-3.742990	9906.912018
HLA B*1503	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.011374	0.268381	-3.742993	10265.365629
HLA A*2403	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.393159	0.650029	-3.743130	24726.274539
HLA A*3002	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.337532	0.594015	-3.743517	21753.657177
HLA B*4001	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.408975	0.665274	-3.743701	25643.388972
HLA A*3201	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.366485	0.622672	-3.743813	23253.320833
HLA B*1509	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.520005	0.776187	-3.743818	33113.495876
HLA A*0203	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.436222	0.692320	-3.743902	27303.756211
HLA B*4801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.423782	0.679867	-3.743915	26532.726143
HLA A*0201	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.384052	0.639976	-3.744076	24213.194079
HLA B*1517	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.447298	0.703210	-3.744088	28009.017175
HLA A*6801	1:352-360	9	GHHIALDEA	1.224342	-0.303653	-4.664846	0.920689	-3.744157	46221.718061
HLA B*4402	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.422840	0.678487	-3.744353	26475.229350
HLA A*0212	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.394143	0.649772	-3.744371	24782.386234
HLA A*0206	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.520792	0.776187	-3.744605	33173.562304
HLA A*3002	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.424656	0.679867	-3.744789	26586.176457
HLA B*1501	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.295357	0.550534	-3.744823	19740.433011
HLA B*1517	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.423335	0.678487	-3.744849	26505.467724
HLA A*2402	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.535573	0.790719	-3.744854	34322.010542
HLA B*1801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.521105	0.776187	-3.744918	33197.439777
HLA B*5801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.351122	0.606197	-3.744925	22445.108096
HLA A*2402	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.513523	0.768573	-3.744950	32622.917936
HLA B*1502	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.601199	0.856154	-3.745045	39920.735621
HLA B*4402	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.394914	0.649772	-3.745142	24826.400220
HLA A*2501	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.448395	0.703210	-3.745186	28079.869130
HLA A*6901	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.357540	0.612321	-3.745220	22779.306300
HLA B*4002	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.607502	0.862113	-3.745389	40504.400042
HLA A*2602	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.605764	0.860349	-3.745414	40342.572190
HLA A*2501	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.461992	0.716494	-3.745498	28972.872089
HLA A*6802	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.385481	0.639976	-3.745505	24292.967546
HLA A*1101	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.367956	0.622434	-3.745522	23332.203808
HLA A*8001	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.368320	0.622672	-3.745648	23351.776831
HLA A*0202	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-3.925971	0.180214	-3.745757	8432.777523
HLA B*0802	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.439723	0.693953	-3.745770	27524.733975
HLA A*2601	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.396037	0.650029	-3.746008	24890.682558
HLA B*4601	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.401337	0.655319	-3.746018	25196.327478
HLA B*3901	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.483461	0.737370	-3.746091	30441.156163
HLA A*3002	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.514888	0.768573	-3.746315	32725.617832
HLA A*6801	1:171-179	9	VRGPVTFAA	1.047952	-0.164687	-4.629590	0.883265	-3.746325	42617.670982
HLA B*3901	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.449593	0.703210	-3.746384	28157.449684
HLA B*4801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.442016	0.695627	-3.746389	27670.450352
HLA A*0101	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.396204	0.649772	-3.746432	24900.244959
HLA B*1501	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.396521	0.650029	-3.746492	24918.437122
HLA B*1502	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.614577	0.867880	-3.746696	41169.586312
HLA A*3002	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.273257	0.526478	-3.746780	18761.062008
HLA B*5701	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.412215	0.665274	-3.746941	25835.410105
HLA A*2902	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.341049	0.594015	-3.747035	21930.546745
HLA A*3201	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.545932	0.798809	-3.747122	35150.507503
HLA B*1509	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.536552	0.789406	-3.747147	34399.525783
HLA A*8001	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.425873	0.678719	-3.747154	26660.783988
HLA A*2301	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.535244	0.787998	-3.747246	34296.025426
HLA A*3301	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.515971	0.768573	-3.747398	32807.336036
HLA A*2402	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.593976	0.846543	-3.747433	39262.343523
HLA B*5701	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.426164	0.678719	-3.747445	26678.674742
HLA B*1509	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.469973	0.722436	-3.747536	29510.240550
HLA A*2602	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.582417	0.834835	-3.747581	38231.096343
HLA B*1503	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.426183	0.678487	-3.747696	26679.829396
HLA A*3201	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.608085	0.860349	-3.747736	40558.779343
HLA A*0212	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.414128	0.666384	-3.747744	25949.431073
HLA B*4402	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.413381	0.665274	-3.748106	25904.827483

HLA A*8001	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.434632	0.686428	-3.748204	27203.939243
HLA B*7301	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.569255	0.821048	-3.748207	37089.838080
HLA A*1101	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.384139	0.635887	-3.748252	24218.041220
HLA A*1101	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.485829	0.737370	-3.748460	30607.610348
HLA B*4001	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.414910	0.666384	-3.748526	25996.220926
HLA B*4001	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.398330	0.649772	-3.748558	25022.454226
HLA B*0702	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.414001	0.665274	-3.748727	25941.851468
HLA A*0202	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.486104	0.737370	-3.748734	30626.989783
HLA A*0301	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.361492	0.612666	-3.748827	22987.531010
HLA A*3002	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.539633	0.790719	-3.748914	34644.366990
HLA B*0802	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.486302	0.737370	-3.748932	30640.910790
HLA A*2603	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.646276	0.897326	-3.748949	44286.948250
HLA B*5801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.349818	0.600860	-3.748958	22377.817987
HLA B*0702	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.404314	0.655319	-3.748995	25369.624649
HLA A*2602	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.605341	0.856154	-3.749187	40303.306520
HLA A*6801	1:443-451	9	KPRKAFSPI	0.736033	0.187427	-4.672705	0.923460	-3.749245	47065.763857
HLA A*0250	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.548095	0.798809	-3.749286	35326.082223
HLA B*4601	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.407892	0.658550	-3.749342	25579.515096
HLA B*0702	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.452676	0.703210	-3.749466	28358.015858
HLA B*5301	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.580157	0.830606	-3.749551	38032.646583
HLA B*0801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.332302	0.582728	-3.749575	21493.261690
HLA A*3301	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.622421	0.872828	-3.749593	41920.015396
HLA B*5301	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.540594	0.790719	-3.749875	34721.107532
HLA B*5101	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.505572	0.755651	-3.749921	32031.121616
HLA B*0803	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.526121	0.776187	-3.749934	33583.096873
HLA B*0702	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.428455	0.678487	-3.749968	26819.766976
HLA A*6801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.275696	0.525631	-3.750065	18866.710448
HLA B*0801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.372751	0.622672	-3.750079	23591.255830
HLA A*6802	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.387424	0.637330	-3.750093	24401.897249
HLA B*5301	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.606255	0.856154	-3.750101	40388.211995
HLA A*0216	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.466719	0.716494	-3.750225	29289.955570
HLA A*6901	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.400264	0.649772	-3.750492	25134.111051
HLA B*4601	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.400332	0.649772	-3.750560	25138.054571
HLA A*2403	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.446201	0.695627	-3.750573	27938.343996
HLA A*0201	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.346923	0.595974	-3.750949	22229.166132
HLA A*0206	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.360503	0.609548	-3.750955	22935.235029
HLA B*3501	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.454191	0.703210	-3.750982	28457.140550
HLA B*4501	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-3.947088	0.196045	-3.751043	8852.945975
HLA A*2603	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.541775	0.790719	-3.751057	34815.718383
HLA A*3002	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.459022	0.707963	-3.751058	28775.428535
HLA A*8001	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.400849	0.649772	-3.751077	25167.991081
HLA A*3301	1:345-353	9	RDHLDTHGH	1.109634	-0.225157	-4.635569	0.884477	-3.751092	43208.496188
HLA A*3002	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.513053	0.761813	-3.751240	32587.639750
HLA A*1101	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.424654	0.673165	-3.751488	26586.032629
HLA A*6901	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.204497	0.452989	-3.751508	16013.910272
HLA B*5101	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.504442	0.752921	-3.751521	31947.879970
HLA A*3301	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.521020	0.769405	-3.751615	33190.975006
HLA A*0201	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.389040	0.637330	-3.751710	24492.890435
HLA A*0219	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.418390	0.666384	-3.752006	26205.340458
HLA A*2501	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.407385	0.655319	-3.752066	25549.641968
HLA B*3801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.521535	0.769461	-3.752074	33230.321839
HLA B*1503	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.507893	0.755651	-3.752242	32202.785376
HLA A*8001	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.446196	0.693953	-3.752243	27938.041711
HLA A*3201	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.466369	0.714055	-3.752314	29266.355227
HLA B*2705	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.448007	0.695627	-3.752380	28054.815332
HLA A*3101	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.353297	0.600860	-3.752437	22557.830260
HLA A*8001	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.429898	0.677348	-3.752549	26909.001565
HLA A*2601	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.402352	0.649772	-3.752580	25255.281976
HLA A*0101	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.375183	0.622434	-3.752749	23723.719323
HLA A*0206	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.439202	0.686428	-3.752773	27491.696739
HLA B*5101	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.436594	0.683810	-3.752783	27327.104415
HLA A*3301	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.614924	0.862113	-3.752811	41202.562500
HLA A*3101	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.365552	0.612666	-3.752887	23203.432664
HLA B*5701	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.402709	0.649772	-3.752938	25276.058015
HLA B*0803	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.439469	0.686428	-3.753041	27508.656850

HLA B*0702	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.411597	0.658550	-3.753047	25798.677599
HLA A*2601	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.390924	0.637857	-3.753067	24599.389369
HLA B*1509	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-3.992945	0.239809	-3.753136	9838.866373
HLA A*6901	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.359596	0.606197	-3.753400	22887.391248
HLA A*0212	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.412281	0.658550	-3.753731	25839.323869
HLA A*2601	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.393720	0.639976	-3.753744	24758.265387
HLA A*8001	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.432233	0.678487	-3.753746	27054.092591
HLA B*0803	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.494377	0.740545	-3.753832	31215.971127
HLA B*4601	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.349829	0.595974	-3.753855	22378.423303
HLA A*2301	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.540319	0.786321	-3.753997	34699.137516
HLA B*1503	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.460603	0.706599	-3.754004	28880.386662
HLA B*5401	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.528177	0.774156	-3.754021	33742.444451
HLA A*2402	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.588897	0.834835	-3.754061	38805.799190
HLA B*5301	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.600614	0.846543	-3.754071	39866.996103
HLA B*4001	1:380-388	9	WELLKFFND	0.942251	-0.784797	-3.911550	0.157454	-3.754096	8157.357649
HLA B*4402	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.427271	0.673165	-3.754105	26746.740227
HLA A*8001	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.420495	0.666384	-3.754111	26332.672932
HLA B*3901	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.277881	0.523691	-3.754190	18961.871771
HLA B*4501	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.404244	0.650029	-3.754214	25365.507578
HLA A*2501	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.427438	0.673165	-3.754272	26757.015680
HLA B*0702	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.431636	0.677348	-3.754288	27016.942772
HLA A*2902	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.148594	0.394299	-3.754295	14079.711132
HLA A*2603	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.522888	0.768573	-3.754315	33334.032219
HLA B*5801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.350342	0.595974	-3.754367	22404.830996
HLA B*0801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.309604	0.555221	-3.754383	20398.768619
HLA A*8001	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.409762	0.655319	-3.754444	25689.904953
HLA A*3301	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.585234	0.830606	-3.754628	38479.886721
HLA B*5401	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.433145	0.678487	-3.754658	27110.939773
HLA B*4601	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.404716	0.650029	-3.754687	25393.104721
HLA A*3002	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.448891	0.693953	-3.754938	28111.940225
HLA B*1517	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.450592	0.695627	-3.754964	28222.263855
HLA B*2705	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.432329	0.677348	-3.754981	27060.094002
HLA B*1801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.358126	0.603125	-3.755001	22810.012123
HLA A*0206	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.510671	0.755651	-3.755019	32409.365515
HLA B*1801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.450766	0.695627	-3.755138	28233.564387
HLA B*1503	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.516955	0.761813	-3.755142	32881.786202
HLA B*1509	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.439232	0.683810	-3.755422	27493.630258
HLA B*0702	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.449492	0.693953	-3.755539	28150.900312
HLA B*4402	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.458785	0.703210	-3.755575	28759.709970
HLA A*2603	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.617720	0.862113	-3.755607	41468.670694
HLA A*0202	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-3.750276	-0.005447	-3.755723	5626.990142
HLA A*3001	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-3.936167	0.180214	-3.755954	8633.112645
HLA B*7301	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.405743	0.649772	-3.755971	25453.208125
HLA B*5101	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.416950	0.660945	-3.756005	26118.580621
HLA B*1509	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.411337	0.655319	-3.756018	25783.190204
HLA A*0216	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.442460	0.686428	-3.756032	27698.757000
HLA A*0250	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.545478	0.789406	-3.756073	35113.825709
HLA B*4601	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.379036	0.622672	-3.756364	23935.137826
HLA A*2403	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.435219	0.678719	-3.756500	27240.756709
HLA A*6801	1:4-12	9	TETVRVRFC	0.906845	-0.011390	-4.652004	0.895455	-3.756549	44874.931551
HLA B*0803	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.509533	0.752921	-3.756612	32324.616276
HLA B*4403	1:376-384	9	LGDAWELLK	0.881918	0.032559	-4.671145	0.914477	-3.756668	46896.999099
HLA B*1517	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.494194	0.737370	-3.756824	31202.801660
HLA A*2403	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.449152	0.692320	-3.756832	28128.826450
HLA A*2301	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.266996	0.510101	-3.756895	18492.517626
HLA A*2603	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.551321	0.794424	-3.756897	35589.453432
HLA B*2705	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.473828	0.716494	-3.757335	29773.387824
HLA A*0301	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.367061	0.609548	-3.757513	23284.161750
HLA B*5801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.353906	0.596390	-3.757515	22589.459573
HLA A*1101	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.436244	0.678719	-3.757524	27305.085636
HLA A*2501	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.464207	0.706599	-3.757608	29121.055594
HLA A*0301	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.364039	0.606197	-3.757843	23122.733291
HLA A*0250	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.519667	0.761813	-3.757853	33087.709712
HLA B*0802	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.450315	0.692320	-3.757995	28204.253445
HLA A*0203	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.223002	0.464975	-3.758026	16710.980586

HLA B*0802	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.466054	0.707963	-3.758090	29245.146998
HLA B*1502	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.579193	0.821048	-3.758145	37948.381585
HLA A*0219	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.450472	0.692320	-3.758152	28214.478284
HLA A*0101	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.364598	0.606197	-3.758402	23152.524225
HLA A*1101	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.416959	0.658550	-3.758409	26119.145822
HLA B*2705	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.465643	0.707098	-3.758544	29217.472825
HLA A*2602	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.603412	0.844865	-3.758547	40124.695564
HLA B*4001	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.394486	0.635887	-3.758599	24801.968181
HLA B*3901	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.435964	0.677348	-3.758616	27287.512912
HLA A*6801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.437355	0.678719	-3.758636	27375.045478
HLA A*0212	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.381357	0.622672	-3.758685	24063.412938
HLA B*0801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.368308	0.609548	-3.758760	23351.145187
HLA B*4403	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.619214	0.860349	-3.758865	41611.597256
HLA A*3301	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.607803	0.848752	-3.759051	40532.457668
HLA A*3201	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.454783	0.695627	-3.759156	28495.962401
HLA B*3501	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.355236	0.595974	-3.759261	22658.734441
HLA A*0219	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.417814	0.658550	-3.759264	26170.630310
HLA B*0802	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.475952	0.716494	-3.759459	29919.352394
HLA A*0202	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.336588	0.577123	-3.759465	21706.399264
HLA A*0101	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.141066	0.381582	-3.759484	13837.766395
HLA A*0212	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.224492	0.464975	-3.759516	16768.395478
HLA B*2705	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.443367	0.683810	-3.759557	27756.658456
HLA A*0101	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.369112	0.609548	-3.759564	23394.389050
HLA B*0803	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.513880	0.754283	-3.759596	32649.754896
HLA B*0801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.269783	0.510101	-3.759682	18611.549449
HLA B*1502	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.594345	0.834602	-3.759743	39295.705262
HLA B*5701	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.415084	0.655319	-3.759765	26006.630124
HLA B*4001	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.372476	0.612666	-3.759811	23576.328304
HLA A*2902	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.425095	0.665274	-3.759821	26613.085952
HLA A*1101	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.454062	0.693953	-3.760109	28448.674561
HLA B*3901	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.485324	0.725139	-3.760186	30572.030532
HLA A*6801	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.662522	0.902312	-3.760211	45975.074694
HLA B*5401	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.549618	0.789406	-3.760212	35450.138945
HLA A*2602	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.603656	0.843357	-3.760299	40147.277212
HLA A*2501	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.444173	0.683810	-3.760363	27808.211304
HLA A*3301	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.620737	0.860349	-3.760387	41757.727199
HLA B*1517	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.446936	0.686428	-3.760508	27985.691938
HLA B*5801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.354526	0.594015	-3.760511	22621.745131
HLA A*2603	1:83-91	9	GPYRQSQRA	1.285016	-0.382704	-4.662847	0.902312	-3.760535	46009.410878
HLA B*3801	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.482972	0.722436	-3.760536	30406.921306
HLA B*5101	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.483019	0.722436	-3.760583	30410.211445
HLA B*4801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.419210	0.658550	-3.760660	26254.864223
HLA A*0212	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.383166	0.622434	-3.760733	24163.860912
HLA A*0301	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.361640	0.600860	-3.760780	22995.367025
HLA B*7301	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.410881	0.650029	-3.760852	25756.144464
HLA A*0203	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.357327	0.596390	-3.760936	22768.094809
HLA B*1503	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.152527	0.391537	-3.760990	14207.798283
HLA A*0212	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.411031	0.650029	-3.761002	25765.063632
HLA A*2602	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.559902	0.798809	-3.761092	36299.583131
HLA A*6801	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.629959	0.868794	-3.761164	42653.883788
HLA A*0250	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.538582	0.777400	-3.761182	34560.690488
HLA A*0219	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.357707	0.596390	-3.761317	22788.057560
HLA A*2601	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.367540	0.606197	-3.761343	23309.872740
HLA B*1503	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.286978	0.525631	-3.761347	19363.257070
HLA B*2705	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.469399	0.707963	-3.761436	29471.312349
HLA A*0301	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.343173	0.581735	-3.761438	22038.061645
HLA A*2403	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.383902	0.622434	-3.761468	24204.812126
HLA B*5701	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.399465	0.637857	-3.761608	25087.922806
HLA A*0211	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.514542	0.752921	-3.761621	32699.603009
HLA B*5101	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.440374	0.678719	-3.761655	27566.011791
HLA B*1502	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.439023	0.677348	-3.761675	27480.395808
HLA B*1501	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.324401	0.562720	-3.761681	21105.760634
HLA A*2902	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.428110	0.666384	-3.761726	26798.446935
HLA B*3801	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.553983	0.791821	-3.762162	35808.265493
HLA B*3901	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.411952	0.649772	-3.762180	25819.760976

HLA B*1503	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.420739	0.658550	-3.762189	26347.492612
HLA B*4801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.440689	0.678487	-3.762202	27586.002331
HLA A*2402	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.476352	0.714055	-3.762297	29946.881315
HLA A*2301	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.536484	0.774156	-3.762329	34394.129376
HLA A*0203	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.412544	0.650029	-3.762515	25854.984856
HLA B*4801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.384999	0.622434	-3.762565	24266.040917
HLA B*1517	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.470692	0.707963	-3.762728	29559.133030
HLA B*1517	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.423982	0.660945	-3.763037	26544.929773
HLA B*1503	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.503732	0.740545	-3.763187	31895.726570
HLA A*0216	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.357266	0.594015	-3.763251	22764.892540
HLA A*2603	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.606894	0.843615	-3.763279	40447.686587
HLA A*2403	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.441864	0.678487	-3.763377	27660.721948
HLA A*0211	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.519042	0.755651	-3.763390	33040.129731
HLA A*0250	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.466608	0.703210	-3.763399	29282.509112
HLA B*5101	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.488700	0.725139	-3.763562	30810.624037
HLA B*5801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.346308	0.582728	-3.763580	22197.681032
HLA B*4402	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.441039	0.677348	-3.763690	27608.247640
HLA A*2301	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.525543	0.761813	-3.763729	33538.433115
HLA B*0802	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.366894	0.603125	-3.763769	23275.219971
HLA B*5101	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.490160	0.726109	-3.764051	30914.307663
HLA A*0301	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.360503	0.596390	-3.764113	22935.235029
HLA B*1502	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.425173	0.660945	-3.764228	26617.837513
HLA A*0219	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.217218	0.452989	-3.764228	16489.880280
HLA A*0202	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.478407	0.714055	-3.764353	30088.975507
HLA B*0802	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.448184	0.683810	-3.764373	28066.200649
HLA B*7301	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.553793	0.789406	-3.764387	35792.577712
HLA A*2601	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.360362	0.595974	-3.764388	22927.791612
HLA A*2402	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.540596	0.776187	-3.764409	34721.295370
HLA B*1509	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.401753	0.637330	-3.764423	25220.465786
HLA B*2705	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.478494	0.714055	-3.764440	30094.998896
HLA B*0802	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.437679	0.673165	-3.764514	27395.490352
HLA B*4002	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.540302	0.775701	-3.764601	34697.823512
HLA A*0202	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.274716	0.510101	-3.764616	18824.196560
HLA B*4801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.377330	0.612666	-3.764665	23841.315037
HLA B*3501	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.471293	0.706599	-3.764695	29600.098769
HLA A*2602	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.540448	0.775701	-3.764747	34709.463569
HLA A*0206	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.341912	0.577123	-3.764789	21974.131549
HLA A*2403	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.404767	0.639976	-3.764792	25396.127126
HLA B*1517	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.458770	0.693953	-3.764818	28758.776464
HLA A*3201	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.556688	0.791821	-3.764867	36031.931408
HLA B*3901	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.387572	0.622672	-3.764900	24410.215395
HLA A*0216	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.423547	0.658550	-3.764997	26518.376114
HLA A*2402	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.534483	0.769405	-3.765077	34235.963866
HLA B*1501	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-3.896165	0.131008	-3.765157	7873.450039
HLA B*4801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.402505	0.637330	-3.765175	25264.164375
HLA B*4601	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.405212	0.639976	-3.765236	25422.107159
HLA B*4402	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.374809	0.609548	-3.765261	23703.321609
HLA A*0101	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.361405	0.595974	-3.765431	22982.930151
HLA A*0203	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.444227	0.678719	-3.765508	27811.671624
HLA B*4601	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.402874	0.637330	-3.765543	25285.631674
HLA A*3201	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.610418	0.844865	-3.765553	40777.248198
HLA A*2602	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.534960	0.769405	-3.765554	34273.582711
HLA A*0202	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.556274	0.790719	-3.765556	35997.640274
HLA A*8001	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.305885	0.540290	-3.765594	20224.822421
HLA A*6802	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.371818	0.606197	-3.765622	23540.642648
HLA A*3301	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.368795	0.603125	-3.765670	23377.309546
HLA A*2601	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.388403	0.622672	-3.765732	24457.008209
HLA A*2402	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.275891	0.510101	-3.765790	18875.183896
HLA A*0250	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.560386	0.794424	-3.765961	36340.059285
HLA A*3301	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.633849	0.867880	-3.765969	43037.727213
HLA B*4403	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.633863	0.867880	-3.765983	43039.124212
HLA B*7301	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.506552	0.740545	-3.766007	32103.462953
HLA A*0211	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.552334	0.786321	-3.766013	35672.532835
HLA B*3801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.543573	0.777400	-3.766172	34960.104072
HLA B*5701	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.406238	0.639976	-3.766262	25482.279210

HLA A*8001	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.446147	0.679867	-3.766280	27934.867915
HLA B*7301	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.601006	0.834602	-3.766404	39903.030275
HLA A*2501	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.460366	0.693953	-3.766413	28864.610764
HLA B*0802	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.403762	0.637330	-3.766432	25337.392131
HLA A*3002	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.153584	0.387024	-3.766560	14242.428595
HLA A*0301	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.360694	0.594015	-3.766679	22945.287475
HLA B*4403	1:454-462	9	AATGTTVSP	0.728010	0.134103	-4.628803	0.862113	-3.766689	42540.504375
HLA A*0201	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.376329	0.609548	-3.766781	23786.433303
HLA A*0216	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.462492	0.695627	-3.766865	29006.276958
HLA B*5701	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.402817	0.635887	-3.766930	25282.348868
HLA B*4001	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.360950	0.594015	-3.766935	22958.821794
HLA B*4601	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.389569	0.622434	-3.767135	24522.721947
HLA A*2902	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.422560	0.655319	-3.767241	26458.190696
HLA A*3002	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.544644	0.777400	-3.767244	35046.453948
HLA A*0211	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.461235	0.693953	-3.767282	28922.445735
HLA B*5401	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.447159	0.679867	-3.767292	28000.078587
HLA A*0250	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.493439	0.726109	-3.767331	31148.662695
HLA B*1501	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.114930	0.347215	-3.767716	13029.577203
HLA B*0803	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.445096	0.677348	-3.767748	27867.396859
HLA B*4002	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.611365	0.843615	-3.767750	40866.247138
HLA B*5401	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.544003	0.776187	-3.767816	34994.732053
HLA A*2402	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.559697	0.791821	-3.767876	36282.502376
HLA B*0803	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.493059	0.725139	-3.767920	31121.375902
HLA B*3901	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.460246	0.692320	-3.767926	28856.647991
HLA A*3201	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.434329	0.666384	-3.767945	27184.960898
HLA B*4402	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.179710	0.411532	-3.768178	15125.520342
HLA A*6801	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.602961	0.834602	-3.768359	40083.039732
HLA B*3801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.544564	0.776187	-3.768378	35040.008228
HLA B*1502	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.560350	0.791821	-3.768530	36337.110470
HLA A*0219	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.433868	0.665274	-3.768594	27156.150920
HLA B*4801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.391321	0.622672	-3.768650	24621.890168
HLA A*0203	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.418472	0.649772	-3.768700	26210.302808
HLA B*2705	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.461052	0.692320	-3.768732	28910.243866
HLA B*5101	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.434204	0.665274	-3.768930	27177.167431
HLA A*3201	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.612309	0.843357	-3.768952	40955.218760
HLA A*2301	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.495192	0.726109	-3.769083	31274.625769
HLA B*0702	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.365423	0.595974	-3.769449	23196.529651
HLA A*2603	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.561288	0.791821	-3.769467	36415.630500
HLA B*4601	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.407420	0.637857	-3.769563	25551.715363
HLA B*1801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.447004	0.677348	-3.769656	27990.082868
HLA B*2705	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.365712	0.595974	-3.769738	23211.970138
HLA B*1509	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.456294	0.686428	-3.769866	28595.259885
HLA B*3901	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.477007	0.707098	-3.769909	29992.116041
HLA B*3801	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.539353	0.769405	-3.769948	34622.070927
HLA A*0203	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.382297	0.612321	-3.769976	24115.541479
HLA A*1101	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.462370	0.692320	-3.770050	28998.118227
HLA A*0203	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-3.950565	0.180214	-3.770351	8924.112813
HLA A*2902	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.371308	0.600860	-3.770448	23513.023421
HLA A*0301	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.347609	0.577123	-3.770486	22264.309021
HLA B*4001	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.410472	0.639976	-3.770496	25731.911079
HLA A*8001	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.366476	0.595974	-3.770501	23252.817647
HLA A*3002	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.558541	0.787998	-3.770544	36186.058900
HLA A*0301	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.237397	0.466843	-3.770554	17274.171590
HLA A*2301	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.294574	0.523921	-3.770654	19704.902771
HLA A*0219	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.420683	0.650029	-3.770654	26344.071946
HLA A*3001	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.294358	0.523691	-3.770667	19695.097888
HLA A*6801	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.615535	0.844865	-3.770671	41260.557615
HLA B*3501	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.408026	0.637330	-3.770696	25587.404106
HLA B*1501	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.408085	0.637330	-3.770755	25590.864965
HLA B*3801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.546531	0.775701	-3.770830	35199.031855
HLA B*1801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.525122	0.754283	-3.770839	33505.971217
HLA B*4403	1:96-104	9	DVLARLLAA	1.127174	-0.243179	-4.654842	0.883995	-3.770847	45169.156137
HLA B*4801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.420941	0.650029	-3.770912	26359.753647
HLA A*0202	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.429512	0.658550	-3.770962	26885.137900
HLA A*2501	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.448365	0.677348	-3.771016	28077.894382

HLA A*2601	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.380587	0.609548	-3.771039	24020.751630
HLA A*0211	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.511599	0.740545	-3.771053	32478.695339
HLA B*1509	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.437463	0.666384	-3.771079	27381.858740
HLA B*1501	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.353948	0.582728	-3.771220	22591.659396
HLA B*2705	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.457723	0.686428	-3.771294	28689.470629
HLA B*4501	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.570110	0.798809	-3.771301	37162.947336
HLA B*1509	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.383982	0.612666	-3.771316	24209.264677
HLA A*8001	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.409224	0.637857	-3.771368	25658.098345
HLA A*2301	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.525658	0.754283	-3.771374	33547.324814
HLA A*6801	1:89-97	9	QRAEIYRDV	0.611829	0.260999	-4.644253	0.872828	-3.771425	44081.143113
HLA B*1502	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.606266	0.834835	-3.771431	40389.304489
HLA B*4001	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.367413	0.595974	-3.771439	23303.064128
HLA B*3901	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.334198	0.562720	-3.771478	21587.301683
HLA A*0216	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.426824	0.655319	-3.771506	26719.261941
HLA A*2402	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.548984	0.777400	-3.771583	35398.395787
HLA A*6801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.463906	0.692320	-3.771586	29100.897238
HLA B*1509	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.451550	0.679867	-3.771684	28284.625816
HLA A*6901	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.348904	0.577123	-3.771781	22330.774575
HLA A*2603	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.632188	0.860349	-3.771839	42873.431274
HLA A*2402	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.497986	0.726109	-3.771877	31476.443751
HLA A*3301	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.616921	0.844865	-3.772057	41392.464891
HLA B*5301	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.562291	0.790220	-3.772072	36499.848667
HLA B*3901	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.438487	0.666384	-3.772103	27446.520880
HLA B*2705	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.438847	0.666384	-3.772463	27469.248127
HLA A*2301	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.486741	0.714055	-3.772686	30671.924329
HLA A*3301	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.616118	0.843357	-3.772761	41315.952097
HLA B*3501	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.378977	0.606197	-3.772781	23931.900883
HLA A*0206	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.466883	0.693953	-3.772930	29301.049549
HLA A*1101	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.368905	0.595974	-3.772931	23383.254328
HLA B*0801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.385257	0.612321	-3.772937	24280.485639
HLA A*1101	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.480355	0.707098	-3.773257	30224.221536
HLA A*2603	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.641241	0.867880	-3.773361	43776.477043
HLA B*0702	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.423441	0.650029	-3.773412	26511.921134
HLA B*3901	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.467370	0.693953	-3.773417	29333.880623
HLA A*0212	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.336412	0.562720	-3.773692	21697.593859
HLA B*0803	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.487883	0.714055	-3.773828	30752.673247
HLA A*6801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.439206	0.665274	-3.773932	27491.994194
HLA B*4601	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.386312	0.612321	-3.773991	24339.535604
HLA A*2902	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.414278	0.639976	-3.774302	25958.417175
HLA B*3901	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.469938	0.695627	-3.774310	29507.845940
HLA A*0203	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.138890	0.364577	-3.774313	13768.618655
HLA B*5101	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.452930	0.678487	-3.774443	28374.589382
HLA A*0216	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.482432	0.707963	-3.774469	30369.110277
HLA B*0702	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.454382	0.679867	-3.774515	28469.613231
HLA B*4002	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.182962	0.408334	-3.774628	15239.194472
HLA A*1101	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.491135	0.716494	-3.774641	30983.791469
HLA B*1517	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.491384	0.716494	-3.774890	31001.564165
HLA B*5301	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-3.912532	0.137558	-3.774974	8175.825029
HLA B*4002	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.643985	0.868794	-3.775191	44053.965447
HLA B*1509	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.109536	0.334311	-3.775225	12868.736429
HLA B*4001	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.278102	0.502859	-3.775243	18971.516895
HLA B*0702	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.352419	0.577123	-3.775296	22512.235177
HLA B*1501	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.376202	0.600860	-3.775342	23779.485492
HLA B*5801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.357101	0.581735	-3.775366	22756.273284
HLA B*1503	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.469338	0.693953	-3.775386	29467.167291
HLA B*1502	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.543963	0.768573	-3.775390	34991.513801
HLA A*2603	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.549564	0.774156	-3.775408	35445.728249
HLA A*0211	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.489478	0.714055	-3.775424	30865.845225
HLA A*0203	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.213989	0.438531	-3.775458	16367.762330
HLA A*2402	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.569908	0.794424	-3.775484	37145.661278
HLA B*7301	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.551220	0.775701	-3.775520	35581.175390
HLA B*0802	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.482143	0.706599	-3.775544	30348.908896
HLA B*2705	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.434141	0.658550	-3.775591	27173.198034
HLA A*6901	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.369607	0.594015	-3.775593	23421.108679
HLA A*2902	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.033309	0.257713	-3.775596	10797.151981

HLA A*2403	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.436612	0.660945	-3.775668	27328.287133
HLA B*5701	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.425744	0.650029	-3.775715	26652.852414
HLA B*3801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.537607	0.761813	-3.775794	34483.185180
HLA A*8001	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.353044	0.577123	-3.775921	22544.654291
HLA B*1801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.479216	0.703210	-3.776006	30145.023282
HLA A*2402	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.564175	0.787998	-3.776178	36658.555740
HLA A*2603	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.575023	0.798809	-3.776213	37585.724236
HLA B*2705	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.398743	0.622434	-3.776310	25046.290464
HLA B*4002	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.449565	0.673165	-3.776400	28155.621799
HLA A*8001	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.441701	0.665274	-3.776427	27650.398616
HLA A*0216	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.426470	0.650029	-3.776441	26697.444068
HLA A*0203	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.379637	0.603125	-3.776513	23968.309320
HLA B*0803	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.514040	0.737370	-3.776670	32661.768052
HLA B*2705	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.303258	0.526478	-3.776780	20102.866697
HLA A*3101	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.386359	0.609548	-3.776811	24342.169230
HLA B*5101	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.454208	0.677348	-3.776859	28458.218221
HLA A*0212	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.414250	0.637330	-3.776920	25956.732044
HLA B*5801	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.354066	0.577123	-3.776943	22597.771141
HLA B*0802	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.454328	0.677348	-3.776979	28466.071050
HLA A*2402	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.551345	0.774156	-3.777189	35591.378834
HLA B*1801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-3.974671	0.197447	-3.777224	9433.454691
HLA B*4001	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.380601	0.603125	-3.777476	24021.531340
HLA A*1101	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.485442	0.707963	-3.777478	30580.301215
HLA A*3002	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.287693	0.510101	-3.777592	19395.128205
HLA A*6801	1:295-303	9	HDLFGLDEM	0.942327	-0.093575	-4.626385	0.848752	-3.777633	42304.348842
HLA B*2705	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.456442	0.678719	-3.777723	28605.007469
HLA A*2301	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.484944	0.707098	-3.777845	30545.248879
HLA A*2602	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.532189	0.754283	-3.777906	34055.672596
HLA A*0206	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.515285	0.737370	-3.777915	32755.551606
HLA B*3501	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.340206	0.562255	-3.777951	21887.995663
HLA B*4002	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.438910	0.660945	-3.777966	27473.260771
HLA A*0201	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.384275	0.606197	-3.778079	24225.641394
HLA A*2603	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.486210	0.707963	-3.778247	30634.446678
HLA B*2705	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.458115	0.679867	-3.778248	28715.401886
HLA A*0301	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.361180	0.582728	-3.778452	22970.997080
HLA B*3501	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.437005	0.658550	-3.778455	27352.988071
HLA B*0702	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.388027	0.609548	-3.778480	24435.847816
HLA A*0202	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.472444	0.693953	-3.778492	29678.668154
HLA A*0101	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.374981	0.596390	-3.778590	23712.684418
HLA B*0803	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.486570	0.707963	-3.778606	30659.813706
HLA A*6802	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.288790	0.510101	-3.778689	19444.190360
HLA A*2403	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.384928	0.606197	-3.778732	24262.102938
HLA B*5301	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.533068	0.754283	-3.778785	34124.647143
HLA B*4402	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.385065	0.606197	-3.778868	24269.716940
HLA A*3002	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.036589	0.257713	-3.778876	10879.002977
HLA B*1801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.439843	0.660945	-3.778898	27532.329216
HLA A*3001	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.291673	0.512773	-3.778900	19573.688938
HLA A*2402	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.516441	0.737370	-3.779071	32842.852057
HLA B*4002	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.640033	0.860662	-3.779371	43654.917625
HLA B*4501	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.648181	0.868794	-3.779387	44481.680571
HLA B*5101	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.452692	0.673165	-3.779527	28359.089775
HLA A*0101	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.362348	0.582728	-3.779620	23032.842647
HLA A*0201	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.392043	0.612321	-3.779722	24662.817066
HLA B*2705	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.417098	0.637330	-3.779767	26127.483952
HLA A*0301	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.166863	0.387024	-3.779839	14684.641215
HLA A*2902	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.438410	0.658550	-3.779860	27441.621390
HLA A*2602	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.520466	0.740545	-3.779920	33148.626005
HLA A*2602	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.574346	0.794424	-3.779922	37527.209467
HLA A*2603	1:348-356	9	LDTHGHHIA	1.233621	-0.388756	-4.624893	0.844865	-3.780029	42159.270909
HLA B*4402	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.438673	0.658550	-3.780123	27458.253515
HLA B*1503	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.453301	0.673165	-3.780135	28398.853285
HLA B*1801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.517719	0.737370	-3.780349	32939.650271
HLA B*4402	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.416348	0.635887	-3.780461	26082.433210
HLA B*4601	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.390318	0.609548	-3.780770	24565.078687
HLA B*5301	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.568790	0.787998	-3.780792	37050.130272

HLA A*2602	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.549461	0.768573	-3.780888	35437.291925
HLA A*2602	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.458357	0.677348	-3.781008	28731.407100
HLA A*6801	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.556824	0.775701	-3.781123	36043.239049
HLA B*4801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.417126	0.635887	-3.781239	26129.180168
HLA A*3201	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.555710	0.774156	-3.781554	35950.932225
HLA A*3301	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.637733	0.856154	-3.781579	43424.320087
HLA B*0803	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.454793	0.673165	-3.781627	28496.579048
HLA B*4501	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.642324	0.860662	-3.781662	43885.790032
HLA B*1509	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.543568	0.761813	-3.781755	34959.725814
HLA B*4001	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.394096	0.612321	-3.781775	24779.704980
HLA B*0802	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.485165	0.703210	-3.781955	30560.785992
HLA B*5101	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.489957	0.707963	-3.781994	30899.928113
HLA B*1502	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.522566	0.740545	-3.782021	33309.335694
HLA A*3201	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.616891	0.834835	-3.782055	41389.553921
HLA A*2402	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.536383	0.754283	-3.782100	34386.129364
HLA A*6801	1:146-154	9	AYLAEGRQP	0.600807	0.296519	-4.679436	0.897326	-3.782110	47800.934385
HLA A*0201	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.376134	0.594015	-3.782120	23775.755097
HLA A*0201	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.385448	0.603125	-3.782323	24291.127704
HLA B*1501	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.392097	0.609548	-3.782549	24665.885988
HLA B*4801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.422532	0.639976	-3.782556	26456.473121
HLA A*2301	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.523149	0.740545	-3.782604	33354.055240
HLA A*2602	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.613315	0.830606	-3.782709	41050.157676
HLA B*2705	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.395057	0.612321	-3.782736	24834.594365
HLA A*0101	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.376839	0.594015	-3.782824	23814.373687
HLA A*3101	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.422995	0.639976	-3.783019	26484.684089
HLA B*3901	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.433112	0.650029	-3.783083	27108.886511
HLA B*0803	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.477110	0.693953	-3.783158	29999.256068
HLA B*4001	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.392762	0.609548	-3.783214	24703.678348
HLA B*3901	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.448562	0.665274	-3.783288	28090.656739
HLA B*4403	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.536318	0.752921	-3.783396	34380.921054
HLA A*2403	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.438849	0.655319	-3.783530	27469.396733
HLA B*2705	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.204638	0.421060	-3.783579	16019.109125
HLA A*6901	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.346397	0.562720	-3.783677	22202.244807
HLA A*8001	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.406236	0.622434	-3.783802	25482.141354
HLA B*5101	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.434026	0.650029	-3.783996	27165.995793
HLA A*0211	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.378054	0.594015	-3.784039	23881.073644
HLA A*2501	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.470581	0.686428	-3.784153	29551.618138
HLA A*6901	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.346474	0.562255	-3.784219	22206.208846
HLA A*0202	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.393842	0.609548	-3.784294	24765.231219
HLA B*5101	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.491510	0.707098	-3.784412	31010.622100
HLA A*3201	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.573923	0.789406	-3.784518	37490.684006
HLA A*0301	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.169086	0.384545	-3.784541	14759.986247
HLA A*0216	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.450935	0.666384	-3.784551	28244.563841
HLA B*0803	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.463209	0.678487	-3.784722	29054.177291
HLA B*3501	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.397115	0.612321	-3.784794	24952.566387
HLA B*4601	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.391058	0.606197	-3.784862	24606.976097
HLA B*4001	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.422351	0.637330	-3.785021	26445.454669
HLA A*3301	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.619884	0.834835	-3.785049	41675.804268
HLA B*1502	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.575869	0.790719	-3.785150	37658.996020
HLA A*1101	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.388276	0.603125	-3.785152	24449.864529
HLA B*4402	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.388286	0.603125	-3.785161	24450.393619
HLA A*2301	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.540866	0.755651	-3.785215	34742.903502
HLA B*5401	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.554688	0.769405	-3.785283	35866.428303
HLA B*0803	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.480914	0.695627	-3.785287	30263.161905
HLA B*0801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.031712	0.246392	-3.785319	10757.505202
HLA A*0219	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.379391	0.594015	-3.785376	23954.698267
HLA B*3901	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-3.891649	0.106226	-3.785424	7792.007571
HLA A*0203	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.379466	0.594015	-3.785451	23958.845578
HLA B*1501	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.379499	0.594015	-3.785484	23960.660253
HLA B*3801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.541139	0.755651	-3.785487	34764.713154
HLA B*4801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.392045	0.606197	-3.785848	24662.950489
HLA A*6901	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.381837	0.595974	-3.785862	24089.984399
HLA B*1509	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.511009	0.725139	-3.785870	32434.623026
HLA B*1509	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.502403	0.716494	-3.785909	31798.211315
HLA B*1517	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.392191	0.606197	-3.785994	24671.224154

HLA B*2705	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.464508	0.678487	-3.786021	29141.227912
HLA A*2902	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.311681	0.525631	-3.786050	20496.556147
HLA B*5701	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.423392	0.637330	-3.786062	26508.909347
HLA A*0203	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.426047	0.639976	-3.786071	26671.459284
HLA B*4002	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.642230	0.856154	-3.786076	43876.294369
HLA B*4501	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.577910	0.791821	-3.786090	37836.455061
HLA B*4001	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.382955	0.596390	-3.786564	24152.098633
HLA B*1801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.424494	0.637857	-3.786637	26576.254158
HLA A*3201	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.436502	0.649772	-3.786730	27321.339395
HLA B*0802	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.473187	0.686428	-3.786759	29729.447971
HLA B*0801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.389916	0.603125	-3.786792	24542.364260
HLA A*3002	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.500854	0.714055	-3.786800	31685.048811
HLA A*2602	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.452204	0.665274	-3.786929	28327.196460
HLA A*0219	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.409394	0.622434	-3.786960	25668.094430
HLA A*6901	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-3.714423	-0.072551	-3.786974	5181.112389
HLA B*0702	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.427106	0.639976	-3.787130	26736.613362
HLA B*0803	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.490533	0.703210	-3.787324	30940.910737
HLA A*2602	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.622081	0.834602	-3.787479	41887.144808
HLA B*4601	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.383888	0.596390	-3.787497	24204.026466
HLA B*5301	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.556220	0.768573	-3.787647	35993.161459
HLA A*3301	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.622269	0.834602	-3.787667	41905.277116
HLA B*4402	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.427926	0.639976	-3.787950	26787.141144
HLA A*3001	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.246661	0.458535	-3.788126	17646.608415
HLA B*5401	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.557966	0.769461	-3.788505	36138.128842
HLA A*2602	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.410942	0.622434	-3.788508	25759.767503
HLA B*5401	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.484429	0.695627	-3.788802	30509.081345
HLA B*7301	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.236927	0.448098	-3.788829	17255.491427
HLA A*0211	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.514987	0.726109	-3.788878	32733.054440
HLA A*2403	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.371734	0.582728	-3.789006	23536.058413
HLA B*0803	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.495695	0.706599	-3.789096	31310.853879
HLA B*5401	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.544841	0.755651	-3.789190	35062.383751
HLA A*3001	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.170825	0.381582	-3.789243	14819.193599
HLA B*1502	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.385276	0.595974	-3.789302	24281.536500
HLA B*0802	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.469190	0.679867	-3.789323	29457.125913
HLA B*1801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.469240	0.679867	-3.789373	29460.472659
HLA A*0212	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.395689	0.606197	-3.789492	24870.761471
HLA B*0702	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.395776	0.606197	-3.789579	24875.740247
HLA B*4501	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.558410	0.768573	-3.789837	36175.097857
HLA A*6802	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.367044	0.577123	-3.789921	23283.280013
HLA A*6801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.412359	0.622434	-3.789925	25843.937281
HLA B*5801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.352198	0.562255	-3.789942	22500.789950
HLA B*0702	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.371691	0.581735	-3.789957	23533.766630
HLA A*0211	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.352893	0.562720	-3.790173	22536.849941
HLA A*8001	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.255267	0.464975	-3.790292	17999.788918
HLA B*1509	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.527685	0.737370	-3.790316	33704.314548
HLA A*0216	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.440153	0.649772	-3.790381	27551.997222
HLA A*3001	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.293277	0.502859	-3.790419	19646.146605
HLA A*8001	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.440604	0.650029	-3.790575	27580.630314
HLA A*0202	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.387191	0.596390	-3.790801	24388.831604
HLA B*1517	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.483156	0.692320	-3.790836	30419.754863
HLA B*1502	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.580283	0.789406	-3.790878	38043.758836
HLA A*6802	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.440917	0.650029	-3.790888	27600.482139
HLA A*0219	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.440748	0.649772	-3.790976	27589.733513
HLA A*8001	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.430978	0.639976	-3.791002	26976.049325
HLA A*2602	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.577328	0.786321	-3.791007	37785.725725
HLA A*2501	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.470875	0.679867	-3.791008	29571.608769
HLA B*1517	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.428885	0.637857	-3.791028	26846.331953
HLA A*0250	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.581799	0.790719	-3.791080	38176.739786
HLA A*3301	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.637693	0.846543	-3.791150	43420.326618
HLA B*4501	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.581378	0.790220	-3.791159	38139.788464
HLA A*2601	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.394286	0.603125	-3.791162	24790.565851
HLA A*6801	1:7-15	9	VRVRFCPSP	0.669607	0.198273	-4.659189	0.867880	-3.791308	45623.492145
HLA A*3002	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.590210	0.798809	-3.791400	38923.330520
HLA A*6901	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.373228	0.581735	-3.791493	23617.178156
HLA A*1101	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.452478	0.660945	-3.791534	28345.132033

HLA B*4001	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.392456	0.600860	-3.791596	24686.310715
HLA B*5101	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.498545	0.706599	-3.791946	31516.997462
HLA B*3801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.545022	0.752921	-3.792101	35076.992432
HLA A*2301	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.545062	0.752921	-3.792141	35080.218545
HLA A*6801	1:357-365	9	LDEAAFAAA	1.202039	-0.358682	-4.635527	0.843357	-3.792170	43204.288835
HLA B*4403	1:81-89	9	PYGPYRQSQ	1.093382	-0.224588	-4.661012	0.868794	-3.792217	45815.425533
HLA B*4501	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.627146	0.834835	-3.792311	42378.565102
HLA B*4402	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.405127	0.612666	-3.792461	25417.156533
HLA B*4402	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.393368	0.600860	-3.792508	24738.182616
HLA B*0802	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.428535	0.635887	-3.792648	26824.700557
HLA B*1509	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.442695	0.650029	-3.792666	27713.745775
HLA B*4001	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.442730	0.650029	-3.792701	27715.994790
HLA B*1509	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.470123	0.677348	-3.792775	29520.459736
HLA B*0801	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.370007	0.577123	-3.792884	23442.658539
HLA B*4403	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.591904	0.798809	-3.793094	39075.448619
HLA B*1502	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.569342	0.776187	-3.793155	37097.262944
HLA A*2501	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.454236	0.660945	-3.793291	28460.065750
HLA B*3901	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.500121	0.706599	-3.793523	31631.613189
HLA A*3301	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.563092	0.769461	-3.793631	36567.244719
HLA B*1517	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.376414	0.582728	-3.793686	23791.066305
HLA B*5101	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.489387	0.695627	-3.793759	30859.333661
HLA B*0803	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.500967	0.707098	-3.793869	31693.277684
HLA A*0203	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.431220	0.637330	-3.793890	26991.085070
HLA A*3101	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.400212	0.606197	-3.794015	25131.119829
HLA B*0702	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.416527	0.622434	-3.794093	26093.159248
HLA A*2601	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.395038	0.600860	-3.794178	24833.519569
HLA B*1503	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.029494	0.235091	-3.794403	10702.707362
HLA B*5401	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.189409	0.394899	-3.794510	15467.103729
HLA B*5401	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.547532	0.752921	-3.794610	35280.245540
HLA B*4402	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.417297	0.622672	-3.794626	26139.501192
HLA B*5301	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.568783	0.774156	-3.794627	37049.528965
HLA A*2603	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.650782	0.856154	-3.794628	44748.869379
HLA A*8001	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.404218	0.609548	-3.794670	25363.998152
HLA B*4402	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.084627	0.289933	-3.794694	12151.409758
HLA B*1501	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.159392	0.364577	-3.794815	14434.175376
HLA B*4501	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.651111	0.856154	-3.794957	44782.774316
HLA A*2603	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.629576	0.834602	-3.794974	42616.287664
HLA A*6901	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.395917	0.600860	-3.795057	24883.816058
HLA B*1502	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.503115	0.707963	-3.795151	31850.377572
HLA B*5801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.357900	0.562720	-3.795180	22798.168834
HLA B*1502	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.468392	0.673165	-3.795226	29402.993386
HLA B*1509	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.142462	0.347179	-3.795283	13882.305223
HLA A*6802	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.445078	0.649772	-3.795306	27866.190809
HLA A*3201	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.549609	0.754283	-3.795325	35449.371828
HLA B*1501	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.248463	0.452989	-3.795474	17719.983111
HLA A*3301	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.590088	0.794424	-3.795663	38912.382373
HLA B*4601	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.377415	0.581735	-3.795680	23845.958729
HLA A*2402	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.582109	0.786321	-3.795788	38204.011737
HLA A*0206	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.445867	0.650029	-3.795838	27916.889883
HLA B*4801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.377589	0.581735	-3.795854	23855.506935
HLA A*3001	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.160416	0.364340	-3.796076	14468.261618
HLA B*1509	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.491722	0.695627	-3.796095	31025.724538
HLA B*7301	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.564669	0.768573	-3.796096	36700.226338
HLA A*0211	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.418531	0.622434	-3.796097	26213.847918
HLA B*0702	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.358353	0.562255	-3.796098	22821.985029
HLA A*3201	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.564765	0.768573	-3.796192	36708.367551
HLA A*0301	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.320186	0.523921	-3.796265	20901.912834
HLA B*4501	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.565839	0.769461	-3.796378	36799.234638
HLA B*1502	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.322012	0.525631	-3.796381	20989.958607
HLA B*4403	1:249-257	9	TVLGEGTKK	0.662472	0.198190	-4.657154	0.860662	-3.796492	45410.247638
HLA A*3301	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.513253	0.716494	-3.796759	32602.628315
HLA B*1509	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.446605	0.649772	-3.796833	27964.352750
HLA B*4402	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.390863	0.594015	-3.796848	24595.929533
HLA B*7301	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.452220	0.655319	-3.796901	28328.269209
HLA B*7301	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.573322	0.776187	-3.797135	37438.797910

HLA A*0202	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.552874	0.755651	-3.797223	35716.946884
HLA B*0702	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.400358	0.603125	-3.797233	25139.550550
HLA A*0250	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.589125	0.791821	-3.797304	38826.168236
HLA B*0801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.393706	0.596390	-3.797316	24757.461763
HLA A*0101	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.264233	0.466843	-3.797390	18375.241135
HLA B*5701	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.406997	0.609548	-3.797449	25526.845723
HLA B*1801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.522648	0.725139	-3.797510	33315.643284
HLA A*0250	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.573752	0.776187	-3.797565	37475.881037
HLA B*0802	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.379391	0.581735	-3.797656	23954.698267
HLA B*1801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.145206	0.347463	-3.797743	13970.301768
HLA B*3901	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.410587	0.612666	-3.797922	25738.733116
HLA A*0201	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.398830	0.600860	-3.797970	25051.304379
HLA A*3002	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.535354	0.737370	-3.797984	34304.746806
HLA A*2501	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.476629	0.678487	-3.798142	29966.004517
HLA B*3801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.506225	0.707963	-3.798262	32079.331039
HLA A*0211	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.246436	0.448098	-3.798338	17637.446039
HLA A*2301	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.523522	0.725139	-3.798384	33382.757819
HLA A*3101	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.381155	0.582728	-3.798427	24052.220028
HLA B*7301	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.586484	0.787998	-3.798486	38590.793705
HLA A*3101	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.375704	0.577123	-3.798581	23752.228516
HLA A*1101	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.477233	0.678487	-3.798746	30007.696473
HLA B*0803	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.482632	0.683810	-3.798822	30383.078438
HLA A*2603	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.629446	0.830606	-3.798841	42603.609333
HLA A*0101	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.399747	0.600860	-3.798887	25104.214840
HLA A*1101	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.465398	0.666384	-3.799014	29201.038866
HLA A*0206	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.402190	0.603125	-3.799065	25245.856384
HLA A*0101	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.349637	0.550534	-3.799103	22368.498192
HLA B*0702	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.393187	0.594015	-3.799172	24727.879788
HLA A*8001	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.412013	0.612666	-3.799348	25823.392964
HLA A*2403	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.395398	0.595974	-3.799423	24854.083106
HLA B*1503	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.252060	0.452486	-3.799575	17867.359066
HLA A*3001	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.191152	0.391537	-3.799616	15529.315594
HLA A*2602	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.507626	0.707963	-3.799662	32182.931160
HLA B*0802	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.466073	0.666384	-3.799688	29246.412729
HLA A*1101	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.465008	0.665274	-3.799734	29174.826890
HLA B*0803	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.460685	0.660945	-3.799741	28885.855569
HLA A*2301	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.537328	0.737370	-3.799958	34460.992849
HLA B*0801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.340307	0.540290	-3.800017	21893.087956
HLA B*5701	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.406285	0.606197	-3.800089	25485.036485
HLA A*2603	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.569532	0.769405	-3.800127	37113.522564
HLA A*2602	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.483992	0.683810	-3.800182	30478.397346
HLA A*2501	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.450336	0.650029	-3.800307	28205.626715
HLA B*5101	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.503587	0.703210	-3.800377	31885.030118
HLA B*7301	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.586712	0.786321	-3.800390	38611.049895
HLA A*3201	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.594970	0.794424	-3.800546	39352.293687
HLA B*4501	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.576496	0.775701	-3.800795	37713.431500
HLA B*3801	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.555099	0.754283	-3.800816	35900.400227
HLA A*2501	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.438163	0.637330	-3.800833	27426.037923
HLA A*0202	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.587858	0.786321	-3.801537	38713.118740
HLA B*7301	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.518078	0.716494	-3.801585	32966.926136
HLA A*0216	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.493940	0.692320	-3.801620	31184.576185
HLA A*2602	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.437519	0.635887	-3.801632	27385.414159
HLA A*2902	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.451503	0.649772	-3.801732	28281.565648
HLA B*3801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.570416	0.768573	-3.801843	37189.092694
HLA B*1502	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.600703	0.798809	-3.801893	39875.192635
HLA A*0201	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.398337	0.596390	-3.801947	25022.860335
HLA A*3002	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.497586	0.695627	-3.801959	31447.508766
HLA A*3201	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.414285	0.612321	-3.801964	25958.838475
HLA B*4801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.414330	0.612321	-3.802009	25961.506866
HLA B*0803	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.452020	0.649772	-3.802249	28315.245716
HLA A*3301	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.594080	0.791821	-3.802259	39271.690452
HLA A*0301	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.365010	0.562720	-3.802289	23174.453807
HLA B*3801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.542873	0.740545	-3.802327	34903.788653
HLA A*1101	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.479772	0.677348	-3.802424	30183.698323
HLA B*1502	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.588868	0.786321	-3.802547	38803.280051

HLA A*2402	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.498312	0.695627	-3.802685	31500.122139
HLA A*2902	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.315536	0.512773	-3.802763	20679.327036
HLA B*1517	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.475962	0.673165	-3.802796	29919.999842
HLA A*2602	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.592212	0.789406	-3.802806	39103.151028
HLA B*4501	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.528113	0.725139	-3.802975	33737.516153
HLA B*0801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.440440	0.637330	-3.803109	27570.187721
HLA A*2402	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.497135	0.693953	-3.803182	31414.861238
HLA B*0802	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.461735	0.658550	-3.803185	28955.792463
HLA B*7301	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.572617	0.769405	-3.803212	37378.085267
HLA B*0702	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.441182	0.637857	-3.803325	27617.359955
HLA A*2403	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.406562	0.603125	-3.803438	25501.310483
HLA B*0801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-3.969770	0.166266	-3.803504	9327.596314
HLA A*2603	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.573190	0.769461	-3.803729	37427.457402
HLA A*3001	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.256228	0.452486	-3.803743	18039.660149
HLA A*0201	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.381078	0.577123	-3.803955	24047.926457
HLA A*0212	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.400407	0.596390	-3.804016	25142.406758
HLA B*4601	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.407166	0.603125	-3.804041	25536.790673
HLA A*0211	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.459456	0.655319	-3.804138	28804.242249
HLA B*0802	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.453912	0.649772	-3.804140	28438.826399
HLA A*3002	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.442040	0.637857	-3.804183	27671.947334
HLA A*0301	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.366595	0.562255	-3.804340	23259.234085
HLA B*5701	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.400318	0.595974	-3.804343	25137.238619
HLA B*1517	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.481758	0.677348	-3.804409	30321.994623
HLA A*0219	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.185030	0.380458	-3.804572	15311.916709
HLA B*4001	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.410886	0.606197	-3.804689	25756.423141
HLA A*0250	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.469992	0.665274	-3.804717	29511.517755
HLA B*1502	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.460154	0.655319	-3.804835	28850.560293
HLA B*1517	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.483628	0.678719	-3.804909	30452.850922
HLA B*3801	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.483731	0.678719	-3.805012	30460.100633
HLA B*1509	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.512153	0.707098	-3.805055	32520.188470
HLA B*5801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.355612	0.550534	-3.805078	22678.355931
HLA A*0206	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.521574	0.716494	-3.805081	33233.378110
HLA B*0802	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.483602	0.678487	-3.805115	30451.038764
HLA B*4402	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.401116	0.595974	-3.805142	25183.517657
HLA A*0212	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.414746	0.609548	-3.805198	25986.378223
HLA A*3001	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.220342	0.415126	-3.805216	16608.955352
HLA B*5701	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.387976	0.582728	-3.805248	24432.939694
HLA A*6901	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.315379	0.510101	-3.805278	20671.832912
HLA B*4002	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.636023	0.830606	-3.805417	43253.634111
HLA B*4403	1:230-238	9	QALIRIGVA	1.048756	-0.205141	-4.649140	0.843615	-3.805525	44579.970517
HLA B*1801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.315973	0.510101	-3.805873	20700.145861
HLA A*2601	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.383108	0.577123	-3.805985	24160.593038
HLA B*0803	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.471312	0.665274	-3.806038	29601.379862
HLA B*4002	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.604871	0.798809	-3.806061	40259.722818
HLA A*2301	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.522580	0.716494	-3.806086	33310.416910
HLA A*3201	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.418815	0.612666	-3.806150	26231.013031
HLA B*1503	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.418571	0.612321	-3.806250	26216.258867
HLA B*0801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.369271	0.562720	-3.806551	23402.996785
HLA B*0802	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.429345	0.622672	-3.806674	26874.813244
HLA B*4402	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.429463	0.622434	-3.807029	26882.083715
HLA B*0801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.332732	0.525631	-3.807101	21514.550764
HLA B*0803	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.443078	0.635887	-3.807191	27738.194865
HLA B*4601	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.408066	0.600860	-3.807206	25589.757439
HLA A*2403	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.416771	0.609548	-3.807223	26107.844133
HLA B*4501	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.584747	0.777400	-3.807347	38436.819252
HLA B*4002	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.628455	0.821048	-3.807407	42506.457374
HLA B*4001	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.384531	0.577123	-3.807408	24239.930932
HLA B*0801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.429853	0.622434	-3.807419	26906.235788
HLA B*5401	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.484800	0.677348	-3.807452	30535.170511
HLA B*0801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.408449	0.600860	-3.807589	25612.332745
HLA B*5301	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.597181	0.789406	-3.807775	39553.135412
HLA B*1501	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.189428	0.381582	-3.807846	15467.773146
HLA B*4002	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.642932	0.834835	-3.808097	43947.324202
HLA B*5801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.363348	0.555221	-3.808127	23085.985644
HLA B*4601	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.370458	0.562255	-3.808203	23467.021049

HLA A*6901	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.391046	0.582728	-3.808319	24606.310500
HLA B*1517	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.458120	0.649772	-3.808348	28715.712582
HLA A*0206	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.370672	0.562255	-3.808416	23478.576705
HLA B*5101	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.448412	0.639976	-3.808436	28080.932513
HLA A*2902	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.458582	0.650029	-3.808553	28746.332614
HLA A*0206	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.504259	0.695627	-3.808631	31934.401724
HLA A*8001	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.411943	0.603125	-3.808818	25819.202253
HLA A*2602	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.048896	0.239809	-3.809087	11191.690670
HLA A*6802	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.371395	0.562255	-3.809140	23517.730397
HLA A*6801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.188432	0.379131	-3.809301	15432.333937
HLA A*2501	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.475776	0.666384	-3.809392	29907.215328
HLA A*3301	1:184-192	9	DFALTRASG	0.793377	-0.725463	-3.877369	0.067914	-3.809455	7539.962675
HLA A*2601	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.403522	0.594015	-3.809507	25323.414595
HLA B*2705	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.464943	0.655319	-3.809624	29170.407912
HLA B*0702	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.447042	0.637330	-3.809711	27992.505745
HLA B*2705	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.404058	0.594015	-3.810043	25354.669152
HLA B*4501	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.550612	0.740545	-3.810067	35531.355336
HLA B*1801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.488776	0.678487	-3.810289	30815.958324
HLA A*2501	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.406316	0.595974	-3.810341	25486.828874
HLA B*4402	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.373202	0.562720	-3.810482	23615.772768
HLA B*1801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.517146	0.706599	-3.810547	32896.198191
HLA B*4002	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.645475	0.834602	-3.810873	44205.324231
HLA A*0203	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.191571	0.380458	-3.811113	15544.276910
HLA B*5801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.351740	0.540290	-3.811449	22477.065744
HLA A*0250	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.505405	0.693953	-3.811453	32018.820757
HLA A*0250	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.548991	0.737370	-3.811621	35398.970296
HLA A*0211	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.498063	0.686428	-3.811635	31482.063627
HLA A*2902	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.393375	0.581735	-3.811640	24738.584112
HLA A*6801	1:269-277	9	AHRDRGFIP	0.775084	0.085265	-4.672092	0.860349	-3.811743	46999.354785
HLA A*2501	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.434491	0.622672	-3.811819	27195.110458
HLA B*4801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.408165	0.595974	-3.812190	25595.572485
HLA B*3801	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.526248	0.714055	-3.812193	33592.909071
HLA B*1501	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.374483	0.562255	-3.812227	23685.504013
HLA B*4002	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.604102	0.791821	-3.812282	40188.564969
HLA A*2601	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.394037	0.581735	-3.812302	24776.353820
HLA B*4501	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.203896	0.391537	-3.812359	15991.747452
HLA A*0301	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.367629	0.555221	-3.812408	23314.665178
HLA B*7301	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.603283	0.790719	-3.812564	40112.758482
HLA B*1503	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.462692	0.650029	-3.812663	29019.618288
HLA B*1509	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.409086	0.596390	-3.812695	25649.910011
HLA B*7301	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.110123	0.297408	-3.812715	12886.152813
HLA B*4403	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.567122	0.754283	-3.812838	36908.092891
HLA A*3101	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.338735	0.525631	-3.813104	21813.995358
HLA B*2705	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.453237	0.639976	-3.813261	28394.705452
HLA B*7301	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.587579	0.774156	-3.813423	38688.204152
HLA B*5101	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.505854	0.692320	-3.813534	32051.922545
HLA B*4501	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.634625	0.821048	-3.813577	43114.629518
HLA B*0802	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.474611	0.660945	-3.813666	29827.072718
HLA A*6802	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.339346	0.525631	-3.813715	21844.699884
HLA B*1501	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.390861	0.577123	-3.813738	24595.796472
HLA B*4601	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.407892	0.594015	-3.813878	25579.515096
HLA A*6801	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.670071	0.856154	-3.813918	46781.197949
HLA B*0801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.395675	0.581735	-3.813940	24869.954196
HLA B*4001	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.376320	0.562255	-3.814065	23785.918581
HLA B*1502	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.528139	0.714055	-3.814084	33739.523891
HLA A*3201	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.521199	0.707098	-3.814100	33204.624333
HLA B*0802	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.410106	0.595974	-3.814131	25710.203981
HLA B*1502	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.520778	0.706599	-3.814179	33172.485530
HLA A*0101	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.396128	0.581735	-3.814394	24895.934690
HLA A*2602	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.591963	0.777400	-3.814562	39080.733823
HLA B*5701	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.157028	0.342354	-3.814675	14355.832941
HLA B*1517	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.396410	0.581735	-3.814675	24912.102047
HLA B*0803	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.493402	0.678719	-3.814683	31145.966638
HLA B*3801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.552073	0.737370	-3.814703	35651.117992
HLA A*0250	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.601086	0.786321	-3.814765	39910.370563

HLA B*3901	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.417946	0.603125	-3.814821	26178.560002
HLA B*5801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.338747	0.523921	-3.814826	21814.585422
HLA A*2402	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.338754	0.523921	-3.814833	21814.939469
HLA A*2902	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.411224	0.596390	-3.814833	25776.495831
HLA B*0803	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.531367	0.716494	-3.814873	33991.250511
HLA A*2602	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.605695	0.790719	-3.814977	40336.243470
HLA A*2603	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.507381	0.692320	-3.815061	32164.829219
HLA B*5301	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.590880	0.775701	-3.815179	38983.389516
HLA A*0201	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.397961	0.582728	-3.815233	25001.210362
HLA A*0206	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.421522	0.606197	-3.815325	26395.000217
HLA A*2403	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.452657	0.637330	-3.815327	28356.788575
HLA B*4403	1:204-212	9	DALMKITHV	0.852595	-0.031547	-4.636502	0.821048	-3.815454	43301.395924
HLA B*1503	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.452941	0.637330	-3.815611	28375.356909
HLA A*0301	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.366182	0.550534	-3.815648	23237.098567
HLA A*3201	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.606654	0.790719	-3.815936	40425.373359
HLA B*0802	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.471399	0.655319	-3.816080	29607.305642
HLA A*0301	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.196603	0.380458	-3.816145	15725.451415
HLA B*4501	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.650763	0.834602	-3.816161	44746.932729
HLA A*8001	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.398008	0.581735	-3.816273	25003.915584
HLA B*5701	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.417429	0.600860	-3.816569	26147.421453
HLA A*2601	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.399310	0.582728	-3.816582	25078.966695
HLA A*3002	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.602904	0.786321	-3.816583	40077.835795
HLA B*3801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.519841	0.703210	-3.816631	33100.958427
HLA A*0250	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.489920	0.673165	-3.816754	30897.253585
HLA B*1517	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.472139	0.655319	-3.816820	29657.802913
HLA A*2902	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.197313	0.380458	-3.816855	15751.164445
HLA A*6901	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.340911	0.523691	-3.817220	21923.547995
HLA A*0201	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.398960	0.581735	-3.817225	25058.759351
HLA B*1509	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.482683	0.665274	-3.817409	30386.694773
HLA B*4601	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.400343	0.582728	-3.817616	25138.734550
HLA B*4801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.420751	0.603125	-3.817626	26348.205307
HLA A*6802	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.380375	0.562720	-3.817655	24009.059012
HLA B*1503	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.510010	0.692320	-3.817690	32360.134912
HLA A*0101	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.379964	0.562255	-3.817709	23986.339658
HLA A*2402	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.579602	0.761813	-3.817789	37984.120001
HLA B*4801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.380772	0.562720	-3.818052	24031.019842
HLA A*3301	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.103432	0.285370	-3.818062	12689.132839
HLA A*1101	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.473394	0.655319	-3.818075	29743.604646
HLA B*3901	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.176985	0.358727	-3.818258	15030.897783
HLA B*3901	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.496776	0.678487	-3.818289	31388.869506
HLA A*0216	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.497147	0.678719	-3.818428	31415.711004
HLA B*4601	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.395555	0.577123	-3.818432	24863.093414
HLA B*7301	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.424679	0.606197	-3.818483	26587.614778
HLA A*3201	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.574175	0.755651	-3.818523	37512.392076
HLA B*1801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.483799	0.665274	-3.818525	30464.879795
HLA B*4002	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.571489	0.752921	-3.818568	37281.149757
HLA A*2602	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.556030	0.737370	-3.818660	35977.392674
HLA A*2603	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.502673	0.683810	-3.818863	31818.000321
HLA A*3002	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.415307	0.596390	-3.818917	26019.999392
HLA B*4801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.428471	0.609548	-3.818924	26820.782639
HLA A*0219	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.414955	0.595974	-3.818980	25998.893160
HLA B*0803	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.511427	0.692320	-3.819107	32465.871323
HLA A*0101	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.322138	0.502859	-3.819280	20996.091383
HLA A*3001	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.292984	0.473598	-3.819386	19632.865662
HLA A*2501	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.455338	0.635887	-3.819451	28532.367395
HLA A*3201	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.588875	0.769405	-3.819470	38803.909820
HLA A*3002	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.572450	0.752921	-3.819529	37363.731022
HLA B*0801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.459522	0.639976	-3.819546	28808.605757
HLA B*4402	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.332349	0.512773	-3.819576	21495.587339
HLA B*5701	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.413602	0.594015	-3.819587	25918.004204
HLA B*1501	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.284605	0.464975	-3.819630	19257.744986
HLA A*2501	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.469519	0.649772	-3.819748	29479.444734
HLA A*0212	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.396925	0.577123	-3.819802	24941.634542
HLA B*4403	1:234-242	9	RIGVAERIP	0.716991	0.139163	-4.676180	0.856154	-3.820026	47443.858265
HLA B*4501	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.650719	0.830606	-3.820113	44742.333523

HLA A*0202	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-3.931652	0.111406	-3.820246	8543.812275
HLA B*1503	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.333153	0.512773	-3.820380	21535.394904
HLA A*3002	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.560933	0.740545	-3.820388	36385.894964
HLA A*0206	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.528365	0.707963	-3.820401	33757.051042
HLA B*5301	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.596648	0.776187	-3.820461	39504.592201
HLA A*0216	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.416985	0.596390	-3.820594	26120.700187
HLA B*5301	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.089241	0.268538	-3.820703	12281.207086
HLA B*0802	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.433387	0.612666	-3.820721	27126.050702
HLA B*5301	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.590198	0.769461	-3.820737	38922.277680
HLA A*0219	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.458084	0.637330	-3.820754	28713.382444
HLA A*2301	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.516504	0.695627	-3.820877	32847.649664
HLA B*3501	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.470694	0.649772	-3.820922	29559.292942
HLA A*0201	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.383671	0.562720	-3.820951	24191.982883
HLA A*0250	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.561629	0.740545	-3.821083	36444.207363
HLA A*3002	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.433781	0.612666	-3.821116	27150.715729
HLA A*2301	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.524532	0.703210	-3.821323	33460.504932
HLA A*0202	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-3.904802	0.083388	-3.821414	8031.594671
HLA A*0301	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.347224	0.525631	-3.821593	22244.564401
HLA B*3901	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.431173	0.609548	-3.821625	26988.164853
HLA A*2301	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.515640	0.693953	-3.821687	32782.320327
HLA A*0212	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.425062	0.603125	-3.821938	26611.070394
HLA B*5101	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.434672	0.612666	-3.822006	27206.441253
HLA B*3901	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.480656	0.658550	-3.822106	30245.158024
HLA B*1509	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.516185	0.693953	-3.822232	32823.491061
HLA A*6901	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.372807	0.550534	-3.822273	23594.319055
HLA B*5401	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.545100	0.722436	-3.822663	35083.255158
HLA A*1101	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.404596	0.581735	-3.822861	25386.099619
HLA A*2902	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.432531	0.609548	-3.822983	27072.686652
HLA A*3002	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.481631	0.658550	-3.823081	30313.137831
HLA B*5301	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.592576	0.769405	-3.823171	39135.954055
HLA A*3001	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.271357	0.448098	-3.823259	18679.131757
HLA A*6801	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.526473	0.703210	-3.823264	33610.360058
HLA B*3501	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.145018	0.321711	-3.823306	13964.256853
HLA B*3801	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.530460	0.707098	-3.823362	33920.343457
HLA B*0802	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.473452	0.650029	-3.823423	29747.627658
HLA A*2501	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.461357	0.637857	-3.823500	28930.583175
HLA A*0201	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.385901	0.562255	-3.823646	24316.503525
HLA B*1517	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.463643	0.639976	-3.823667	29083.270125
HLA B*4402	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.436058	0.612321	-3.823737	27293.418448
HLA A*8001	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.386080	0.562255	-3.823824	24326.503349
HLA A*2902	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.149327	0.325371	-3.823956	14103.496138
HLA A*0201	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.002451	0.178488	-3.823963	10056.597732
HLA B*7301	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.585835	0.761813	-3.824022	38533.215652
HLA B*4501	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.235922	0.411532	-3.824390	17215.583720
HLA A*2402	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.580149	0.755651	-3.824498	38032.029331
HLA B*0803	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.504386	0.679867	-3.824519	31943.732212
HLA B*2705	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.474557	0.650029	-3.824527	29823.361643
HLA B*1502	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.577476	0.752921	-3.824555	37798.606165
HLA B*7301	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.518673	0.693953	-3.824720	33012.078926
HLA A*0203	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-3.819351	-0.005447	-3.824798	6597.068801
HLA B*5701	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.421228	0.596390	-3.824838	26377.156998
HLA B*1509	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.428093	0.603125	-3.824968	26797.432118
HLA A*2301	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.532951	0.707963	-3.824987	34115.417863
HLA A*6801	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.655617	0.830606	-3.825011	45249.867003
HLA A*0203	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.233015	0.407915	-3.825101	17100.761094
HLA A*2402	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.491508	0.666384	-3.825124	31010.454336
HLA A*0211	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.520846	0.695627	-3.825219	33177.690263
HLA A*6802	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.212504	0.387024	-3.825480	16311.895693
HLA A*3201	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.532175	0.706599	-3.825577	34054.567189
HLA B*5301	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.603146	0.777400	-3.825746	40100.174133
HLA A*2603	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.563132	0.737370	-3.825762	36570.607894
HLA A*3201	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.578836	0.752921	-3.825915	37917.189338
HLA A*0202	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.566494	0.740545	-3.825949	36854.819835
HLA B*5801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.352430	0.526478	-3.825953	22512.844129
HLA A*3002	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.491308	0.665274	-3.826034	30996.197749

HLA B*7301	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.503439	0.677348	-3.826090	31874.164818
HLA A*8001	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.463491	0.637330	-3.826160	29073.045000
HLA A*0101	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.403287	0.577123	-3.826164	25309.718613
HLA B*0802	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.403344	0.577123	-3.826221	25313.004973
HLA A*0212	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.438654	0.612321	-3.826333	27457.065172
HLA B*4501	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.462231	0.635887	-3.826344	28988.863984
HLA B*5701	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.408160	0.581735	-3.826425	25595.295549
HLA B*7301	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.580727	0.754283	-3.826444	38082.677295
HLA A*0301	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.366882	0.540290	-3.826592	23274.590398
HLA A*2902	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.293590	0.466843	-3.826746	19660.287394
HLA A*0203	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.115809	0.288865	-3.826944	13055.966616
HLA B*4601	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.389865	0.562720	-3.827145	24539.443462
HLA B*5401	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.552292	0.725139	-3.827153	35669.059284
HLA B*4403	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.117111	0.289933	-3.827178	13095.155070
HLA A*1101	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.467308	0.639976	-3.827332	29329.754894
HLA B*0702	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.423780	0.596390	-3.827389	26532.582604
HLA B*0803	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.465530	0.637857	-3.827673	29209.886772
HLA B*1503	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.428666	0.600860	-3.827806	26832.828432
HLA A*3002	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.534414	0.706599	-3.827816	34230.593117
HLA A*2602	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.589641	0.761813	-3.827828	38872.405704
HLA A*3002	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.501052	0.673165	-3.827886	31699.450742
HLA A*2902	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.465267	0.637330	-3.827936	29192.193640
HLA A*0219	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.434134	0.606197	-3.827937	27172.757025
HLA B*1509	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.437752	0.609548	-3.828204	27400.085141
HLA B*0702	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.440569	0.612321	-3.828248	27578.392282
HLA B*3501	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.410082	0.581735	-3.828347	25708.813125
HLA B*3901	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.465864	0.637330	-3.828533	29232.334552
HLA A*2603	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.663582	0.834835	-3.828747	46087.384395
HLA B*4403	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.604497	0.775701	-3.828796	40225.107407
HLA A*2402	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.535918	0.707098	-3.828820	34349.316104
HLA A*0101	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.384054	0.555221	-3.828833	24213.325070
HLA B*5401	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.535570	0.706599	-3.828972	34321.824865
HLA B*3801	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.554387	0.725139	-3.829249	35841.600625
HLA A*2601	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.391589	0.562255	-3.829334	24637.079845
HLA B*7301	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.585001	0.755651	-3.829350	38459.283218
HLA A*2501	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.469397	0.639976	-3.829421	29471.152913
HLA B*5701	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.391824	0.562255	-3.829569	24650.411838
HLA B*4002	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.599281	0.769461	-3.829820	39744.895157
HLA B*1509	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.452511	0.622672	-3.829840	28347.278931
HLA A*1101	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.479996	0.650029	-3.829967	30199.214904
HLA A*3201	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.567354	0.737370	-3.829984	36927.865386
HLA A*3002	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.272959	0.442758	-3.830201	18748.176536
HLA B*0802	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.452756	0.622434	-3.830322	28363.232405
HLA A*0206	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.295523	0.464975	-3.830548	19748.016809
HLA B*5801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.356232	0.525631	-3.830601	22710.768543
HLA B*2705	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.295650	0.464975	-3.830675	19753.786720
HLA A*0101	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.393457	0.562720	-3.830737	24743.268710
HLA A*6802	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.212363	0.381582	-3.830782	16306.601819
HLA B*1517	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.480888	0.650029	-3.830859	30261.361035
HLA A*0219	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.212580	0.381582	-3.830998	16314.719795
HLA A*2402	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.088823	0.257713	-3.831109	12269.386464
HLA A*0201	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.356779	0.525631	-3.831148	22739.413611
HLA B*4402	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.413989	0.582728	-3.831261	25941.149765
HLA A*3201	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.469244	0.637857	-3.831388	29460.791416
HLA B*1501	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.355374	0.523921	-3.831454	22665.967889
HLA B*4001	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.121452	0.289933	-3.831519	13226.730171
HLA A*0202	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.517996	0.686428	-3.831568	32960.684568
HLA B*5101	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.469477	0.637857	-3.831620	29476.574224
HLA A*6801	1:400-408	9	KELGPDGAA	1.015651	-0.169108	-4.678238	0.846543	-3.831695	47669.231300
HLA B*4403	1:436-444	9	LIEGLALKP	0.728591	0.106011	-4.666352	0.834602	-3.831750	46382.281147
HLA B*1509	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.467698	0.635887	-3.831811	29356.106064
HLA A*0202	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.435010	0.603125	-3.831885	27227.643982
HLA A*2301	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.538500	0.706599	-3.831902	34554.147175
HLA A*0219	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.435043	0.603125	-3.831918	27229.706240
HLA B*4001	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.355908	0.523921	-3.831987	22693.819812

HLA B*4402	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.428377	0.596390	-3.831987	26814.979368
HLA A*3201	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.618347	0.786321	-3.832026	41528.612999
HLA A*0211	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.540126	0.707963	-3.832163	34683.748014
HLA A*0202	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.585107	0.752921	-3.832186	38468.647079
HLA A*0250	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.585231	0.752921	-3.832310	38479.678549
HLA B*4002	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.620539	0.787998	-3.832542	41738.755517
HLA A*3001	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.154383	0.321711	-3.832672	14268.649689
HLA A*0216	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.445078	0.612321	-3.832757	27866.190809
HLA A*6801	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.667816	0.834835	-3.832980	46538.869907
HLA A*2603	1:333-341	9	RMLDVGDFT	0.912031	-0.136330	-4.608700	0.775701	-3.833000	40616.307751
HLA B*5401	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.245028	0.412011	-3.833017	17580.383985
HLA A*0211	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.499506	0.666384	-3.833122	31586.810585
HLA B*5101	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.488451	0.655319	-3.833133	30792.960803
HLA B*5101	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.455624	0.622434	-3.833191	28551.205158
HLA B*5701	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.300114	0.466843	-3.833271	19957.878846
HLA B*3901	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.429775	0.596390	-3.833385	26901.432745
HLA B*0702	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.434279	0.600860	-3.833419	27181.872653
HLA A*0202	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.101905	0.268381	-3.833524	12644.590778
HLA B*1501	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.048196	0.214632	-3.833564	11173.662555
HLA B*5801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.230892	0.397240	-3.833651	17017.333312
HLA B*1517	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.429627	0.595974	-3.833653	26892.265679
HLA B*4403	1:418-426	9	TSVTDWTAP	0.685195	0.106626	-4.625485	0.791821	-3.833664	42216.785505
HLA B*3801	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.529307	0.695627	-3.833679	33830.361916
HLA A*3101	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.430102	0.596390	-3.833712	26921.669546
HLA B*4801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.430107	0.596390	-3.833716	26921.960834
HLA A*2402	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.248954	0.415126	-3.833828	17740.029839
HLA B*4801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.434723	0.600860	-3.833863	27209.679490
HLA A*2601	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.357961	0.523921	-3.834040	22801.375784
HLA B*4403	1:316-324	9	PARFDQKKA	1.207624	-0.372789	-4.668892	0.834835	-3.834056	46654.323598
HLA B*5101	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.456736	0.622672	-3.834064	28624.357751
HLA B*3801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.550833	0.716494	-3.834339	35549.428676
HLA B*4403	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.514225	0.679867	-3.834358	32675.730062
HLA A*0211	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.550889	0.716494	-3.834395	35554.044619
HLA A*2501	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.456900	0.622434	-3.834466	28635.199626
HLA A*1101	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.484269	0.649772	-3.834498	30497.859958
HLA B*1501	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.351317	0.516619	-3.834697	22455.188679
HLA B*0801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.351357	0.516619	-3.834737	22457.253936
HLA A*0219	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.444298	0.609548	-3.834750	27816.185732
HLA A*0301	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.358520	0.523691	-3.834829	22830.752686
HLA A*2602	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.604323	0.769461	-3.834862	40209.007240
HLA A*2601	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.390086	0.555221	-3.834864	24551.925668
HLA A*2403	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.397602	0.562720	-3.834882	24980.525097
HLA A*0216	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.444528	0.609548	-3.834980	27830.936925
HLA B*7301	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.508204	0.673165	-3.835038	32225.789770
HLA A*2603	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.500345	0.665274	-3.835070	31647.874102
HLA B*5101	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.493829	0.658550	-3.835279	31176.648053
HLA A*0211	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.199864	0.364577	-3.835287	15843.977112
HLA A*2601	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.398135	0.562720	-3.835415	25011.221146
HLA B*1502	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.612913	0.777400	-3.835513	41012.200103
HLA B*5801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.352146	0.516619	-3.835527	22498.112120
HLA A*3101	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.386141	0.550534	-3.835607	24329.925286
HLA A*0212	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.436528	0.600860	-3.835668	27322.965303
HLA B*4501	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.531311	0.695627	-3.835683	33986.837464
HLA B*4403	1:212-220	9	VLRGEDLLP	0.739933	0.090673	-4.666298	0.830606	-3.835692	46376.510277
HLA B*5301	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.561854	0.726109	-3.835745	36463.139554
HLA B*1502	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.597632	0.761813	-3.835819	39594.240547
HLA A*0203	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.436779	0.600860	-3.835919	27338.786003
HLA B*4002	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.626643	0.790719	-3.835925	42329.531136
HLA B*4601	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.302856	0.466843	-3.836013	20084.278315
HLA B*0803	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.491409	0.655319	-3.836091	31003.409085
HLA A*2402	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.448555	0.612321	-3.836234	28090.200841
HLA B*7301	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.544280	0.707963	-3.836317	35017.078664
HLA A*2301	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.515240	0.678719	-3.836521	32752.184905
HLA A*8001	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.303458	0.466843	-3.836614	20112.112937
HLA B*4501	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.550873	0.714055	-3.836818	35552.698240

HLA A*1101	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.449490	0.612666	-3.836824	28150.748020
HLA A*3101	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.312165	0.475212	-3.836953	20519.411004
HLA A*0203	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.232026	0.394899	-3.837128	17061.857348
HLA A*2402	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.577744	0.740545	-3.837199	37821.924789
HLA A*3301	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.636016	0.798809	-3.837206	43252.932124
HLA A*0211	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.495932	0.658550	-3.837382	31327.966767
HLA B*4002	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.632005	0.794424	-3.837581	42855.343730
HLA B*4002	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.614992	0.777400	-3.837592	41209.027145
HLA A*2403	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.393060	0.555221	-3.837839	24720.656989
HLA B*2705	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.419670	0.581735	-3.837935	26282.718025
HLA A*3002	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.593692	0.755651	-3.838040	39236.650937
HLA A*3002	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.296625	0.458535	-3.838090	19798.185847
HLA A*0250	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.524547	0.686428	-3.838118	33461.591056
HLA A*3301	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.624705	0.786321	-3.838384	42141.028699
HLA B*0803	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.504823	0.666384	-3.838439	31975.891430
HLA B*5801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.351291	0.512773	-3.838518	22453.852438
HLA A*0301	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.365066	0.526478	-3.838588	23177.462912
HLA B*1801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.478579	0.639976	-3.838603	30100.860649
HLA A*6901	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.364413	0.525631	-3.838782	23142.631384
HLA B*5701	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.415946	0.577123	-3.838823	26058.315741
HLA A*3001	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.247352	0.408334	-3.839018	17674.697808
HLA B*0803	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.433112	0.594015	-3.839097	27108.886511
HLA A*2601	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.362850	0.523691	-3.839159	23059.523586
HLA A*6801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.494506	0.655319	-3.839187	31225.260630
HLA B*1801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.488989	0.649772	-3.839218	30831.132753
HLA A*0201	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.394820	0.555221	-3.839599	24821.028479
HLA A*6901	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.278203	0.438531	-3.839672	18975.930662
HLA A*3201	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.601574	0.761813	-3.839761	39955.305261
HLA A*1101	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-3.767230	-0.072551	-3.839781	5850.999191
HLA A*2301	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.523649	0.683810	-3.839839	33392.511483
HLA A*3101	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.402606	0.562720	-3.839886	25270.042141
HLA A*2501	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.498451	0.658550	-3.839901	31510.178061
HLA B*5801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.363644	0.523691	-3.839953	23101.727479
HLA A*0216	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.221639	0.381582	-3.840057	16658.628122
HLA A*0216	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.443212	0.603125	-3.840087	27746.749635
HLA A*3002	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.517449	0.677348	-3.840100	32919.163661
HLA B*5301	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.595868	0.755651	-3.840216	39433.702348
HLA A*3002	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.449774	0.609548	-3.840226	28169.181436
HLA A*6901	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.366725	0.526478	-3.840247	23266.155758
HLA A*0101	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.380558	0.540290	-3.840268	24019.192285
HLA A*2601	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.390889	0.550534	-3.840355	24597.393250
HLA B*1501	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.307254	0.466843	-3.840411	20288.711509
HLA A*0203	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.357089	0.516619	-3.840470	22755.657748
HLA A*3002	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.519009	0.678487	-3.840522	33037.627418
HLA A*0219	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.315741	0.475212	-3.840529	20689.062266
HLA B*0702	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.222194	0.381582	-3.840612	16679.910339
HLA B*0801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.402890	0.562255	-3.840635	25286.589240
HLA A*2602	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.616935	0.776187	-3.840749	41393.808485
HLA B*0803	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.499313	0.658550	-3.840763	31572.801439
HLA B*7301	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.547903	0.707098	-3.840805	35310.414663
HLA A*0250	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.596516	0.755651	-3.840865	39492.625947
HLA A*0203	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.249267	0.408334	-3.840932	17752.798654
HLA B*1502	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.595271	0.754283	-3.840987	39379.553242
HLA A*8001	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.447234	0.606197	-3.841038	28004.926280
HLA A*0301	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.353819	0.512773	-3.841046	22584.938386
HLA A*2902	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.381447	0.540290	-3.841156	24068.360302
HLA A*6802	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.442068	0.600860	-3.841208	27673.743818
HLA B*4601	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.223040	0.381582	-3.841458	16712.427121
HLA B*1801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.477414	0.635887	-3.841527	30020.199127
HLA B*5301	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.535535	0.693953	-3.841582	34319.039819
HLA A*0216	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.418716	0.577123	-3.841593	26225.053620
HLA A*2602	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.594690	0.752921	-3.841769	39326.967746
HLA A*3101	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.397089	0.555221	-3.841868	24951.081534
HLA B*4801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.404159	0.562255	-3.841904	25360.567974
HLA A*0219	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.404756	0.562720	-3.842036	25395.440184

HLA B*5401	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.545281	0.703210	-3.842071	35097.872534
HLA A*8001	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.367888	0.525631	-3.842257	23328.543580
HLA B*4402	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.404547	0.562255	-3.842291	25383.215727
HLA B*0802	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.454666	0.612321	-3.842345	28488.255444
HLA B*0802	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.480212	0.637857	-3.842355	30214.249090
HLA B*4002	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.582910	0.740545	-3.842365	38274.554483
HLA B*4001	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.405240	0.562720	-3.842520	25423.757582
HLA A*0250	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.436713	0.594015	-3.842699	27334.645122
HLA B*1503	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.307835	0.464975	-3.842859	20315.840271
HLA B*4801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.436892	0.594015	-3.842877	27345.886115
HLA B*0803	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.480285	0.637330	-3.842954	30219.316643
HLA A*0201	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.393669	0.550534	-3.843135	24755.318894
HLA A*0219	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.383434	0.540290	-3.843144	24178.768023
HLA B*5801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.353328	0.510101	-3.843227	22559.416776
HLA B*4501	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.537210	0.693953	-3.843258	34451.672602
HLA A*2301	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.466134	0.622434	-3.843700	29250.526735
HLA B*4001	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.426477	0.582728	-3.843749	26697.877363
HLA B*5101	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.450042	0.606197	-3.843845	28186.559499
HLA B*3501	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.444723	0.600860	-3.843863	27843.436401
HLA B*3901	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.440083	0.595974	-3.844108	27547.525987
HLA A*2403	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.440914	0.596390	-3.844524	27600.332824
HLA A*0216	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.481885	0.637330	-3.844554	30330.854003
HLA B*1502	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.523111	0.678487	-3.844624	33351.168297
HLA A*3201	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.622043	0.777400	-3.844643	41883.519288
HLA A*6801	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.620906	0.776187	-3.844719	41773.995503
HLA A*0202	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.450930	0.606197	-3.844734	28244.258243
HLA A*0250	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.467177	0.622434	-3.844743	29320.870679
HLA A*6901	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.400111	0.555221	-3.844890	25125.274376
HLA B*3801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.531541	0.686428	-3.845113	34004.861013
HLA B*4501	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.598053	0.752921	-3.845131	39632.600998
HLA A*3301	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.599472	0.754283	-3.845188	39762.315227
HLA B*0802	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.451628	0.606197	-3.845431	28289.675817
HLA B*5801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.293700	0.448098	-3.845602	19665.286949
HLA A*0212	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.401145	0.555221	-3.845923	25185.152591
HLA A*1101	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.452135	0.606197	-3.845939	28322.752646
HLA B*5101	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.481861	0.635887	-3.845974	30329.213182
HLA A*3101	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.210334	0.364340	-3.845993	16230.560264
HLA A*2403	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.408529	0.562255	-3.846274	25617.044214
HLA B*1502	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.299285	0.452989	-3.846296	19919.801836
HLA A*0206	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.409025	0.562720	-3.846305	25646.302423
HLA A*0212	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.371943	0.525631	-3.846312	23547.393286
HLA A*2402	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.530242	0.683810	-3.846431	33903.281757
HLA A*2402	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.571614	0.725139	-3.846475	37291.840695
HLA B*4402	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.423599	0.577123	-3.846476	26521.532455
HLA B*4501	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.526624	0.679867	-3.846757	33621.999085
HLA A*2402	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.524314	0.677348	-3.846966	33443.674527
HLA B*5301	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.584390	0.737370	-3.847020	38405.225526
HLA B*1509	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.550353	0.703210	-3.847144	35510.217350
HLA A*6901	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.387565	0.540290	-3.847274	24409.819228
HLA A*1101	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.312304	0.464975	-3.847328	20525.961506
HLA A*6901	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.360132	0.512773	-3.847359	22915.639226
HLA A*0202	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.285895	0.438531	-3.847364	19315.026071
HLA B*5801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.350227	0.502859	-3.847368	22398.892608
HLA A*3002	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.409831	0.562255	-3.847575	25693.935676
HLA A*8001	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.448496	0.600860	-3.847636	28086.401976
HLA B*5401	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.540041	0.692320	-3.847721	34676.993804
HLA A*3001	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.300831	0.452989	-3.847842	19990.836852
HLA A*2501	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.424968	0.577123	-3.847845	26605.312500
HLA A*0212	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.429611	0.581735	-3.847876	26891.247309
HLA B*4601	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.398471	0.550534	-3.847937	25030.577666
HLA A*0301	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.364558	0.516619	-3.847939	23150.395029
HLA A*0216	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.410733	0.562720	-3.848013	25747.367672
HLA A*0101	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.371945	0.523921	-3.848024	23547.520675
HLA A*2902	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.350891	0.502859	-3.848033	22433.211546
HLA B*3501	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.410963	0.562720	-3.848243	25761.021751

HLA B*0702	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.410996	0.562720	-3.848276	25762.972925
HLA B*1502	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.513586	0.665274	-3.848312	32627.683416
HLA B*3801	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.540666	0.692320	-3.848346	34726.930978
HLA A*2902	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.365127	0.516619	-3.848508	23180.723216
HLA A*3201	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.507116	0.658550	-3.848566	32145.172306
HLA B*1503	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.488689	0.639976	-3.848713	30809.790638
HLA B*4002	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.610559	0.761813	-3.848746	40790.486370
HLA B*3901	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.471293	0.622434	-3.848859	29600.098769
HLA A*2501	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.458444	0.609548	-3.848896	28737.158724
HLA B*3801	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.532873	0.683810	-3.849063	34109.327906
HLA A*2402	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.602028	0.752921	-3.849107	39997.044726
HLA A*3001	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.287679	0.438531	-3.849147	19394.498662
HLA A*2301	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.527815	0.678487	-3.849328	33714.344553
HLA A*6802	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.443550	0.594015	-3.849536	27768.373442
HLA A*0212	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.432482	0.582728	-3.849754	27069.611162
HLA B*7301	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.574910	0.725139	-3.849772	37575.965442
HLA A*6801	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.557912	0.707963	-3.849948	36133.632546
HLA B*3801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.556598	0.706599	-3.850000	36024.524876
HLA A*0212	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.412319	0.562255	-3.850063	25841.560572
HLA B*5401	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.490051	0.639976	-3.850075	30906.615444
HLA A*3301	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.639587	0.789406	-3.850181	43610.068708
HLA B*4601	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.405458	0.555221	-3.850237	25436.551994
HLA A*0211	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.456475	0.606197	-3.850278	28607.174050
HLA A*3001	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.287749	0.437367	-3.850382	19397.646580
HLA A*2403	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.401053	0.550534	-3.850519	25179.839445
HLA A*0206	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.444634	0.594015	-3.850619	27837.713053
HLA B*4403	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.645045	0.794424	-3.850620	44161.582187
HLA B*2705	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.405923	0.555221	-3.850702	25463.813159
HLA A*6901	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.374668	0.523921	-3.850747	23695.628917
HLA A*0206	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.245839	0.394899	-3.850940	17613.226860
HLA A*3002	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.432792	0.581735	-3.851057	27088.948620
HLA A*0201	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.353948	0.502859	-3.851089	22591.659396
HLA A*0203	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.413874	0.562720	-3.851154	25934.274078
HLA A*3301	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.627393	0.776187	-3.851206	42402.644591
HLA A*3101	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.374955	0.523691	-3.851264	23711.273347
HLA B*1501	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.231766	0.380458	-3.851308	17051.614817
HLA A*2403	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.433109	0.581735	-3.851374	27108.739855
HLA A*0201	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.391791	0.540290	-3.851501	24648.544924
HLA B*4402	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.406823	0.555221	-3.851602	25516.628560
HLA A*2902	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.414414	0.562720	-3.851694	25966.563518
HLA A*0202	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.491703	0.639976	-3.851727	31024.381802
HLA A*3301	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.517068	0.665274	-3.851794	32890.325878
HLA A*8001	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.445876	0.594015	-3.851862	27917.493998
HLA B*4402	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.402434	0.550534	-3.851900	25260.064418
HLA A*6801	1:163-171	9	DDLAWNDLV	0.956505	-0.187932	-4.620485	0.768573	-3.851913	41733.562393
HLA B*5401	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.510520	0.658550	-3.851970	32398.146268
HLA B*4501	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.009438	0.157454	-3.851985	10219.707052
HLA B*3501	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.429486	0.577123	-3.852363	26883.538045
HLA B*5301	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.605383	0.752921	-3.852462	40307.231366
HLA A*2301	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.538930	0.686428	-3.852502	34588.373055
HLA A*6802	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.435438	0.582728	-3.852710	27254.465518
HLA B*1502	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.539165	0.686428	-3.852737	34607.090044
HLA B*0802	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.492845	0.639976	-3.852869	31106.058622
HLA B*1501	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.408146	0.555221	-3.852925	25594.464756
HLA A*2603	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.629150	0.776187	-3.852964	42574.578648
HLA B*5701	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.403555	0.550534	-3.853021	25325.332623
HLA B*7301	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.408245	0.555221	-3.853023	25600.280872
HLA B*1517	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.415836	0.562720	-3.853116	26051.690872
HLA B*5101	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.490460	0.637330	-3.853130	30935.722178
HLA A*2902	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.290533	0.437367	-3.853166	19522.398884
HLA B*1509	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.434961	0.581735	-3.853226	27224.550889
HLA A*1101	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.454095	0.600860	-3.853235	28450.829301
HLA A*0250	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.533223	0.679867	-3.853356	34136.833615
HLA A*2902	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.291901	0.438531	-3.853369	19583.963108
HLA A*2301	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.545692	0.692320	-3.853372	35131.116498

HLA A*0206	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.150892	0.297408	-3.853484	14154.402492
HLA A*2403	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.370181	0.516619	-3.853561	23452.045260
HLA A*2301	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.530937	0.677348	-3.853589	33957.615495
HLA A*3101	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.238288	0.384545	-3.853743	17309.625987
HLA A*8001	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.436631	0.582728	-3.853903	27329.469903
HLA B*4002	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.489831	0.635887	-3.853944	30890.902511
HLA A*8001	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.450397	0.596390	-3.854006	28209.594317
HLA A*0216	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.379736	0.525631	-3.854105	23973.755906
HLA B*4501	1:130-138	9	LGYDNFDRH	1.014767	-0.220343	-4.648555	0.794424	-3.854130	44519.958944
HLA B*3801	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.548121	0.693953	-3.854169	35328.184497
HLA A*2902	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.364286	0.510101	-3.854185	23135.871622
HLA A*8001	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.378207	0.523921	-3.854286	23889.472728
HLA B*1502	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.610087	0.755651	-3.854435	40746.155403
HLA B*5401	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.562599	0.707963	-3.854635	36525.725113
HLA B*7301	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.624256	0.769461	-3.854795	42097.507334
HLA B*0801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.241826	0.387024	-3.854802	17451.228638
HLA B*3501	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.367575	0.512773	-3.854802	23311.764374
HLA B*4001	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.381331	0.526478	-3.854854	24061.980997
HLA A*2602	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.571597	0.716494	-3.855104	37290.428508
HLA A*6901	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.322063	0.466843	-3.855220	20992.456929
HLA B*4002	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.641546	0.786321	-3.855225	43807.275238
HLA A*3002	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.456261	0.600860	-3.855401	28593.094207
HLA B*7301	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.581585	0.726109	-3.855476	38157.950005
HLA A*2501	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.437308	0.581735	-3.855573	27372.083719
HLA A*0216	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.462100	0.606197	-3.855903	28980.083028
HLA B*5301	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.578430	0.722436	-3.855993	37881.718831
HLA A*0101	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.382490	0.526478	-3.856012	24126.241769
HLA B*5101	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.505800	0.649772	-3.856028	32047.934655
HLA A*0203	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.437811	0.581735	-3.856076	27403.791177
HLA B*0803	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.468742	0.612666	-3.856076	29426.703914
HLA B*5401	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.359004	0.502859	-3.856145	22856.210308
HLA A*3101	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.380154	0.523921	-3.856234	23996.852799
HLA A*3301	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.633666	0.777400	-3.856266	43019.570356
HLA A*2603	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.642608	0.786321	-3.856287	43914.526925
HLA B*5101	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.465856	0.609548	-3.856309	29231.860125
HLA B*4501	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.647039	0.790719	-3.856321	44364.882674
HLA A*0211	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.433565	0.577123	-3.856442	27137.205914
HLA B*5701	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.411802	0.555221	-3.856581	25810.822872
HLA B*5701	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.419348	0.562720	-3.856628	26263.245679
HLA B*4601	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.396960	0.540290	-3.856670	24943.658596
HLA A*3001	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.253947	0.397240	-3.856707	17945.146230
HLA A*0203	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.257478	0.400734	-3.856744	18091.654177
HLA B*1503	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.071441	0.214632	-3.856809	11788.033358
HLA A*3301	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.597512	0.740545	-3.856967	39583.317831
HLA A*6802	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.257803	0.400734	-3.857068	18105.165810
HLA A*3301	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-3.979708	0.122535	-3.857174	9543.508479
HLA B*2705	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.439975	0.582728	-3.857247	27540.671503
HLA A*2402	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.565240	0.707963	-3.857276	36748.504294
HLA A*2501	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.460413	0.603125	-3.857288	28867.734019
HLA A*0219	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.469696	0.612321	-3.857375	29491.408201
HLA A*0203	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.440179	0.582728	-3.857451	27553.636856
HLA A*0206	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.536374	0.678719	-3.857655	34385.385271
HLA A*0202	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.265600	0.407915	-3.857686	18433.187777
HLA B*1501	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.367843	0.510101	-3.857742	23326.145812
HLA A*2301	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.518772	0.660945	-3.857827	33019.580629
HLA A*2902	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.440597	0.582728	-3.857869	27580.182693
HLA A*0101	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.383556	0.525631	-3.857925	24185.570811
HLA B*0702	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.408555	0.550534	-3.858021	25618.568698
HLA A*0301	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.368282	0.510101	-3.858182	23349.755630
HLA B*5401	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.565430	0.707098	-3.858332	36764.611055
HLA B*4501	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.620312	0.761813	-3.858498	41716.858465
HLA A*3001	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.292016	0.433440	-3.858576	19589.155202
HLA B*5301	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.523870	0.665274	-3.858596	33409.496881
HLA B*3501	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.468227	0.609548	-3.858679	29391.860809
HLA B*0801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.333907	0.475212	-3.858695	21572.825210

HLA A*0211	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.156136	0.297408	-3.858728	14326.351138
HLA B*7301	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.545159	0.686428	-3.858730	35088.000392
HLA A*0219	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.420991	0.562255	-3.858735	26362.748488
HLA A*0203	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.409438	0.550534	-3.858904	25670.732934
HLA A*0219	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.459908	0.600860	-3.859047	28834.176722
HLA B*4601	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.384787	0.525631	-3.859157	24254.228899
HLA B*3501	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.369314	0.510101	-3.859213	23405.275833
HLA A*0250	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.573284	0.714055	-3.859230	37435.557414
HLA A*0211	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.509237	0.649772	-3.859466	32302.589838
HLA B*4001	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.383258	0.523691	-3.859567	24168.959679
HLA B*7301	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.597082	0.737370	-3.859712	39544.149353
HLA A*2402	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.525082	0.665274	-3.859808	33502.889878
HLA B*4801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.410564	0.550534	-3.860030	25737.340716
HLA A*0206	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.456571	0.596390	-3.860181	28613.519981
HLA B*0803	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.441925	0.581735	-3.860190	27664.612900
HLA A*2402	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.566908	0.706599	-3.860309	36889.927512
HLA A*6901	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.363421	0.502859	-3.860562	23089.857640
HLA A*1101	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.470118	0.609548	-3.860571	29520.140332
HLA A*2301	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.533954	0.673165	-3.860789	34194.316345
HLA B*3801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.454969	0.594015	-3.860954	28508.143644
HLA B*0702	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.384748	0.523691	-3.861056	24251.998386
HLA B*4501	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.269414	0.408334	-3.861079	18595.748393
HLA A*0211	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.539823	0.678719	-3.861104	34659.551513
HLA A*6802	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.442855	0.581735	-3.861120	27723.942774
HLA B*0803	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.501256	0.639976	-3.861280	31714.373928
HLA B*3801	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.464555	0.603125	-3.861430	29144.381099
HLA B*4501	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.647862	0.786321	-3.861540	44448.965436
HLA A*0101	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.374328	0.512773	-3.861555	23677.048550
HLA B*1503	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.150642	0.288865	-3.861777	14146.288002
HLA B*3801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.540283	0.678487	-3.861797	34696.321853
HLA B*1801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.374621	0.512773	-3.861848	23693.065241
HLA A*2301	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.541954	0.679867	-3.862087	34830.035864
HLA B*4001	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.402442	0.540290	-3.862151	25260.474384
HLA B*3801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.535354	0.673165	-3.862189	34304.746806
HLA A*0202	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.365160	0.502859	-3.862301	23182.478955
HLA B*4002	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.616585	0.754283	-3.862302	41360.455478
HLA B*1501	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.130780	0.268381	-3.862399	13513.876614
HLA A*0250	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.546244	0.683810	-3.862434	35175.807931
HLA B*4801	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.439674	0.577123	-3.862551	27521.607131
HLA A*2403	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.337821	0.475212	-3.862609	21768.137233
HLA A*2402	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.579125	0.716494	-3.862631	37942.428453
HLA A*0202	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.558262	0.695627	-3.862634	36162.770652
HLA A*0201	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.244333	0.381582	-3.862751	17552.254566
HLA B*1509	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.500615	0.637857	-3.862758	31667.569549
HLA A*2601	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.389294	0.526478	-3.862816	24507.205029
HLA A*0101	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.379452	0.516619	-3.862832	23958.067902
HLA B*1801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.458829	0.595974	-3.862855	28762.666272
HLA A*2902	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.425271	0.562255	-3.863016	26623.886181
HLA B*4801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.445846	0.582728	-3.863118	27915.530670
HLA A*2601	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.403428	0.540290	-3.863138	25317.935313
HLA B*2705	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.440684	0.577123	-3.863561	27585.703858
HLA A*2403	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.311968	0.448098	-3.863869	20510.088472
HLA A*3101	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.376665	0.512773	-3.863892	23804.841944
HLA A*3301	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.625767	0.761813	-3.863954	42244.200978
HLA B*1503	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.339492	0.475212	-3.864279	21852.028112
HLA A*0211	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.514481	0.650029	-3.864452	32695.003901
HLA A*3201	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.460946	0.596390	-3.864556	28903.206668
HLA B*3501	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.458651	0.594015	-3.864636	28750.842887
HLA B*3901	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.477094	0.612321	-3.864773	29998.120041
HLA A*0219	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.441901	0.577123	-3.864778	27663.116315
HLA B*5401	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.474352	0.609548	-3.864804	29809.328271
HLA B*4601	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.340018	0.475212	-3.864806	21878.524782
HLA A*0211	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.557186	0.692320	-3.864866	36073.280010
HLA B*1517	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.458900	0.594015	-3.864885	28767.334736
HLA B*0802	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.474585	0.609548	-3.865037	29825.297798

HLA A*0206	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.477538	0.612321	-3.865217	30028.807876
HLA A*0201	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.391782	0.526478	-3.865304	24648.011547
HLA B*1517	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.427832	0.562255	-3.865577	26781.345153
HLA B*0801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.389275	0.523691	-3.865584	24506.144402
HLA B*3801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.503467	0.637857	-3.865610	31876.234114
HLA B*4002	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.503007	0.637330	-3.865676	31842.452436
HLA A*6802	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.154561	0.288865	-3.865696	14274.517473
HLA A*0301	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.368769	0.502859	-3.865910	23375.918432
HLA A*3001	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.211095	0.345166	-3.865929	16259.034203
HLA A*2301	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.532399	0.666384	-3.866014	34072.073674
HLA A*3201	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.582642	0.716494	-3.866149	38250.956795
HLA A*0212	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.376287	0.510101	-3.866186	23784.117140
HLA B*5301	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.591420	0.725139	-3.866281	39031.925743
HLA B*0702	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.406584	0.540290	-3.866293	25502.552147
HLA A*3001	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.119267	0.252948	-3.866320	13160.351010
HLA A*0203	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.421665	0.555221	-3.866444	26403.712090
HLA B*3901	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.247169	0.380458	-3.866711	17667.241166
HLA B*5401	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.473121	0.606197	-3.866924	29724.944987
HLA A*3002	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.553570	0.686428	-3.867142	35774.187220
HLA A*2501	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.258876	0.391537	-3.867340	18149.982940
HLA B*4002	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.643618	0.776187	-3.867432	44016.802108
HLA B*1509	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.526118	0.658550	-3.867568	33582.915192
HLA A*3101	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.377711	0.510101	-3.867610	23862.218773
HLA B*7301	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.590062	0.722436	-3.867626	38910.066814
HLA A*2601	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.393340	0.525631	-3.867709	24736.576698
HLA B*0803	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.473941	0.606197	-3.867744	29781.120223
HLA A*2602	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.561739	0.693953	-3.867786	36453.475019
HLA B*5301	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.528773	0.660945	-3.867829	33788.842214
HLA B*4001	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.423063	0.555221	-3.867842	26488.839512
HLA B*1517	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.505199	0.637330	-3.867868	32003.581177
HLA B*4601	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.391843	0.523691	-3.868152	24651.478709
HLA B*4002	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.551986	0.683810	-3.868176	35643.982568
HLA B*4403	1:147-155	9	YLAEGRQPV	0.580541	0.209679	-4.658404	0.790220	-3.868184	45541.129354
HLA A*2603	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.645684	0.777400	-3.868283	44226.613341
HLA A*3201	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.609201	0.740545	-3.868656	40663.137157
HLA A*0201	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.392592	0.523921	-3.868672	24694.057842
HLA A*3101	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.409187	0.540290	-3.868897	25655.877522
HLA B*0802	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.469839	0.600860	-3.868979	29501.142067
HLA B*1501	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.260603	0.391537	-3.869066	18222.295818
HLA B*0803	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.519237	0.650029	-3.869208	33054.968768
HLA A*1101	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.463288	0.594015	-3.869274	29059.521899
HLA A*2301	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.509261	0.639976	-3.869285	32304.337419
HLA A*6802	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.419837	0.550534	-3.869303	26292.815212
HLA B*1501	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.281326	0.412011	-3.869314	19112.854354
HLA A*3201	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.534616	0.665274	-3.869342	34246.522622
HLA A*0202	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.585861	0.716494	-3.869367	38535.508785
HLA A*0301	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.344654	0.475212	-3.869441	22113.300575
HLA A*0201	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.379696	0.510101	-3.869595	23971.551186
HLA B*5801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.334572	0.464975	-3.869596	21605.878472
HLA B*5401	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.492063	0.622434	-3.869629	31050.071718
HLA B*1509	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.463646	0.594015	-3.869631	29083.427463
HLA B*4403	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.639154	0.769461	-3.869694	43566.679989
HLA A*0216	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.410148	0.540290	-3.869858	25712.707711
HLA B*5301	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.565489	0.695627	-3.869861	36769.583703
HLA A*6802	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.425304	0.555221	-3.870083	26625.902709
HLA A*2402	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.507992	0.637857	-3.870135	32210.103174
HLA A*3101	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.335281	0.464975	-3.870306	21641.206716
HLA B*0802	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.432818	0.562255	-3.870563	27090.560699
HLA B*5701	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.396286	0.525631	-3.870655	24904.960170
HLA A*0212	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.421336	0.550534	-3.870802	26383.721900
HLA A*0211	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.483196	0.612321	-3.870875	30422.552639
HLA A*6801	1:19-27	9	PHVGLVRTA	1.198003	-0.399194	-4.670045	0.798809	-3.871236	46778.414140
HLA A*2602	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.008193	0.136944	-3.871249	10190.446655
HLA B*0802	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.465450	0.594015	-3.871435	29204.514509
HLA A*0211	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.467865	0.596390	-3.871475	29367.383973

HLA A*6801	1:10-18	9	RFCPSPTGT	0.873191	-0.103730	-4.641001	0.769461	-3.871540	43752.327466
HLA A*0219	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.454306	0.582728	-3.871579	28464.685099
HLA B*3901	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.511596	0.639976	-3.871620	32478.519633
HLA A*0101	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.381851	0.510101	-3.871750	24090.766357
HLA B*7301	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.509656	0.637857	-3.871799	32333.710930
HLA A*0211	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.052025	0.180214	-3.871812	11272.628952
HLA B*5701	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.395788	0.523921	-3.871867	24876.413132
HLA B*1801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.530446	0.658550	-3.871896	33919.242443
HLA A*3301	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.597094	0.725139	-3.871955	39545.219015
HLA A*6901	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.252509	0.380458	-3.872051	17885.830750
HLA A*3101	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.434481	0.562255	-3.872226	27194.521975
HLA A*0206	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.564749	0.692320	-3.872429	36706.977460
HLA B*1502	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.575718	0.703210	-3.872509	37645.959493
HLA B*4403	1:116-124	9	EVEARHVAA	1.183323	-0.395325	-4.660514	0.787998	-3.872516	45762.910103
HLA B*4801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.427811	0.555221	-3.872590	26780.041227
HLA A*0211	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.398285	0.525631	-3.872654	25019.882353
HLA A*6801	1:261-269	9	RDPQSNLFA	1.010830	-0.221424	-4.662071	0.789406	-3.872666	45927.345236
HLA A*2301	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.253035	0.380348	-3.872688	17907.518209
HLA A*3201	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.339713	0.466843	-3.872869	21863.143341
HLA A*6901	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.348117	0.475212	-3.872904	22290.340876
HLA B*5701	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.413350	0.540290	-3.873060	25903.005698
HLA B*1517	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.473936	0.600860	-3.873076	29780.797999
HLA A*2602	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.479357	0.606197	-3.873160	30154.809745
HLA A*2902	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.270469	0.397240	-3.873228	18640.973118
HLA B*3501	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.260277	0.387024	-3.873253	18208.598265
HLA A*0202	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.485811	0.612321	-3.873490	30606.285707
HLA B*7301	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.580093	0.706599	-3.873494	38027.091674
HLA B*4601	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.390140	0.516619	-3.873520	24554.980792
HLA B*0802	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.469961	0.596390	-3.873571	29509.442325
HLA B*1503	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.470163	0.596390	-3.873773	29523.174801
HLA B*4002	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.647951	0.774156	-3.873795	44458.104007
HLA B*4002	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.643266	0.769405	-3.873861	43981.097694
HLA A*0203	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.332542	0.458535	-3.874007	21505.125131
HLA B*4402	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.347656	0.473598	-3.874058	22266.718100
HLA A*0203	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.377074	0.502859	-3.874215	23827.260485
HLA B*3901	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.456017	0.581735	-3.874282	28577.011443
HLA A*6801	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.660821	0.786321	-3.874500	45795.353565
HLA A*0201	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.387278	0.512773	-3.874505	24393.713905
HLA A*0101	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.266157	0.391537	-3.874621	18456.836931
HLA B*1502	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.554488	0.679867	-3.874622	35849.939255
HLA A*2501	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.480870	0.606197	-3.874673	30260.051378
HLA B*0803	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.475546	0.600860	-3.874686	29891.363647
HLA A*0203	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.384802	0.510101	-3.874701	24255.016188
HLA A*2301	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.512628	0.637857	-3.874771	32555.745879
HLA B*5401	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.163955	0.288865	-3.875090	14586.620282
HLA A*0250	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.536233	0.660945	-3.875288	34374.225815
HLA B*1503	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.458317	0.582728	-3.875589	28728.764849
HLA A*2603	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.616360	0.740545	-3.875815	41338.980529
HLA B*3501	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.458545	0.582728	-3.875817	28743.844490
HLA A*0201	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.392534	0.516619	-3.875914	24690.718265
HLA A*2301	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.541223	0.665274	-3.875949	34771.484450
HLA A*2301	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.513297	0.637330	-3.875967	32605.979643
HLA B*1509	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.476880	0.600860	-3.876020	29983.355604
HLA B*4402	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.416437	0.540290	-3.876147	26087.795678
HLA B*5101	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.438407	0.562255	-3.876152	27441.472934
HLA A*0201	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.400099	0.523691	-3.876408	25124.594761
HLA A*1101	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.402928	0.526478	-3.876450	25288.778097
HLA B*4501	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.650615	0.774156	-3.876460	44731.684543
HLA A*2902	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.427125	0.550534	-3.876591	26737.770524
HLA A*0216	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.438873	0.562255	-3.876617	27470.882837
HLA B*1517	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.486168	0.609548	-3.876620	30631.463702
HLA B*4403	1:153-161	9	QPVVRLRMP	0.777747	0.008574	-4.663049	0.786321	-3.876728	46030.821758
HLA B*5401	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.526842	0.650029	-3.876813	33638.919231
HLA B*5401	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.514787	0.637857	-3.876930	32718.005913
HLA A*3301	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.630050	0.752921	-3.877129	42662.884096

HLA A*0203	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.417603	0.540290	-3.877312	26157.891192
HLA A*2602	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.532662	0.655319	-3.877343	34092.724457
HLA A*2602	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.580582	0.703210	-3.877372	38069.906007
HLA B*4403	1:235-243	9	IGVAERIPK	0.603044	0.187675	-4.668274	0.790719	-3.877555	46587.990987
HLA B*0803	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.440278	0.562720	-3.877558	27559.898177
HLA B*4001	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.403243	0.525631	-3.877612	25307.117214
HLA A*0101	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.401398	0.523691	-3.877707	25199.871770
HLA A*8001	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.428436	0.550534	-3.877902	26818.606265
HLA B*5801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.353128	0.475212	-3.877916	22549.045425
HLA B*1509	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.490251	0.612321	-3.877930	30920.830828
HLA A*0212	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.418568	0.540290	-3.878278	26216.117041
HLA B*7301	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.388582	0.510101	-3.878481	24467.065814
HLA B*3801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.528306	0.649772	-3.878534	33752.485803
HLA B*4403	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.656038	0.777400	-3.878637	45293.706847
HLA B*4001	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.389021	0.510101	-3.878921	24491.830428
HLA B*4501	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.655295	0.776187	-3.879109	45216.342271
HLA B*5301	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.558997	0.679867	-3.879130	36224.056774
HLA B*4501	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.601621	0.722436	-3.879185	39959.628571
HLA A*6801	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.619767	0.740545	-3.879221	41664.532718
HLA B*2705	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.475705	0.596390	-3.879315	29902.361880
HLA B*4402	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.403320	0.523921	-3.879399	25311.635605
HLA B*2705	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.403414	0.523921	-3.879493	25317.113523
HLA A*2902	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.332490	0.452989	-3.879501	21502.565796
HLA A*2301	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.529307	0.649772	-3.879535	33830.361916
HLA A*3001	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.300608	0.421060	-3.879548	19980.565412
HLA A*2601	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.389860	0.510101	-3.879759	24539.177952
HLA B*4002	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.492504	0.612666	-3.879839	31081.667542
HLA A*2603	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.535183	0.655319	-3.879864	34291.201785
HLA B*1801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.486097	0.606197	-3.879901	30626.492721
HLA A*3301	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.572380	0.692320	-3.880060	37357.667504
HLA A*2603	1:178-186	9	AAGSVPDFA	1.016320	-0.262037	-4.634350	0.754283	-3.880066	43087.348445
HLA A*0219	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.435290	0.555221	-3.880068	27245.178152
HLA A*2601	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.355353	0.475212	-3.880141	22664.864332
HLA A*2602	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.558628	0.678487	-3.880141	36193.302840
HLA B*3801	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.560071	0.679867	-3.880204	36313.725009
HLA B*5801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.353812	0.473598	-3.880214	22584.571843
HLA A*6901	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.281001	0.400734	-3.880267	19098.590697
HLA A*2601	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.393044	0.512773	-3.880271	24719.720854
HLA B*1501	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.420617	0.540290	-3.880327	26340.081730
HLA B*1517	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.476770	0.596390	-3.880379	29975.732861
HLA A*2603	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.493049	0.612666	-3.880384	31120.702456
HLA B*5101	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.492737	0.612321	-3.880416	31098.318690
HLA A*3002	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.535822	0.655319	-3.880503	34341.698084
HLA B*0803	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.503178	0.622672	-3.880506	31855.030201
HLA B*3901	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.347753	0.466843	-3.880909	22271.657528
HLA A*2602	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.636645	0.755651	-3.880994	43315.687883
HLA A*0202	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.272623	0.391537	-3.881086	18733.678290
HLA A*3301	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.564932	0.683810	-3.881122	36722.470021
HLA B*5101	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.444077	0.562720	-3.881357	27802.043975
HLA A*0212	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.329497	0.448098	-3.881399	21354.875379
HLA A*2601	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.398130	0.516619	-3.881511	25010.950531
HLA A*0202	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.263227	0.381582	-3.881646	18332.743722
HLA B*5101	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.478102	0.596390	-3.881712	30067.821803
HLA A*3001	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.106825	0.225072	-3.881753	12788.647012
HLA A*8001	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.444822	0.562720	-3.882101	27849.763576
HLA A*6801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.273779	0.391537	-3.882242	18783.607492
HLA A*3002	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.599192	0.716494	-3.882698	39736.725408
HLA B*5301	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.505184	0.622434	-3.882751	32002.542379
HLA A*0216	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.483684	0.600860	-3.882824	30456.805095
HLA A*1101	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.465596	0.582728	-3.882868	29214.311730
HLA B*0803	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.486060	0.603125	-3.882935	30623.841861
HLA A*2402	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.569452	0.686428	-3.883024	37106.696671
HLA B*0801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.243074	0.359537	-3.883536	17501.432004
HLA B*1517	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.460720	0.577123	-3.883598	28888.199703
HLA B*3801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.544562	0.660945	-3.883617	35039.818666

HLA A*3201	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.577589	0.693953	-3.883636	37808.422780
HLA B*4601	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.342194	0.458535	-3.883659	21988.401494
HLA B*1509	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.506127	0.622434	-3.883693	32072.042950
HLA B*2705	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.486868	0.603125	-3.883743	30680.885951
HLA A*0250	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.600254	0.716494	-3.883760	39834.011323
HLA B*0801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.396587	0.512773	-3.883814	24922.211976
HLA A*3001	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.284570	0.400734	-3.883836	19256.182315
HLA B*0803	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.479862	0.595974	-3.883887	30189.903999
HLA B*4001	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.434423	0.550534	-3.883889	27190.844239
HLA A*2301	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.487352	0.603125	-3.884227	30715.096930
HLA A*1101	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.480719	0.596390	-3.884329	30249.576166
HLA A*0101	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.357982	0.473598	-3.884384	22802.485987
HLA A*0216	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.401055	0.516619	-3.884436	25179.975666
HLA A*2603	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.561866	0.677348	-3.884517	36464.125875
HLA B*0801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.411165	0.526478	-3.884687	25773.009867
HLA B*1509	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.563210	0.678487	-3.884723	36577.137294
HLA B*4002	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.577093	0.692320	-3.884773	37765.289594
HLA A*2602	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.577135	0.692320	-3.884815	37768.967282
HLA B*4002	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.598948	0.714055	-3.884893	39714.374684
HLA A*2402	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.577293	0.692320	-3.884972	37782.659600
HLA A*6802	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.096990	0.211872	-3.885117	12502.292521
HLA B*4601	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.409062	0.523921	-3.885142	25648.522417
HLA B*3801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.543697	0.658550	-3.885147	34970.129415
HLA B*4002	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.534976	0.649772	-3.885204	34274.880650
HLA A*2402	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.564368	0.678719	-3.885649	36674.821483
HLA B*3501	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.402293	0.516619	-3.885674	25251.866500
HLA B*5701	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.409372	0.523691	-3.885681	25666.844706
HLA A*0250	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.581421	0.695627	-3.885793	38143.502622
HLA A*0219	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.436382	0.550534	-3.885848	27313.802359
HLA A*3001	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.293764	0.407915	-3.885849	19668.159608
HLA A*3301	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.641546	0.755651	-3.885895	43807.275238
HLA B*1502	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.498794	0.612666	-3.886128	31535.076012
HLA A*3002	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.552665	0.666384	-3.886281	35699.754023
HLA A*0202	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.480303	0.594015	-3.886289	30220.624537
HLA A*2402	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.412798	0.526478	-3.886320	25870.095510
HLA B*4403	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.578646	0.692320	-3.886326	37900.577627
HLA A*6901	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.402996	0.516619	-3.886377	25292.745883
HLA A*2301	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.545022	0.658550	-3.886472	35076.992432
HLA A*0203	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.334591	0.448098	-3.886493	21606.813575
HLA B*4403	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.524370	0.637857	-3.886514	33448.017047
HLA B*0802	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.469284	0.582728	-3.886557	29463.500994
HLA B*7301	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.589773	0.703210	-3.886563	38884.184031
HLA A*0202	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.065633	0.178924	-3.886709	11631.438513
HLA B*4501	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.656216	0.769405	-3.886811	45312.333255
HLA A*8001	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.410564	0.523691	-3.886873	25737.340716
HLA A*2403	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.427167	0.540290	-3.886877	26740.374321
HLA A*0203	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.360571	0.473598	-3.886973	22938.833546
HLA B*1501	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.413461	0.526478	-3.886983	25909.592757
HLA A*0203	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.411135	0.523921	-3.887214	25771.197352
HLA B*5701	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.413782	0.526478	-3.887305	25928.802895
HLA B*4801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.345941	0.458535	-3.887406	22178.955364
HLA B*4601	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.413989	0.526478	-3.887511	25941.149765
HLA B*3501	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.427983	0.540290	-3.887692	26790.619341
HLA B*5701	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.404375	0.516619	-3.887756	25373.193318
HLA A*0250	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.595731	0.707963	-3.887768	39421.331035
HLA A*2301	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.537824	0.650029	-3.887794	34500.352071
HLA B*1501	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.390666	0.502859	-3.887807	24584.754927
HLA A*0216	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.411821	0.523921	-3.887900	25811.939966
HLA A*3002	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.580220	0.692320	-3.887900	38038.202304
HLA A*3301	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.625274	0.737370	-3.887904	42196.235576
HLA A*0202	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.209713	0.321711	-3.888002	16207.396149
HLA A*3002	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.548965	0.660945	-3.888020	35396.863809
HLA A*8001	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.400928	0.512773	-3.888155	25172.620813
HLA B*3801	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.553704	0.665274	-3.888429	35785.220381
HLA A*0216	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.471209	0.582728	-3.888481	29594.334533

HLA B*5301	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.526351	0.637857	-3.888494	33600.906315
HLA A*2603	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.644185	0.755651	-3.888533	44074.227906
HLA B*5301	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.595677	0.707098	-3.888579	39416.426245
HLA A*2402	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.482843	0.594015	-3.888828	30397.875258
HLA A*2601	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.391721	0.502859	-3.888862	24644.544872
HLA B*1502	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.605383	0.716494	-3.888889	40307.231366
HLA A*3101	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.405557	0.516619	-3.888937	25442.332225
HLA A*2902	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.412676	0.523691	-3.888985	25862.818908
HLA A*0219	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.470765	0.581735	-3.889030	29564.090706
HLA B*5801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.347865	0.458535	-3.889330	22277.441664
HLA B*4402	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.415874	0.526478	-3.889396	26053.945957
HLA B*1801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.512186	0.622672	-3.889514	32522.651592
HLA B*4801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.430064	0.540290	-3.889774	26919.339355
HLA B*4402	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.323367	0.433440	-3.889928	21055.581257
HLA B*4402	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.406624	0.516619	-3.890004	25504.897676
HLA B*0803	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.499689	0.609548	-3.890141	31600.142127
HLA B*1509	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.338458	0.448098	-3.890360	21800.074469
HLA A*2301	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.499929	0.609548	-3.890381	31617.584172
HLA A*2402	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.563651	0.673165	-3.890486	36614.357331
HLA A*2603	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.615902	0.725139	-3.890763	41295.393859
HLA A*2603	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.569549	0.678719	-3.890829	37114.928051
HLA A*1101	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.414967	0.523921	-3.891046	25999.596426
HLA B*4002	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.617469	0.726109	-3.891360	41444.673163
HLA A*0301	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.365165	0.473598	-3.891567	23182.729785
HLA A*6801	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.628960	0.737370	-3.891590	42555.926511
HLA B*7301	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.558165	0.666384	-3.891781	36154.750441
HLA B*4801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.144797	0.252948	-3.891849	13957.157421
HLA A*6901	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.340049	0.448098	-3.891950	21880.063522
HLA B*4403	1:101-109	9	LLAAGEAYH	0.930216	-0.156060	-4.666127	0.774156	-3.891971	46358.198793
HLA B*4403	1:79-87	9	GGPYGPYRQ	1.003223	-0.227036	-4.668175	0.776187	-3.891989	46577.406683
HLA A*2301	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.547480	0.655319	-3.892161	35276.046822
HLA A*3001	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.287493	0.394899	-3.892594	19386.211588
HLA A*0202	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.600599	0.707963	-3.892636	39865.702068
HLA B*3901	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.493569	0.600860	-3.892709	31157.932168
HLA B*3901	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.433027	0.540290	-3.892737	27103.607406
HLA A*3301	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.505523	0.612666	-3.892857	32027.482842
HLA B*1501	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.405646	0.512773	-3.892873	25447.563090
HLA B*4403	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.618047	0.725139	-3.892908	41499.865809
HLA B*5401	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.488959	0.595974	-3.892985	30828.964520
HLA B*1801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.515471	0.622434	-3.893037	32769.553706
HLA A*6801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.528950	0.635887	-3.893063	33802.554537
HLA B*5301	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.601083	0.707963	-3.893120	39910.154653
HLA A*0212	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.419875	0.526478	-3.893397	26295.091170
HLA B*1509	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.489429	0.595974	-3.893454	30862.338828
HLA A*3201	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.419160	0.525631	-3.893530	26251.881638
HLA A*0212	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.072033	0.178488	-3.893545	11804.114849
HLA A*2601	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.358570	0.464975	-3.893594	22833.346582
HLA B*5101	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.448893	0.555221	-3.893672	28112.092308
HLA B*7301	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-3.859598	-0.034117	-3.893715	7237.651898
HLA B*4801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.417673	0.523921	-3.893752	26162.136876
HLA A*0250	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.531628	0.637857	-3.893771	34011.668308
HLA A*0202	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.352369	0.458535	-3.893834	22509.677760
HLA B*4801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.419548	0.525631	-3.893917	26275.325362
HLA B*3901	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.487965	0.594015	-3.893950	30758.496698
HLA B*1501	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.236436	0.342354	-3.894082	17235.992240
HLA B*0803	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.506416	0.612321	-3.894095	32093.391315
HLA A*0301	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.347099	0.452989	-3.894110	22238.187262
HLA B*2705	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.360954	0.466843	-3.894111	22959.070205
HLA A*3001	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.058557	0.164416	-3.894140	11443.444835
HLA A*0211	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.503728	0.609548	-3.894180	31895.381467
HLA B*4402	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.241814	0.347463	-3.894351	17450.756599
HLA B*4601	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.407150	0.512773	-3.894377	25535.823633
HLA B*0802	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.418089	0.523691	-3.894398	26187.200438
HLA B*4001	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.361269	0.466843	-3.894426	22975.719846
HLA B*5301	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.597679	0.703210	-3.894469	39598.524788

HLA B*5701	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.404664	0.510101	-3.894563	25390.082675
HLA A*2603	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.567916	0.673165	-3.894750	36975.642649
HLA A*0212	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.353504	0.458535	-3.894969	22568.571929
HLA B*4801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.418681	0.523691	-3.894990	26222.925586
HLA A*0202	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.544769	0.649772	-3.894997	35056.504053
HLA B*4403	1:106-114	9	EAYHAFSTP	0.667866	0.046189	-4.609095	0.714055	-3.895041	40653.239124
HLA B*4001	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.407838	0.512773	-3.895065	25576.332500
HLA A*0203	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.337941	0.442758	-3.895183	21774.143986
HLA B*3801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.572779	0.677348	-3.895431	37392.040451
HLA B*5301	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.587849	0.692320	-3.895529	38712.281014
HLA B*1502	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.587872	0.692320	-3.895552	38714.375362
HLA B*1517	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.446097	0.550534	-3.895563	27931.694480
HLA B*1503	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.348598	0.452989	-3.895609	22315.075185
HLA B*0803	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.518090	0.622434	-3.895656	32967.817885
HLA A*3001	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-3.897006	0.001267	-3.895740	7888.713643
HLA A*2501	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.489758	0.594015	-3.895743	30885.722338
HLA A*2501	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.419489	0.523691	-3.895798	26271.771937
HLA A*0201	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.343902	0.448098	-3.895804	22075.051930
HLA B*3501	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.446391	0.550534	-3.895857	27950.589290
HLA B*5801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.348995	0.452989	-3.896006	22335.486546
HLA B*5101	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.499132	0.603125	-3.896007	31559.652166
HLA A*6901	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.184931	0.288865	-3.896066	15308.438002
HLA A*2402	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.518760	0.622672	-3.896088	33018.687479
HLA B*1501	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.304080	0.407915	-3.896166	20140.966755
HLA A*0219	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.399051	0.502859	-3.896192	25064.046948
HLA B*1801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.420077	0.523691	-3.896386	26307.327820
HLA A*2301	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.490434	0.594015	-3.896420	30933.881286
HLA B*5401	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.532314	0.635887	-3.896427	34065.438579
HLA B*4002	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.297227	0.400734	-3.896493	19825.623976
HLA A*0206	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.422285	0.525631	-3.896654	26441.449097
HLA B*4801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.409438	0.512773	-3.896665	25670.732934
HLA A*3001	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.291059	0.394299	-3.896761	19546.070763
HLA A*2603	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.613357	0.716494	-3.896863	41054.155253
HLA A*6901	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.339821	0.442758	-3.897063	21868.584768
HLA A*0216	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.452286	0.555221	-3.897065	28332.560612
HLA A*0212	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.284128	0.387024	-3.897105	19236.607595
HLA B*5801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.281690	0.384545	-3.897145	19128.887831
HLA B*4403	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.659015	0.761813	-3.897201	45605.231266
HLA B*1801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.509526	0.612321	-3.897206	32324.091663
HLA B*1801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.507135	0.609548	-3.897587	32146.563551
HLA A*3201	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.576106	0.678487	-3.897619	37679.578473
HLA A*3001	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.309153	0.411532	-3.897621	20377.591445
HLA A*3201	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.262001	0.364340	-3.897661	18281.045779
HLA A*0206	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.186580	0.288865	-3.897715	15366.686038
HLA B*0801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.279310	0.381582	-3.897728	19024.344084
HLA A*0203	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.261616	0.363771	-3.897844	18264.833629
HLA A*2402	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.520327	0.622434	-3.897893	33138.047200
HLA B*4501	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.624480	0.726109	-3.898371	42119.148465
HLA B*1503	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.475527	0.577123	-3.898404	29890.070004
HLA B*5301	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.504616	0.606197	-3.898419	31960.672283
HLA A*2402	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.578319	0.679867	-3.898452	37872.088069
HLA B*1517	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.050164	0.151627	-3.898537	11224.433207
HLA A*0206	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.535873	0.637330	-3.898543	34345.785592
HLA A*6901	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.372267	0.473598	-3.898669	23564.979502
HLA A*8001	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.401802	0.502859	-3.898944	25223.331187
HLA B*4403	1:470-478	9	LLGRDRSMQ	0.949209	-0.179804	-4.668544	0.769405	-3.899139	46616.984130
HLA B*1502	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.593116	0.693953	-3.899163	39184.680233
HLA B*4001	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.415794	0.516619	-3.899174	26049.154133
HLA A*2902	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.347365	0.448098	-3.899267	22251.786010
HLA A*8001	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.454602	0.555221	-3.899381	28484.094553
HLA A*2402	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.500255	0.600860	-3.899395	31641.368734
HLA B*5101	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.281232	0.381582	-3.899650	19108.718864
HLA B*7301	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.591977	0.692320	-3.899657	39082.002378
HLA A*2902	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.454913	0.555221	-3.899691	28504.442462
HLA B*0702	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.454945	0.555221	-3.899724	28506.601426

HLA B*3801	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.512141	0.612321	-3.899821	32519.308829
HLA A*6802	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.440252	0.540290	-3.899961	27558.258170
HLA B*4403	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.311561	0.411532	-3.900029	20490.901839
HLA A*0202	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.592357	0.692320	-3.900037	39116.268938
HLA A*0212	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.423751	0.523691	-3.900060	26530.860200
HLA A*2301	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.536005	0.635887	-3.900118	34356.192354
HLA A*6801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.496125	0.595974	-3.900150	31341.867278
HLA B*7301	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.565430	0.665274	-3.900156	36764.611055
HLA A*3201	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.592512	0.692320	-3.900192	39130.238000
HLA A*3201	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.578925	0.678719	-3.900206	37924.984995
HLA A*3101	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.403104	0.502859	-3.900245	25299.040890
HLA A*6802	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.423982	0.523691	-3.900291	26544.929773
HLA B*1503	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.281927	0.381582	-3.900345	19139.342688
HLA B*1501	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.424045	0.523691	-3.900354	26548.807395
HLA A*3301	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.555675	0.655319	-3.900356	35948.014985
HLA A*2603	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.662283	0.761813	-3.900469	45949.712247
HLA B*0801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.292067	0.391537	-3.900531	19591.486795
HLA B*3501	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.424459	0.523921	-3.900538	26574.097627
HLA B*3801	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.555898	0.655319	-3.900579	35966.494837
HLA B*4002	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.580464	0.679867	-3.900597	38059.609701
HLA A*2402	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.579109	0.678487	-3.900622	37940.991630
HLA B*1502	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.550800	0.650029	-3.900771	35546.736319
HLA B*5401	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.463049	0.562255	-3.900793	29043.491025
HLA A*3101	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.248024	0.347215	-3.900809	17702.065768
HLA B*1801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-3.922761	0.021903	-3.900858	8370.689762
HLA B*0803	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.497271	0.596390	-3.900881	31424.719938
HLA B*5401	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.550689	0.649772	-3.900918	35537.699185
HLA B*0702	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.417622	0.516619	-3.901002	26159.023307
HLA B*5301	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.607636	0.706599	-3.901037	40516.892054
HLA A*2402	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.537006	0.635887	-3.901119	34435.461381
HLA B*5101	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.502109	0.600860	-3.901249	31776.715484
HLA A*0216	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.349350	0.448098	-3.901252	22353.739709
HLA B*1509	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.463681	0.562255	-3.901425	29085.787630
HLA A*2403	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.425264	0.523691	-3.901573	26623.454088
HLA B*1501	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.360144	0.458535	-3.901609	22916.259090
HLA A*6801	1:182-190	9	VPDFALTRA	1.151379	-0.389566	-4.663450	0.761813	-3.901637	46073.424162
HLA B*1503	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.418470	0.516619	-3.901850	26210.161013
HLA B*5101	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.497833	0.595974	-3.901859	31465.377232
HLA B*4403	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.624364	0.722436	-3.901928	42107.984808
HLA A*2402	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.505112	0.603125	-3.901987	31997.175792
HLA B*4402	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.427644	0.525631	-3.902013	26769.756932
HLA A*6801	1:223-231	9	PRQLALHQA	1.137769	-0.360369	-4.679441	0.777400	-3.902041	47801.451583
HLA B*3801	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.568463	0.666384	-3.902079	37022.279988
HLA B*5701	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.414962	0.512773	-3.902189	25999.315117
HLA A*2601	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.286748	0.384545	-3.902203	19352.993990
HLA A*3201	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.610366	0.707963	-3.902403	40772.395278
HLA B*4601	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.412516	0.510101	-3.902415	25853.306439
HLA B*7301	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.074416	0.171999	-3.902416	11869.045758
HLA B*4801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.171031	0.268381	-3.902650	14826.250256
HLA A*0219	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.428389	0.525631	-3.902758	26815.704709
HLA A*0216	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.453376	0.550534	-3.902842	28403.770019
HLA A*2602	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.117491	0.214632	-3.902859	13106.636721
HLA A*0203	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.267262	0.364340	-3.902921	18503.825881
HLA A*2602	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.512470	0.609548	-3.902922	32543.947778
HLA A*1101	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.465965	0.562720	-3.903244	29239.135522
HLA A*0206	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.294950	0.391537	-3.903414	19721.966369
HLA A*0201	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.377159	0.473598	-3.903561	23831.901439
HLA B*3801	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.540932	0.637330	-3.903602	34748.166648
HLA A*2402	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.564554	0.660945	-3.903609	36690.498963
HLA A*0301	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.362174	0.458535	-3.903639	23023.623713
HLA A*6801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.225380	0.321711	-3.903668	16802.720894
HLA B*0702	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.486567	0.582728	-3.903839	30659.647840
HLA A*3301	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.607147	0.703210	-3.903938	40471.325782
HLA A*3001	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.268622	0.364577	-3.904045	18561.876763
HLA B*0702	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.430743	0.526478	-3.904266	26961.459529

HLA B*5801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.356843	0.452486	-3.904357	22742.735332
HLA A*8001	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.430880	0.526478	-3.904402	26969.920649
HLA A*0101	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.369398	0.464975	-3.904423	23409.834595
HLA B*5101	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.487169	0.582728	-3.904441	30702.138773
HLA B*0803	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.015956	0.111406	-3.904550	10374.231102
HLA B*2705	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.505434	0.600860	-3.904573	32020.899444
HLA A*0250	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.571064	0.666384	-3.904680	37244.662297
HLA A*2602	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.611595	0.706599	-3.904996	40887.918905
HLA A*0203	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.431495	0.526478	-3.905017	27008.174675
HLA A*6802	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.285498	0.380348	-3.905151	19297.374968
HLA A*1101	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.460373	0.555221	-3.905152	28865.079230
HLA A*6802	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.431709	0.526478	-3.905231	27021.474070
HLA A*0211	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.487975	0.582728	-3.905247	30759.162305
HLA B*4002	1:435-443	9	ALIEGLALK	0.478643	0.243793	-4.627701	0.722436	-3.905264	42432.705804
HLA A*0212	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.313462	0.407915	-3.905547	20580.778861
HLA A*2603	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.658514	0.752921	-3.905593	45552.710332
HLA A*2501	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.506467	0.600860	-3.905607	32097.211219
HLA B*3501	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.317658	0.412011	-3.905647	20780.595387
HLA A*6801	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.622574	0.716494	-3.906080	41934.758860
HLA B*4501	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.515694	0.609548	-3.906146	32786.399602
HLA B*4801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.195038	0.288865	-3.906173	15668.894779
HLA A*2501	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.468533	0.562255	-3.906277	29412.538951
HLA A*2602	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.592825	0.686428	-3.906397	39158.402935
HLA B*0702	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.271798	0.365377	-3.906422	18698.139203
HLA B*7301	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.419642	0.512773	-3.906869	26281.011841
HLA A*3301	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.519225	0.612321	-3.906904	33054.074662
HLA A*2301	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.519570	0.612666	-3.906905	33080.371492
HLA B*5301	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.590793	0.683810	-3.906982	38975.587151
HLA A*2603	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.610244	0.703210	-3.907035	40760.927036
HLA B*5801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.349811	0.442758	-3.907053	22377.454805
HLA A*6901	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.372072	0.464975	-3.907097	23554.400712
HLA A*6802	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.382313	0.475212	-3.907101	24116.454733
HLA B*3801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.529972	0.622672	-3.907300	33882.195822
HLA B*4403	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.603167	0.695627	-3.907540	40102.126618
HLA A*3001	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.287935	0.380348	-3.907587	19405.938543
HLA B*1801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.508619	0.600860	-3.907759	32256.662366
HLA A*2403	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.374617	0.466843	-3.907773	23692.808889
HLA A*0211	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.545328	0.637330	-3.907997	35101.670252
HLA A*2501	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.470720	0.562720	-3.908000	29561.052032
HLA A*0212	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.410921	0.502859	-3.908062	25758.513317
HLA A*0250	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.520397	0.612321	-3.908077	33143.425832
HLA A*2402	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.520825	0.612666	-3.908159	33176.074913
HLA A*3101	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.323346	0.415126	-3.908220	21054.556106
HLA A*3101	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.345619	0.437367	-3.908252	22162.523414
HLA A*8001	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.424914	0.516619	-3.908295	26602.002275
HLA A*6801	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.594850	0.686428	-3.908422	39341.437716
HLA A*3002	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.548467	0.639976	-3.908491	35356.290541
HLA A*3301	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.588610	0.679867	-3.908743	38780.195561
HLA A*0250	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.601450	0.692320	-3.909130	39943.850754
HLA B*1501	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.357240	0.448098	-3.909142	22763.537869
HLA A*0250	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.564485	0.655319	-3.909167	36684.743160
HLA B*4601	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.357322	0.448098	-3.909224	22767.848465
HLA B*4002	1:416-424	9	ALTSVTDWT	0.909277	-0.184138	-4.634465	0.725139	-3.909326	43098.771750
HLA B*4403	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.515614	0.606197	-3.909417	32780.369550
HLA A*0101	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.384642	0.475212	-3.909430	24246.095077
HLA B*0702	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.419536	0.510101	-3.909436	26274.614639
HLA A*0301	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.346815	0.437367	-3.909448	22223.634984
HLA B*1509	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.549559	0.639976	-3.909583	35445.344736
HLA A*0201	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.374640	0.464975	-3.909665	23694.090678
HLA A*3001	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.256849	0.347179	-3.909670	18065.442992
HLA A*3301	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.596222	0.686428	-3.909794	39465.928634
HLA B*5301	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.583023	0.673165	-3.909858	38284.494706
HLA A*0201	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.376715	0.466843	-3.909871	23807.546510
HLA A*1101	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.460434	0.550534	-3.909900	28869.139595
HLA A*0301	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.358013	0.448098	-3.909915	22804.089710

HLA A*3301	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.576428	0.666384	-3.910044	37707.515225
HLA A*0206	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.348652	0.438531	-3.910121	22317.851965
HLA B*5301	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.588817	0.678487	-3.910330	38798.662054
HLA B*3501	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.301931	0.391537	-3.910394	20041.514341
HLA A*0250	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.550374	0.639976	-3.910399	35511.946349
HLA A*1101	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.472736	0.562255	-3.910480	29698.584063
HLA A*0216	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.492229	0.581735	-3.910494	31062.000407
HLA A*0212	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.434444	0.523921	-3.910523	27192.168167
HLA B*1503	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.258087	0.347215	-3.910872	18117.021270
HLA A*2301	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.533710	0.622672	-3.911038	34175.083061
HLA A*6802	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.290171	0.379131	-3.911040	19506.141099
HLA B*5101	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.435116	0.523691	-3.911425	27234.273223
HLA B*3901	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.370005	0.458535	-3.911469	23442.531717
HLA A*0201	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.350039	0.438531	-3.911507	22389.200663
HLA A*0219	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.435243	0.523691	-3.911552	27242.230443
HLA B*3801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.493538	0.581735	-3.911803	31155.740953
HLA B*1503	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.291045	0.379131	-3.911914	19545.436321
HLA B*0803	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.387193	0.475212	-3.911981	24388.963545
HLA A*3101	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.354792	0.442758	-3.912034	22635.578427
HLA A*0202	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.591093	0.678719	-3.912374	39002.585760
HLA B*3801	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.525085	0.612666	-3.912419	33503.071125
HLA A*0202	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.549764	0.637330	-3.912433	35462.031381
HLA B*4801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.438917	0.526478	-3.912439	27473.706657
HLA B*5301	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.589834	0.677348	-3.912486	38889.653753
HLA B*4001	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.388053	0.475212	-3.912841	24437.302007
HLA B*3501	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.438562	0.525631	-3.912932	27451.272735
HLA B*5401	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.535606	0.622672	-3.912934	34324.610137
HLA B*5401	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.436704	0.523691	-3.913013	27334.053619
HLA B*5801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.351573	0.438531	-3.913042	22468.433913
HLA A*0211	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.310292	0.397240	-3.913052	20431.128297
HLA B*5301	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.525740	0.612666	-3.913075	33553.677472
HLA B*0802	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.468490	0.555221	-3.913269	29409.674956
HLA B*5401	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.550663	0.637330	-3.913333	35535.584443
HLA A*2402	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.571919	0.658550	-3.913369	37318.076733
HLA B*1509	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.423620	0.510101	-3.913519	26522.823793
HLA B*1801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.475936	0.562255	-3.913680	29918.219392
HLA B*3801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.563720	0.650029	-3.913690	36620.102090
HLA A*0211	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.475999	0.562255	-3.913744	29922.589776
HLA A*0206	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.468988	0.555221	-3.913767	29443.424159
HLA A*0301	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.292918	0.379131	-3.913787	19629.891962
HLA A*3201	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.569107	0.655319	-3.913788	37077.199163
HLA B*0801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.361981	0.448098	-3.913883	23013.412448
HLA B*4002	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.651257	0.737370	-3.913887	44797.797566
HLA A*0250	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.572438	0.658550	-3.913888	37362.720367
HLA A*2603	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.510318	0.596390	-3.913928	32383.076522
HLA B*5801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.351336	0.437367	-3.913968	22456.160541
HLA B*1509	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.454292	0.540290	-3.914002	28463.761169
HLA A*6802	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.426780	0.512773	-3.914007	26716.515665
HLA A*0203	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.437869	0.523691	-3.914178	27407.497714
HLA B*1503	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.381045	0.466843	-3.914201	24046.105173
HLA A*2301	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.510184	0.595974	-3.914210	32373.092296
HLA B*4402	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.438029	0.523691	-3.914338	27417.582033
HLA B*1503	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.508399	0.594015	-3.914384	32240.263069
HLA B*4002	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.610108	0.695627	-3.914480	40748.139341
HLA A*0212	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.431105	0.516619	-3.914486	26983.931098
HLA B*0801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.417368	0.502859	-3.914509	26143.743890
HLA B*1801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.309562	0.394899	-3.914663	20396.782325
HLA A*6901	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.293872	0.379131	-3.914741	19673.054735
HLA A*0301	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.367277	0.452486	-3.914791	23295.753389
HLA B*0802	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.477545	0.562720	-3.914825	30029.295238
HLA B*4801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.262088	0.347215	-3.914873	18284.705387
HLA B*1502	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.581315	0.666384	-3.914931	38134.217906
HLA B*4501	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.621695	0.706599	-3.915097	41849.998100
HLA A*3301	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.621712	0.706599	-3.915113	41851.582957
HLA A*2603	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.564892	0.649772	-3.915120	36719.092880

HLA B*4501	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.527845	0.612666	-3.915180	33716.715718
HLA A*3001	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.273913	0.358727	-3.915186	18789.400568
HLA A*2301	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.521417	0.606197	-3.915220	33221.334437
HLA A*3301	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.592759	0.677348	-3.915411	39152.471791
HLA A*2601	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.389054	0.473598	-3.915456	24493.685471
HLA B*0803	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.492871	0.577123	-3.915748	31107.909761
HLA B*1501	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.189381	0.273594	-3.915787	15466.099658
HLA B*5301	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.555778	0.639976	-3.915802	35956.572894
HLA A*2501	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.363924	0.448098	-3.915826	23116.604624
HLA B*3801	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.551744	0.635887	-3.915857	35624.126611
HLA B*4501	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.576881	0.660945	-3.915937	37746.906527
HLA A*0219	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.442437	0.526478	-3.915959	27697.258569
HLA B*4403	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.624012	0.707963	-3.916049	42073.828739
HLA A*0202	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.478379	0.562255	-3.916124	30087.022234
HLA A*2403	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.441777	0.525631	-3.916146	27655.185769
HLA B*4501	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.538667	0.622434	-3.916233	34567.422046
HLA A*3101	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.374915	0.458535	-3.916380	23709.092767
HLA A*0250	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.595104	0.678719	-3.916385	39364.430377
HLA A*6802	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.419278	0.502859	-3.916419	26258.983587
HLA A*6801	1:317-325	9	ARFDQKKAD	1.403810	-0.650889	-4.669345	0.752921	-3.916424	46703.061218
HLA A*2601	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.383335	0.466843	-3.916492	24173.274860
HLA B*3801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.526062	0.609548	-3.916514	33578.555159
HLA A*2501	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.375112	0.458535	-3.916577	23719.869354
HLA B*5101	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.510598	0.594015	-3.916583	32403.930707
HLA B*0803	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.443182	0.526478	-3.916704	27744.798315
HLA B*3901	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.324683	0.407915	-3.916768	21119.466661
HLA B*5701	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.419640	0.502859	-3.916781	26280.869664
HLA B*2705	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.303888	0.387024	-3.916864	20132.033983
HLA A*0101	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.350403	0.433440	-3.916963	22407.982616
HLA A*3301	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.427217	0.510101	-3.917116	26743.412405
HLA B*1517	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.296287	0.379131	-3.917156	19782.768590
HLA B*0801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.329236	0.412011	-3.917225	21342.055675
HLA B*1501	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.338390	0.421060	-3.917330	21796.654593
HLA A*3001	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.276998	0.359537	-3.917460	18923.340282
HLA B*1801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.511648	0.594015	-3.917633	32482.385377
HLA A*3001	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.299466	0.381754	-3.917712	19928.101386
HLA B*0702	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.443395	0.525631	-3.917764	27758.460439
HLA B*1502	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.530115	0.612321	-3.917794	33893.378901
HLA A*3101	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.329927	0.412011	-3.917916	21376.027382
HLA B*3901	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.495171	0.577123	-3.918048	31273.103076
HLA B*1501	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.082601	0.164416	-3.918185	12094.875713
HLA B*4801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.421108	0.502859	-3.918249	26369.880430
HLA B*4403	1:18-26	9	TPHVGLVRT	1.189163	-0.448618	-4.658881	0.740545	-3.918336	45591.170437
HLA B*3901	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.501115	0.582728	-3.918387	31704.081324
HLA B*5101	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.469096	0.550534	-3.918562	29450.752211
HLA A*6801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.442463	0.523691	-3.918772	27698.906848
HLA A*2602	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.598654	0.679867	-3.918787	39687.527467
HLA B*3901	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.428974	0.510101	-3.918874	26851.851477
HLA B*3501	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.474157	0.555221	-3.918936	29795.946268
HLA A*0212	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.431709	0.512773	-3.918936	27021.474070
HLA A*2301	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.496092	0.577123	-3.918969	31339.493583
HLA B*0801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.050005	0.131008	-3.918997	11220.304807
HLA B*5401	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.481732	0.562720	-3.919012	30320.190252
HLA B*1501	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.172018	0.252948	-3.919070	14859.976072
HLA B*1501	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.361866	0.442758	-3.919108	23007.312756
HLA A*0206	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.240973	0.321711	-3.919262	17416.991722
HLA A*0301	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.283684	0.364340	-3.919344	19216.948811
HLA B*5801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.352959	0.433440	-3.919519	22540.264012
HLA B*3801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.559648	0.639976	-3.919672	36278.380640
HLA A*2402	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.557176	0.637330	-3.919846	36072.499409
HLA B*0802	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.445611	0.525631	-3.919980	27900.432762
HLA B*5301	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.578665	0.658550	-3.920114	37902.217966
HLA B*0803	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.475670	0.555221	-3.920449	29899.935451
HLA A*3101	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.394096	0.473598	-3.920498	24779.704980
HLA A*0212	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.359077	0.438531	-3.920546	22860.043766

HLA A*3001	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.286025	0.365377	-3.920648	19320.773994
HLA A*3101	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.189061	0.268381	-3.920680	15454.724738
HLA B*5701	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.385718	0.464975	-3.920742	24306.244822
HLA B*1517	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.363560	0.442758	-3.920802	23097.228717
HLA A*3301	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.543265	0.622434	-3.920831	34935.336782
HLA B*4801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.437522	0.516619	-3.920902	27385.562311
HLA A*0301	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.364086	0.442758	-3.921328	23125.235255
HLA B*4402	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.431937	0.510101	-3.921836	27035.657560
HLA B*3901	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.477228	0.555221	-3.922007	30007.371798
HLA A*2601	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.370120	0.448098	-3.922022	23448.746794
HLA A*0216	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.088292	0.166266	-3.922026	12254.394650
HLA B*1517	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.387069	0.464975	-3.922093	24381.971644
HLA A*2902	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.157188	0.235091	-3.922097	14361.115028
HLA B*4501	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.608571	0.686428	-3.922143	40604.224414
HLA B*4403	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.572173	0.650029	-3.922144	37339.886863
HLA A*0219	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.446083	0.523921	-3.922162	27930.787851
HLA B*1502	1:5-13	9	ETVRVRFCP	0.711965	-0.016338	-4.618014	0.695627	-3.922386	41496.722792
HLA A*0202	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.572561	0.650029	-3.922532	37373.232511
HLA B*0802	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.473152	0.550534	-3.922618	29727.035573
HLA B*4002	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.588048	0.665274	-3.922774	38730.086585
HLA A*0206	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.463103	0.540290	-3.922813	29047.105058
HLA A*0216	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.006281	0.083388	-3.922893	10145.670159
HLA B*4801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.433156	0.510101	-3.923056	27111.673119
HLA B*3901	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.158208	0.235091	-3.923117	14394.872988
HLA B*4501	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.500610	0.577123	-3.923487	31667.226915
HLA B*4601	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.426369	0.502859	-3.923510	26691.234292
HLA A*2601	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.360926	0.437367	-3.923559	22957.579781
HLA A*2602	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.573421	0.649772	-3.923649	37447.305546
HLA B*4002	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.640263	0.716494	-3.923770	43678.068251
HLA B*1517	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.478995	0.555221	-3.923774	30129.697544
HLA B*0702	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.436558	0.512773	-3.923785	27324.886956
HLA A*1101	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.500986	0.577123	-3.923863	31694.649371
HLA A*0301	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.362399	0.438531	-3.923868	23035.584123
HLA A*2602	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.524732	0.600860	-3.923872	33475.894968
HLA B*5101	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.505664	0.581735	-3.923929	32037.880437
HLA A*6802	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.447913	0.523921	-3.923993	28048.745051
HLA B*0801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.389315	0.464975	-3.924339	24508.398290
HLA B*0803	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.474890	0.550534	-3.924356	29846.280878
HLA B*4801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.391272	0.466843	-3.924429	24619.093091
HLA A*1101	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.448369	0.523691	-3.924678	28078.198181
HLA A*0201	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.367467	0.442758	-3.924709	23305.963849
HLA B*0802	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.465217	0.540290	-3.924927	29188.877372
HLA B*5701	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.373031	0.448098	-3.924933	23606.448223
HLA A*6802	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-3.789334	-0.136008	-3.925342	6156.501547
HLA B*0801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.449318	0.523921	-3.925398	28139.632867
HLA B*0801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.105669	0.180214	-3.925455	12754.653172
HLA B*3901	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.438389	0.512773	-3.925616	27440.285317
HLA A*3201	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.598957	0.673165	-3.925792	39715.234094
HLA A*6802	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.442535	0.516619	-3.925916	27703.552526
HLA B*4601	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.320240	0.394299	-3.925941	20904.513767
HLA B*4501	1:11-19	9	FCPSPTGTP	0.674709	0.062661	-4.663394	0.737370	-3.926024	46067.442499
HLA B*1509	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.508784	0.582728	-3.926056	32268.880027
HLA A*0206	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.452824	0.526478	-3.926346	28367.682570
HLA B*1502	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.488693	0.562255	-3.926438	30810.123995
HLA A*0202	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.285315	0.358727	-3.926588	19289.233746
HLA B*7301	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.605569	0.678719	-3.926849	40324.461603
HLA B*1501	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.324124	0.397240	-3.926884	21092.291714
HLA B*1517	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.452547	0.525631	-3.926916	28349.579359
HLA A*0219	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.443569	0.516619	-3.926950	27769.575258
HLA A*0211	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.527897	0.600860	-3.927037	33720.728838
HLA A*6901	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.385772	0.458535	-3.927237	24309.269374
HLA B*1517	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.450991	0.523691	-3.927300	28248.231279
HLA A*0101	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.365891	0.438531	-3.927359	23221.515738
HLA A*2501	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.510450	0.582728	-3.927722	32392.888584
HLA B*4403	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.621702	0.693953	-3.927750	41850.677317

HLA A*2501	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.440771	0.512773	-3.927998	27591.226128
HLA B*5801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.349061	0.421060	-3.928001	22338.870112
HLA A*2402	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.578044	0.650029	-3.928015	37848.124249
HLA B*0801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.335991	0.407915	-3.928076	21676.592727
HLA B*1509	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.505455	0.577123	-3.928332	32022.458547
HLA B*0702	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.386902	0.458535	-3.928367	24372.608275
HLA B*5101	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.468737	0.540290	-3.928447	29426.385526
HLA A*2601	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.387252	0.458535	-3.928717	24392.262308
HLA A*2403	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.441593	0.512773	-3.928820	27643.518535
HLA B*1517	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.469129	0.540290	-3.928839	29452.982850
HLA B*5701	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.308011	0.379131	-3.928880	20324.084927
HLA B*4001	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.393929	0.464975	-3.928954	24770.188870
HLA A*2902	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.309463	0.380348	-3.929115	20392.148389
HLA B*4002	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.635729	0.706599	-3.929130	43224.394328
HLA B*7301	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.532349	0.603125	-3.929224	34068.203045
HLA B*5101	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.506566	0.577123	-3.929443	32104.505027
HLA A*2603	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.623467	0.693953	-3.929514	42021.055242
HLA A*0250	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.579330	0.649772	-3.929558	37960.290653
HLA A*8001	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.377765	0.448098	-3.929667	23865.188073
HLA A*2301	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.530552	0.600860	-3.929692	33927.500919
HLA A*6901	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.295150	0.365377	-3.929773	19731.037415
HLA A*0219	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.442566	0.512773	-3.929793	27705.500945
HLA A*6901	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.327162	0.397240	-3.929921	21240.349240
HLA A*6801	1:215-223	9	GEDLLPSTP	0.867517	-0.111866	-4.685695	0.755651	-3.930044	48494.826967
HLA B*5701	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.342168	0.412011	-3.930156	21987.093030
HLA A*0101	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.330984	0.400734	-3.930250	21428.129648
HLA B*1503	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.275475	0.345166	-3.930309	18857.118607
HLA B*5401	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.485658	0.555221	-3.930437	30595.525119
HLA A*2601	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.383714	0.452989	-3.930724	24194.338764
HLA A*2402	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.580523	0.649772	-3.930751	38064.757506
HLA A*3301	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.591732	0.660945	-3.930788	39060.019915
HLA A*2301	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.543159	0.612321	-3.930838	34926.832983
HLA A*0203	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.199258	0.268381	-3.930877	15821.878285
HLA B*5301	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.580930	0.650029	-3.930900	38100.399401
HLA A*0203	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.443708	0.512773	-3.930935	27778.440262
HLA B*4402	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.383500	0.452486	-3.931014	24182.430825
HLA A*2501	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.486295	0.555221	-3.931073	30640.413502
HLA B*3801	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.527053	0.595974	-3.931079	33655.301673
HLA A*2501	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.456757	0.525631	-3.931126	28625.751476
HLA B*0801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.368602	0.437367	-3.931235	23366.941416
HLA B*1502	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.527944	0.596390	-3.931554	33724.377544
HLA B*4403	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.592564	0.660945	-3.931619	39134.895463
HLA B*4801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.318661	0.387024	-3.931637	20828.654521
HLA B*4402	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.398588	0.466843	-3.931745	25037.349215
HLA B*0803	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.448421	0.516619	-3.931801	28081.540178
HLA B*4501	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.554503	0.622672	-3.931831	35851.102939
HLA B*4601	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.384997	0.452989	-3.932007	24265.909640
HLA B*0802	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.458486	0.526478	-3.932008	28739.957227
HLA A*0212	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.398880	0.466843	-3.932036	25054.150561
HLA A*2603	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.567930	0.635887	-3.932043	36976.842873
HLA A*6801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.100566	0.168455	-3.932110	12605.659509
HLA A*3001	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.257499	0.325371	-3.932129	18092.535063
HLA B*2705	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.457835	0.525631	-3.932204	28696.921526
HLA A*2403	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.435419	0.502859	-3.932560	27253.285994
HLA B*4002	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.640649	0.707963	-3.932685	43716.837582
HLA B*4001	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.391434	0.458535	-3.932899	24628.284679
HLA A*0202	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.319958	0.387024	-3.932934	20890.947239
HLA A*6901	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.385542	0.452486	-3.933056	24296.384765
HLA A*0301	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.366584	0.433440	-3.933144	23258.604945
HLA A*0201	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.099659	0.166266	-3.933393	12579.363619
HLA A*0301	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.345471	0.412011	-3.933460	22154.971203
HLA B*5401	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.484027	0.550534	-3.933493	30480.870717
HLA A*0211	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.536635	0.603125	-3.933510	34406.039817
HLA A*3002	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.450491	0.516619	-3.933871	28215.699408
HLA A*6801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.071098	0.136944	-3.934154	11778.726328

HLA B*4501	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.650690	0.716494	-3.934197	44739.429004
HLA B*4601	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.399225	0.464975	-3.934250	25074.082891
HLA A*0250	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.530723	0.596390	-3.934333	33940.902278
HLA A*2402	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.589670	0.655319	-3.934351	38874.929331
HLA B*5401	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.530768	0.596390	-3.934378	33944.391171
HLA A*3002	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.497145	0.562720	-3.934425	31415.541049
HLA A*0201	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.392961	0.458535	-3.934426	24715.040714
HLA B*1509	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.294133	0.359537	-3.934595	19684.871907
HLA A*2603	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.530582	0.595974	-3.934608	33929.887075
HLA B*4402	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.335406	0.400734	-3.934672	21647.412662
HLA B*0803	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.475015	0.540290	-3.934724	29854.839754
HLA B*5701	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.409981	0.475212	-3.934769	25702.833302
HLA B*7301	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.531327	0.596390	-3.934937	33988.124543
HLA B*1801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.461562	0.526478	-3.935084	28944.202858
HLA B*2705	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.445190	0.510101	-3.935090	27873.427893
HLA A*0216	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.438006	0.502859	-3.935147	27416.098812
HLA A*0101	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.388164	0.452989	-3.935174	24443.516342
HLA A*6801	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.596173	0.660945	-3.935228	39461.445257
HLA A*2403	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.388222	0.452989	-3.935233	24446.822484
HLA B*4402	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.066470	0.131008	-3.935462	11653.861324
HLA B*3801	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.557959	0.622434	-3.935525	36137.542337
HLA B*0702	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.347630	0.412011	-3.935619	22265.393075
HLA A*0250	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.585706	0.650029	-3.935677	38521.752035
HLA B*7301	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.558123	0.622434	-3.935689	36151.229935
HLA A*3301	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.608996	0.673165	-3.935831	40644.003134
HLA B*7301	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.614381	0.678487	-3.935895	41151.104461
HLA B*4402	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.394557	0.458535	-3.936022	24805.993785
HLA B*2705	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.459743	0.523691	-3.936052	28823.259510
HLA B*4002	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.643332	0.707098	-3.936234	43987.760319
HLA B*4601	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.379022	0.442758	-3.936264	23934.360920
HLA B*4001	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.379038	0.442758	-3.936280	23935.267312
HLA B*4601	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.409889	0.473598	-3.936291	25697.410945
HLA A*3101	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.388911	0.452486	-3.936425	24485.603809
HLA B*3501	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.462955	0.526478	-3.936477	29037.206823
HLA B*1801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.067527	0.131008	-3.936519	11682.266630
HLA A*0301	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.328069	0.391537	-3.936532	21284.750046
HLA B*1501	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.258254	0.321711	-3.936542	18123.981393
HLA B*2705	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.439516	0.502859	-3.936657	27511.633386
HLA A*3101	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.384947	0.448098	-3.936849	24263.153003
HLA A*3001	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.271277	0.334311	-3.936966	18675.696303
HLA B*5401	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.345373	0.408334	-3.937038	22149.937826
HLA A*0203	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.278046	0.340987	-3.937059	18969.053844
HLA A*0206	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.537939	0.600860	-3.937079	34509.498794
HLA B*4402	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.374647	0.437367	-3.937280	23694.475228
HLA A*0250	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.514437	0.577123	-3.937314	32691.643423
HLA A*6901	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.345307	0.407915	-3.937392	22146.582876
HLA B*4402	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.412622	0.475212	-3.937410	25859.601063
HLA A*0203	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.370867	0.433440	-3.937427	23489.121442
HLA A*1101	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.463058	0.525631	-3.937427	29044.119520
HLA A*3201	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.500251	0.562720	-3.937531	31641.026383
HLA A*3002	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.301884	0.364340	-3.937543	20039.346011
HLA A*0201	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.324735	0.387024	-3.937711	21121.980398
HLA A*3201	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.531950	0.594015	-3.937935	34036.885564
HLA A*2403	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.376538	0.438531	-3.938007	23797.888756
HLA B*7301	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.519789	0.581735	-3.938054	33097.019066
HLA A*2603	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.541228	0.603125	-3.938103	34771.860672
HLA B*2705	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.380995	0.442758	-3.938238	24043.373506
HLA A*3101	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.302830	0.364577	-3.938253	20083.083159
HLA A*3201	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.599303	0.660945	-3.938358	39746.830343
HLA A*3201	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.624801	0.686428	-3.938373	42150.376845
HLA B*4002	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.371908	0.433440	-3.938468	23545.482532
HLA A*2301	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.455338	0.516619	-3.938718	28532.367395
HLA B*1501	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.236220	0.297408	-3.938812	17227.415853
HLA B*4002	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.642087	0.703210	-3.938877	43861.817439
HLA B*5301	1:358-366	9	DEAAFAAAA	1.054753	-0.399434	-4.594197	0.655319	-3.938878	39282.314663

HLA B*5801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.350440	0.411532	-3.938908	22409.922296
HLA B*5801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.354120	0.415126	-3.938994	22600.583099
HLA B*4002	1:141-149	9	DAQRAAYLA	1.049780	-0.355827	-4.632975	0.693953	-3.939023	42951.201796
HLA A*2902	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.347005	0.407915	-3.939091	22233.375537
HLA B*3801	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.463061	0.523691	-3.939370	29044.276646
HLA B*7301	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.552050	0.612666	-3.939384	35649.189358
HLA A*0101	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.398133	0.458535	-3.939597	25011.085838
HLA B*1503	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.463533	0.523921	-3.939612	29075.876213
HLA B*0801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.392503	0.452486	-3.940017	24688.981864
HLA B*0801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.406894	0.466843	-3.940050	25520.770160
HLA A*3002	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.324622	0.384545	-3.940077	21116.496267
HLA B*2705	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.415331	0.475212	-3.940118	26021.407084
HLA A*0206	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.304524	0.364340	-3.940184	20161.570801
HLA B*5801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.334492	0.394299	-3.940193	21601.904733
HLA A*0219	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.405193	0.464975	-3.940217	25421.006937
HLA B*0802	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.450336	0.510101	-3.940235	28205.626715
HLA B*4001	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.388394	0.448098	-3.940296	24456.478976
HLA B*5701	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.413942	0.473598	-3.940344	25938.343142
HLA B*0801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.398880	0.458535	-3.940345	25054.150561
HLA B*1801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.503126	0.562720	-3.940406	31851.239119
HLA A*2402	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.580563	0.639976	-3.940587	38068.258411
HLA B*0702	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.407577	0.466843	-3.940734	25560.978582
HLA A*2602	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.613944	0.673165	-3.940779	41109.717425
HLA B*0802	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.407718	0.466843	-3.940875	25569.276852
HLA B*0801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.414555	0.473598	-3.940957	25974.993460
HLA B*7301	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.599514	0.658550	-3.940964	39766.187390
HLA A*2403	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.321330	0.380348	-3.940983	20957.053954
HLA B*0801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.299741	0.358727	-3.941014	19940.719011
HLA A*0206	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.451149	0.510101	-3.941048	28258.472061
HLA B*4501	1:203-211	9	DDALMKITH	1.190427	-0.498107	-4.633370	0.692320	-3.941050	42990.256229
HLA A*3301	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.467553	0.526478	-3.941075	29346.261292
HLA A*0101	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.362197	0.421060	-3.941137	23024.869300
HLA B*1517	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.262990	0.321711	-3.941279	18322.729469
HLA A*2902	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.034907	0.093574	-3.941333	10836.944878
HLA A*0101	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.389489	0.448098	-3.941391	24518.211745
HLA A*3002	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.591488	0.650029	-3.941459	39038.049817
HLA B*1502	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.504271	0.562720	-3.941550	31935.265543
HLA A*0206	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.458174	0.516619	-3.941554	28719.285827
HLA A*3301	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.620389	0.678487	-3.941902	41724.306688
HLA B*5801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.333472	0.391537	-3.941936	21551.245291
HLA A*2603	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.504202	0.562255	-3.941947	31930.255715
HLA A*6901	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.306538	0.364577	-3.941961	20255.262410
HLA A*0301	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.357176	0.415126	-3.942050	22760.213110
HLA B*0702	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.444948	0.502859	-3.942090	27857.900627
HLA B*0702	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.466030	0.523921	-3.942110	29243.564911
HLA B*3801	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.538517	0.596390	-3.942126	34555.455738
HLA B*1517	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.466051	0.523921	-3.942131	29244.988785
HLA B*4403	1:193-201	9	DPLYTLVNP	0.947067	-0.230573	-4.658712	0.716494	-3.942218	45573.415586
HLA A*2603	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.648886	0.706599	-3.942287	44553.931473
HLA B*1503	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.350344	0.407915	-3.942429	22404.952204
HLA A*2603	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.603405	0.660945	-3.942460	40124.044359
HLA B*1502	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.592505	0.649772	-3.942734	39129.602935
HLA A*2603	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.565219	0.622434	-3.942785	36746.715089
HLA B*4403	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.650084	0.707098	-3.942986	44677.027442
HLA A*2403	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.385770	0.442758	-3.943012	24309.137864
HLA B*7301	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.539050	0.595974	-3.943076	34597.917454
HLA B*1502	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.520334	0.577123	-3.943211	33138.585024
HLA B*4501	1:346-354	9	DHLDTHGHH	1.008373	-0.300410	-4.651174	0.707963	-3.943211	44789.316079
HLA A*1101	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.483536	0.540290	-3.943246	30446.426484
HLA B*5801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.355308	0.412011	-3.943297	22662.534779
HLA A*2301	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.539694	0.596390	-3.943303	34649.240309
HLA A*2403	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.416952	0.473598	-3.943354	26118.721920
HLA A*2602	1:29-37	9	FNWAYARHT	0.979245	-0.318300	-4.604302	0.660945	-3.943358	40207.049551
HLA A*0206	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.330399	0.387024	-3.943375	21399.284053
HLA A*2601	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.395863	0.452486	-3.943377	24880.720021

```
HLA A*2301	1:66-74 9	RWLGLDWDE	0.694093	-0.436380	-4.201142	0.257713	-3.943429	15890.674296
HLA B*5801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.351921	0.408334	-3.943586	22486.430774
HLA B*0803	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.526353	0.582728	-3.943626	33601.088093
HLA B*1517	1:42-50 9	VFRIEDTDA	0.672491	-0.155872	-4.460377	0.516619	-3.943758	28865.391546
HLA A*2501	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.494490	0.550534	-3.943956	31224.078176
HLA A*1101	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.456766	0.512773	-3.943993	28626.370932
HLA B*4001	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.397089	0.452989	-3.944100	24951.081534
HLA A*0219	1:30-38 9	NWAYARHTG	1.030515	-0.520414	-4.454299	0.510101	-3.944199	28464.223131
HLA A*2602	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.567098	0.622672	-3.944426	36906.096258
HLA A*6901	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.352896	0.408334	-3.944561	22536.971863
HLA A*0211	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.387489	0.442758	-3.944732	24405.593853
HLA B*5401	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.557087	0.612321	-3.944766	36065.084539
HLA B*4501	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.623314	0.678487	-3.944827	42006.281438
HLA B*1517	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.290007	0.345166	-3.944841	19498.755673
HLA B*4403	1:11-19 9	FCPSPTGTP	0.674709	0.062661	-4.682404	0.737370	-3.945034	48128.661705
HLA A*0216	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.457927	0.512773	-3.945154	28702.976804
HLA B*1517	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.457983	0.512773	-3.945210	28706.703764
HLA B*5401	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.527023	0.581735	-3.945288	33652.934827
HLA A*2402	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.528287	0.582728	-3.945559	33751.025057
HLA A*3002	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.469604	0.523921	-3.945683	29485.186592
HLA A*0301	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.340009	0.394299	-3.945710	21878.051346
HLA B*4501	1:217-225	9	DLLPSTPRQ	0.947510	-0.240412	-4.653096	0.707098	-3.945998	44987.960968
HLA A*0211	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.486436	0.540290	-3.946145	30650.360791
HLA A*2403	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.404704	0.458535	-3.946169	25392.417861
HLA A*0201	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.398793	0.452486	-3.946307	25049.136076
HLA A*2402	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.552529	0.606197	-3.946332	35688.554141
HLA A*3101	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.326997	0.380458	-3.946539	21232.307207
HLA B*1801	1:32-40 9	AYARHTGGT	0.723455	-0.146332	-4.523682	0.577123	-3.946559	33395.040676
HLA A*3101	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.231951	0.285370	-3.946581	17058.903915
HLA A*0219	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.385130	0.438531	-3.946599	24273.393519
HLA A*0203	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.413524	0.466843	-3.946681	25913.377570
HLA B*3501	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.389465	0.442758	-3.946707	24516.885373
HLA B*0803	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.508986	0.562255	-3.946731	32283.896632
HLA A*2602	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.605296	0.658550	-3.946746	40299.164041
HLA B*5401	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.549945	0.603125	-3.946820	35476.806574
HLA B*4001	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.385384	0.438531	-3.946853	24287.579831
HLA B*0802	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.459642	0.512773	-3.946869	28816.555273
HLA B*3501	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.347637	0.400734	-3.946903	22265.754437
HLA A*0101	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.390053	0.442758	-3.947295	24550.066214
HLA B*4002	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.460117	0.512773	-3.947344	28848.063148
HLA B*1517	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.473831	0.526478	-3.947353	29773.548895
HLA A*2402	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.543340	0.595974	-3.947366	34941.385187
HLA A*0101	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.355708	0.408334	-3.947373	22683.386672
HLA A*2902	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.348262	0.400734	-3.947528	22297.818603
HLA B*1501	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.421263	0.473598	-3.947665	26379.297547
HLA B*4403	1:121-129	9	HVAAGRNPK	0.438405	0.287704	-4.673800	0.726109	-3.947691	47184.566729
HLA B*5801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.329328	0.381582	-3.947746	21346.559018
HLA B*5101	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.460580	0.512773	-3.947806	28878.824307
HLA A*0201	1:56-64 9	ESYLALLDA	0.685714	-0.294177	-4.339426	0.391537	-3.947889	21848.718285
HLA A*2403	1:22-30 9	GLVRTALFN	1.049559	-0.584584	-4.412908	0.464975	-3.947933	25876.674201
HLA B*1517	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.224764	0.276822	-3.947942	16778.921739
HLA A*0301	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.369004	0.421060	-3.947944	23388.567966
HLA B*1517	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.245353	0.297408	-3.947945	17593.513779
HLA A*3002	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.329586	0.381582	-3.948005	21359.265876
HLA A*0201	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.355948	0.407915	-3.948033	22695.907016
HLA B*4403	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.631880	0.683810	-3.948070	42843.057831
HLA B*4501	1:175-183	9	VTFAAGSVP	0.636595	0.047215	-4.631998	0.683810	-3.948188	42854.648208
HLA B*2705	1:42-50 9	VFRIEDTDA	0.672491	-0.155872	-4.465018	0.516619	-3.948398	29175.458227
HLA A*0206	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.313234	0.364577	-3.948657	20569.981740
HLA A*2902	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.423918	0.475212	-3.948706	26541.052718
HLA A*2301	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.531499	0.582728	-3.948771	34001.549849
HLA A*2301	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.511103	0.562255	-3.948847	32441.642494
HLA B*1502	1:68-76 9	LGLDWDEGP	0.726280	-0.086304	-4.589280	0.639976	-3.949304	38840.033698
HLA A*6802	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.357705	0.408334	-3.949371	22787.934280
HLA B*5301	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.599162	0.649772	-3.949390	39733.930880
```

HLA A*6901	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.382936	0.433440	-3.949496	24151.053374
HLA B*1517	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.086525	0.136944	-3.949581	12204.642144
HLA A*2402	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.504813	0.555221	-3.949592	31975.199494
HLA B*4501	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.545593	0.595974	-3.949619	35123.135076
HLA A*0212	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.314272	0.364577	-3.949695	20619.226937
HLA B*4501	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.653078	0.703210	-3.949868	44986.013971
HLA A*0203	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.161859	0.211872	-3.949987	14516.400343
HLA B*5701	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.337013	0.387024	-3.949989	21727.664361
HLA B*4801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.392790	0.442758	-3.950032	24705.282130
HLA B*4002	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.627473	0.677348	-3.950124	42410.444690
HLA A*3201	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.587475	0.637330	-3.950145	38678.996097
HLA A*6901	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.362214	0.412011	-3.950202	23025.741250
HLA B*7301	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.314817	0.364577	-3.950240	20645.122258
HLA B*5301	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.553408	0.603125	-3.950283	35760.835840
HLA B*5801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.358344	0.407915	-3.950429	22821.491177
HLA A*8001	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.344863	0.394299	-3.950564	22123.950253
HLA A*0216	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.389141	0.438531	-3.950610	24498.588762
HLA B*1501	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.344980	0.394299	-3.950681	22129.935468
HLA B*5401	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.533592	0.582728	-3.950864	34165.840140
HLA B*0801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.393640	0.442758	-3.950882	24753.711864
HLA A*2601	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.389493	0.438531	-3.950962	24518.477028
HLA A*2601	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.393828	0.442758	-3.951070	24764.427369
HLA B*5801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.352127	0.400734	-3.951393	22497.138443
HLA A*8001	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.461606	0.510101	-3.951506	28947.178125
HLA B*1509	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.464282	0.512773	-3.951509	29126.097364
HLA B*5801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.330644	0.379131	-3.951513	21411.327288
HLA A*6901	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.338566	0.387024	-3.951542	21805.500199
HLA A*2602	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.618115	0.666384	-3.951731	41506.377100
HLA A*0211	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.533808	0.581735	-3.952073	34182.849046
HLA A*6801	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.658827	0.706599	-3.952228	45585.497996
HLA B*4501	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.589559	0.637330	-3.952229	38865.046062
HLA A*3001	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.198243	0.245974	-3.952269	15784.944589
HLA A*2603	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.631063	0.678487	-3.952576	42762.475593
HLA A*3001	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.229411	0.276822	-3.952589	16959.433048
HLA B*5301	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.588525	0.635887	-3.952638	38772.643621
HLA B*4002	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.639209	0.686428	-3.952780	43572.101217
HLA A*0250	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.555952	0.603125	-3.952827	35970.970335
HLA B*3901	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.300201	0.347179	-3.953022	19961.874132
HLA A*6901	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.374095	0.421060	-3.953035	23664.371015
HLA B*1509	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.559253	0.606197	-3.953057	36245.423600
HLA A*0202	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.419959	0.466843	-3.953116	26300.212796
HLA A*0201	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.386679	0.433440	-3.953239	24360.085448
HLA B*7301	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.593276	0.639976	-3.953300	39199.097849
HLA A*6801	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.575984	0.622672	-3.953312	37668.980162
HLA B*3801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.559643	0.606197	-3.953447	36277.988118
HLA B*5701	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.338012	0.384545	-3.953467	21777.678144
HLA A*0101	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.405977	0.452486	-3.953492	25466.981754
HLA B*1509	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.477223	0.523691	-3.953532	30007.047127
HLA B*4002	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.214751	0.261006	-3.953745	16396.476969
HLA B*3901	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.200311	0.246392	-3.953918	15860.271175
HLA A*0301	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.362054	0.407915	-3.954139	23017.272272
HLA B*1502	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.612833	0.658550	-3.954283	41004.657167
HLA B*7301	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.590175	0.635887	-3.954288	38920.172085
HLA A*0219	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.397186	0.442758	-3.954428	24956.616434
HLA A*0211	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.037858	0.083388	-3.954470	10910.830713
HLA A*6802	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.428081	0.473598	-3.954483	26796.707272
HLA A*0301	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.363099	0.408334	-3.954765	23072.750821
HLA A*3101	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.295754	0.340987	-3.954767	19758.489374
HLA A*6901	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.201434	0.246392	-3.955041	15901.337753
HLA A*0216	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.481617	0.526478	-3.955139	30312.153903
HLA B*3801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.517432	0.562255	-3.955177	32917.917062
HLA B*1503	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.376261	0.421060	-3.955201	23782.701819
HLA B*1503	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.403402	0.448098	-3.955304	25316.428718
HLA A*0216	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.478997	0.523691	-3.955306	30129.860542
HLA B*3501	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.430666	0.475212	-3.955454	26956.646628

HLA B*4801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.403651	0.448098	-3.955553	25330.950543
HLA B*3901	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.482129	0.526478	-3.955651	30347.923807
HLA A*0206	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.537586	0.581735	-3.955851	34481.506269
HLA A*3201	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.532995	0.577123	-3.955872	34118.924696
HLA A*1101	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.465995	0.510101	-3.955894	29241.191940
HLA A*0206	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.506634	0.550534	-3.956100	32109.542194
HLA A*0250	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.565653	0.609548	-3.956105	36783.510696
HLA A*0202	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.557061	0.600860	-3.956201	36062.938413
HLA B*4001	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.429860	0.473598	-3.956262	26906.672471
HLA B*0702	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.431502	0.475212	-3.956290	27008.613012
HLA B*3801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.557202	0.600860	-3.956342	36074.646103
HLA B*5701	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.414941	0.458535	-3.956406	25998.049267
HLA A*0212	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.430036	0.473598	-3.956438	26917.591844
HLA A*2602	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.593774	0.637330	-3.956444	39244.080948
HLA A*3002	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.594033	0.637330	-3.956702	39267.441572
HLA A*0219	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.423787	0.466843	-3.956943	26533.013223
HLA A*2501	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.459837	0.502859	-3.956978	28829.497411
HLA B*4002	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.635668	0.678487	-3.957181	43218.314937
HLA A*0301	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.368842	0.411532	-3.957309	23379.839056
HLA B*3901	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.481236	0.523921	-3.957315	30285.599907
HLA B*1502	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.558201	0.600860	-3.957341	36157.684458
HLA A*0211	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.512642	0.555221	-3.957420	32556.802634
HLA B*5401	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.358457	0.400734	-3.957723	22827.418110
HLA A*3201	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.580380	0.622434	-3.957946	38052.198085
HLA B*1801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.226512	0.268538	-3.957974	16846.592281
HLA A*0202	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.484652	0.526478	-3.958175	30524.765196
HLA B*3501	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.416722	0.458535	-3.958187	26104.878250
HLA A*2603	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.644746	0.686428	-3.958318	44131.251131
HLA A*6801	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.636810	0.678487	-3.958323	43332.094304
HLA B*1501	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.342868	0.384545	-3.958323	22022.568043
HLA B*7301	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.595665	0.637330	-3.958335	39415.360066
HLA A*3101	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.411332	0.452989	-3.958343	25782.911237
HLA A*0101	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.342920	0.384545	-3.958375	22025.189271
HLA B*4402	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.411379	0.452989	-3.958390	25785.701041
HLA A*0101	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.136912	0.178488	-3.958424	13706.043480
HLA B*4403	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.089518	0.131008	-3.958510	12289.049505
HLA B*1501	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.411083	0.452486	-3.958597	25768.130310
HLA A*0250	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.564840	0.606197	-3.958644	36714.722923
HLA B*4002	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.156220	0.197447	-3.958773	14329.141553
HLA A*0101	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.353793	0.394899	-3.958894	22583.594423
HLA A*3301	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.555137	0.595974	-3.959162	35903.507836
HLA A*2501	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.499536	0.540290	-3.959246	31589.032118
HLA A*0201	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.356624	0.397240	-3.959384	22731.295892
HLA A*2301	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.522167	0.562720	-3.959447	33278.715808
HLA B*3501	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.462400	0.502859	-3.959541	29000.157694
HLA A*6802	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.318424	0.358727	-3.959697	20817.276878
HLA B*0801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.412744	0.452989	-3.959755	25866.876761
HLA A*6802	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.424778	0.464975	-3.959803	26593.656579
HLA B*5701	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.412460	0.452486	-3.959974	25849.949932
HLA A*1101	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.435313	0.475212	-3.960101	27246.652125
HLA B*1503	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.257612	0.297408	-3.960204	18097.233846
HLA A*2402	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.569798	0.609548	-3.960250	37136.217645
HLA B*4403	1:439-447	9	GLALKPRKA	1.072654	-0.366055	-4.666902	0.706599	-3.960303	46441.034309
HLA B*5801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.347424	0.387024	-3.960400	22254.795706
HLA B*4501	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.610260	0.649772	-3.960489	40762.470650
HLA A*0203	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.372643	0.412011	-3.960632	23585.385761
HLA A*6901	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.301639	0.340987	-3.960652	20028.074476
HLA A*3201	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.566856	0.606197	-3.960659	36885.537224
HLA B*0801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.381916	0.421060	-3.960857	24094.415827
HLA A*3301	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-3.657439	-0.303590	-3.961028	4544.002942
HLA B*4501	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.634242	0.673165	-3.961076	43076.627281
HLA A*2501	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.436316	0.475212	-3.961104	27309.665262
HLA A*2501	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.471281	0.510101	-3.961181	29599.298113
HLA A*0301	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.358602	0.397240	-3.961362	22835.076010
HLA B*0801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.358640	0.397240	-3.961400	22837.052659

HLA B*5101	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.478163	0.516619	-3.961544	30072.051354
HLA A*0301	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.362291	0.400734	-3.961557	23029.852318
HLA B*1801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.478187	0.516619	-3.961567	30073.678262
HLA B*4801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.435247	0.473598	-3.961649	27242.525200
HLA B*4002	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.640411	0.678719	-3.961692	43692.957279
HLA B*4001	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.414250	0.452486	-3.961764	25956.732044
HLA B*1801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.512470	0.550534	-3.961936	32543.947778
HLA B*5801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.356885	0.394899	-3.961986	22744.950082
HLA A*2603	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.543784	0.581735	-3.962049	34977.129942
HLA A*0201	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.370705	0.408334	-3.962370	23480.355004
HLA B*3901	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.435969	0.473598	-3.962371	27287.808159
HLA A*2601	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.395851	0.433440	-3.962412	24880.047020
HLA B*3501	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.232104	0.269593	-3.962511	17064.903611
HLA A*6901	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.374111	0.411532	-3.962579	23665.267183
HLA B*1501	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.396053	0.433440	-3.962614	24891.625167
HLA A*2601	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.363402	0.400734	-3.962668	23088.858353
HLA B*4601	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.415239	0.452486	-3.962753	26015.917519
HLA B*7301	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.322324	0.359537	-3.962787	21005.066637
HLA A*0219	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.374351	0.411532	-3.962819	23678.329487
HLA A*3101	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.401368	0.438531	-3.962837	25198.099562
HLA A*0212	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.405693	0.442758	-3.962935	25450.316609
HLA A*3001	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.231359	0.268381	-3.962978	17035.663492
HLA A*0201	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.384052	0.421060	-3.962992	24213.194079
HLA A*6802	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.429891	0.466843	-3.963047	26908.564845
HLA B*4402	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.428077	0.464975	-3.963101	26796.417340
HLA A*6901	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.400494	0.437367	-3.963127	25147.439914
HLA A*2601	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.375148	0.412011	-3.963136	23721.794260
HLA B*4501	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.642000	0.678719	-3.963280	43853.038677
HLA A*0250	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.600635	0.637330	-3.963304	39868.937235
HLA A*2402	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.559700	0.596390	-3.963309	36282.698661
HLA A*6901	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.322155	0.358727	-3.963428	20996.886504
HLA B*4403	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.601135	0.637330	-3.963805	39914.904945
HLA B*4601	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.401229	0.437367	-3.963862	25190.058028
HLA A*0301	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.304907	0.340987	-3.963920	20179.357356
HLA B*5401	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.564821	0.600860	-3.963961	36713.133977
HLA B*1801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.546900	0.582728	-3.964172	35228.940944
HLA A*2301	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.545925	0.581735	-3.964190	35149.937027
HLA B*4501	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.641579	0.677348	-3.964231	43810.593258
HLA B*0803	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.488061	0.523691	-3.964370	30765.319857
HLA A*0219	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.422934	0.458535	-3.964399	26480.959092
HLA A*0206	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.365207	0.400734	-3.964473	23184.987383
HLA B*5301	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.601913	0.637330	-3.964582	39986.443532
HLA B*5401	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.558750	0.594015	-3.964736	36203.485964
HLA B*7301	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.343866	0.379131	-3.964736	22073.260649
HLA B*1517	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.440146	0.475212	-3.964934	27551.550066
HLA A*3101	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.373369	0.408334	-3.965035	23624.845379
HLA B*4601	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.352066	0.387024	-3.965042	22493.974283
HLA B*0801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.398501	0.433440	-3.965062	25032.338093
HLA A*0201	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.365829	0.400734	-3.965095	23218.249696
HLA A*6901	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.328879	0.363771	-3.965108	21324.513249
HLA B*0801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.360010	0.394899	-3.965111	22909.193638
HLA B*4501	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.571344	0.606197	-3.965147	37268.647267
HLA A*0201	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.402646	0.437367	-3.965279	25272.366286
HLA B*1801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.190457	0.225072	-3.965385	15504.467978
HLA B*1502	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.587936	0.622434	-3.965502	38720.030668
HLA B*7301	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.588370	0.622672	-3.965699	38758.802215
HLA A*3001	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.263570	0.297408	-3.966163	18347.229447
HLA A*3101	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.360762	0.394299	-3.966463	22948.887569
HLA B*4403	1:262-270	9	DPQSNLFAH	1.136197	-0.457478	-4.645254	0.678719	-3.966535	44182.850231
HLA A*0203	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.347012	0.380348	-3.966665	22233.736380
HLA A*0101	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.378695	0.412011	-3.966684	23916.369654
HLA B*1503	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.178568	0.211872	-3.966696	15085.804465
HLA B*4801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.441936	0.475212	-3.966724	27665.361222
HLA A*0219	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.364248	0.397240	-3.967008	23133.869109
HLA A*2603	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.561032	0.594015	-3.967017	36394.163337

HLA B*4601	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.405599	0.438531	-3.967068	25444.809869
HLA B*1502	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.589959	0.622672	-3.967287	38900.805953
HLA A*6802	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.308276	0.340987	-3.967290	20336.513194
HLA A*2603	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.625849	0.658550	-3.967299	42252.200511
HLA A*6802	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.410089	0.442758	-3.967331	25709.230374
HLA A*3001	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.314874	0.347463	-3.967411	20647.802940
HLA B*1801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.493411	0.525631	-3.967780	31146.640630
HLA B*4002	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.626343	0.658550	-3.967793	42300.229529
HLA A*2501	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.484424	0.516619	-3.967805	30508.751245
HLA B*4501	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.626390	0.658550	-3.967840	42304.806568
HLA B*1502	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.605282	0.637330	-3.967952	40297.855978
HLA A*3201	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.571111	0.603125	-3.967986	37248.692305
HLA B*0802	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.491933	0.523921	-3.968013	31040.834332
HLA A*6802	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.426585	0.458535	-3.968050	26704.522087
HLA A*8001	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.441730	0.473598	-3.968132	27652.193701
HLA B*4403	1:240-248	9	RIPKFAHLP	0.576363	0.126847	-4.671406	0.703210	-3.968196	46925.169096
HLA A*2301	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.508500	0.540290	-3.968209	32247.763841
HLA A*1101	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.471260	0.502859	-3.968401	29597.856988
HLA B*5801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.349026	0.380458	-3.968568	22337.057424
HLA B*7301	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.471441	0.502859	-3.968582	29610.188883
HLA A*2403	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.133021	0.164416	-3.968605	13583.802483
HLA A*2601	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.360386	0.391537	-3.968849	22929.032014
HLA A*0202	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.519441	0.550534	-3.968907	33070.530093
HLA A*3301	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.618979	0.650029	-3.968950	41589.091931
HLA A*0219	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.417147	0.448098	-3.969049	26130.452403
HLA B*5801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.350821	0.381754	-3.969067	22429.571006
HLA B*3801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.531846	0.562720	-3.969126	34028.784554
HLA A*0203	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.291099	0.321711	-3.969388	19547.868461
HLA B*1509	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.524641	0.555221	-3.969419	33468.832779
HLA A*0216	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.412467	0.442758	-3.969709	25850.369472
HLA B*5101	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.493695	0.523921	-3.969775	31167.035790
HLA A*3101	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.222946	0.252948	-3.969998	16708.811017
HLA A*6901	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.291795	0.321711	-3.970084	19579.196070
HLA B*1501	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.349216	0.379131	-3.970085	22346.847690
HLA A*2902	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.428624	0.458535	-3.970089	26830.215632
HLA A*0212	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.381731	0.411532	-3.970199	24084.120526
HLA B*1501	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.371043	0.400734	-3.970309	23498.653891
HLA A*3001	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.259297	0.288865	-3.970432	18167.567354
HLA B*5801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.350795	0.380348	-3.970447	22428.236289
HLA B*1801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.494464	0.523921	-3.970543	31222.220125
HLA A*2603	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.580095	0.609548	-3.970548	38027.297397
HLA A*2902	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.444157	0.473598	-3.970559	27807.158249
HLA A*0202	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.533456	0.562720	-3.970736	34155.121484
HLA A*3201	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.610834	0.639976	-3.970858	40816.313168
HLA B*4402	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.409478	0.438531	-3.970947	25673.093932
HLA B*0802	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.487599	0.516619	-3.970979	30732.549239
HLA B*3801	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.548121	0.577123	-3.970998	35328.184497
HLA A*3201	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.621066	0.650029	-3.971037	41789.365833
HLA A*6801	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.629660	0.658550	-3.971110	42624.588250
HLA B*0702	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.413923	0.442758	-3.971166	25937.220578
HLA A*2902	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.362702	0.391537	-3.971166	23051.665708
HLA A*3301	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.607093	0.635887	-3.971206	40466.290351
HLA B*5101	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.496921	0.525631	-3.971290	31399.399511
HLA A*6901	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.386439	0.415126	-3.971313	24346.647049
HLA B*5701	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.424313	0.452989	-3.971323	26565.185820
HLA B*1801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.408693	0.437367	-3.971326	25626.747027
HLA A*8001	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.424435	0.452989	-3.971446	26572.660037
HLA B*4601	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.383636	0.412011	-3.971625	24190.019823
HLA A*0301	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.366539	0.394899	-3.971640	23256.214364
HLA A*6801	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.644819	0.673165	-3.971654	44138.652852
HLA B*4001	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.363238	0.391537	-3.971701	23080.116437
HLA A*0202	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.445341	0.473598	-3.971743	27883.080262
HLA B*4801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.436789	0.464975	-3.971813	27339.377608
HLA A*0101	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.409199	0.437367	-3.971832	25656.571508
HLA A*2602	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.574976	0.603125	-3.971851	37581.657764

HLA B*2705	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.143862	0.171999	-3.971862	13927.138094
HLA B*4001	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.409304	0.437367	-3.971937	25662.818233
HLA A*6901	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.366299	0.394299	-3.972001	23243.384923
HLA B*3501	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.445632	0.473598	-3.972034	27901.791239
HLA A*2603	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.622107	0.650029	-3.972077	41889.637535
HLA A*2601	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.393199	0.421060	-3.972139	24728.548673
HLA A*0101	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.366487	0.394299	-3.972189	23253.446631
HLA B*3801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.439093	0.466843	-3.972250	27484.856147
HLA A*2902	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.383796	0.411532	-3.972264	24198.920302
HLA A*6801	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.649699	0.677348	-3.972351	44637.406587
HLA A*3301	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.622161	0.649772	-3.972389	41894.850080
HLA B*0702	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.420547	0.448098	-3.972449	26335.807169
HLA A*0301	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.354047	0.381582	-3.972465	22596.793151
HLA B*4002	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.582074	0.609548	-3.972526	38200.911670
HLA A*2902	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.415331	0.442758	-3.972573	26021.407084
HLA B*3501	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.353065	0.380458	-3.972607	22545.751994
HLA A*0101	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.384200	0.411532	-3.972668	24221.447900
HLA A*0202	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.496618	0.523921	-3.972698	31377.494277
HLA B*4801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.380692	0.407915	-3.972778	24026.600074
HLA A*3001	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.124418	0.151627	-3.972790	13317.341725
HLA A*2603	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.364439	0.391537	-3.972902	23144.008615
HLA A*0202	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.528224	0.555221	-3.973002	33746.095506
HLA B*5701	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.367528	0.394299	-3.973229	23309.242230
HLA B*4801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.426239	0.452989	-3.973250	26683.293659
HLA B*0801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.258677	0.285370	-3.973307	18141.638760
HLA B*4403	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.596051	0.622434	-3.973617	39450.345752
HLA B*5801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.338023	0.364340	-3.973683	21778.267226
HLA A*2403	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.140591	0.166895	-3.973697	13822.652776
HLA B*4001	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.370961	0.397240	-3.973721	23494.204934
HLA B*1502	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.611614	0.637857	-3.973757	40889.688536
HLA B*1501	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.412370	0.438531	-3.973839	25844.636355
HLA B*4501	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.640362	0.666384	-3.973978	43687.993706
HLA B*1509	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.499651	0.525631	-3.974021	31597.406993
HLA A*0301	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.338653	0.364577	-3.974076	21809.865353
HLA B*3501	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.427092	0.452989	-3.974103	26735.745523
HLA A*0216	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.484211	0.510101	-3.974110	30493.735486
HLA A*2602	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.624153	0.650029	-3.974124	42087.487841
HLA A*8001	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.432926	0.458535	-3.974391	27097.303156
HLA B*4501	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.575253	0.600860	-3.974393	37605.656310
HLA B*5701	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.417239	0.442758	-3.974481	26135.966136
HLA A*0206	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.557219	0.582728	-3.974491	36076.012248
HLA B*4402	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.366083	0.391537	-3.974547	23231.819341
HLA B*1501	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.333508	0.358727	-3.974781	21552.994210
HLA B*0702	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.396246	0.421060	-3.975186	24902.669813
HLA A*0216	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.448832	0.473598	-3.975234	28108.138420
HLA B*1801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.530503	0.555221	-3.975281	33923.646713
HLA A*0211	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.525928	0.550534	-3.975394	33568.202349
HLA B*1501	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.370340	0.394899	-3.975442	23460.674208
HLA A*3101	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.408910	0.433440	-3.975470	25639.504885
HLA A*1101	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.492098	0.516619	-3.975478	31052.591481
HLA B*1501	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.383850	0.408334	-3.975516	24201.931500
HLA B*4002	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.642307	0.666384	-3.975923	43884.128143
HLA B*1503	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.486111	0.510101	-3.976011	30627.486853
HLA B*1509	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.500018	0.523921	-3.976097	31624.084650
HLA A*0206	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.442989	0.466843	-3.976145	27732.493149
HLA B*4801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.428706	0.452486	-3.976221	26835.296311
HLA B*4402	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.384644	0.408334	-3.976310	24246.226246
HLA B*4601	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.373764	0.397240	-3.976523	23646.326849
HLA B*0802	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.451816	0.475212	-3.976604	28301.921988
HLA B*3801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.531858	0.555221	-3.976637	34029.705026
HLA B*4402	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.425029	0.448098	-3.976931	26609.054990
HLA A*0201	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.157146	0.180214	-3.976932	14359.716639
HLA B*3901	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.502579	0.525631	-3.976948	31811.115792
HLA A*0212	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.398121	0.421060	-3.977061	25010.409311
HLA B*4403	1:219-227	9	LPSTPRQLA	1.028911	-0.342483	-4.663493	0.686428	-3.977065	46077.910918

HLA A*0250	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.578087	0.600860	-3.977227	37851.810003
HLA A*3001	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.306904	0.329580	-3.977325	20272.363906
HLA A*0250	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.359016	0.381582	-3.977434	22856.828564
HLA A*0206	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.356575	0.379131	-3.977444	22728.713589
HLA B*1801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.517804	0.540290	-3.977513	32946.066091
HLA B*5401	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.554759	0.577123	-3.977636	35872.249777
HLA A*2603	1:388-396	9	DDQYVIDPK	0.658334	-0.021004	-4.614983	0.637330	-3.977653	41208.135410
HLA B*4501	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.643048	0.665274	-3.977773	43958.975503
HLA A*1101	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.430823	0.452989	-3.977834	26966.419174
HLA A*8001	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.386230	0.408334	-3.977896	24334.927443
HLA A*2601	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.372817	0.394899	-3.977918	23594.829631
HLA B*1502	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.587597	0.609548	-3.978049	38689.878580
HLA A*0206	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.174137	0.196045	-3.978092	14932.665803
HLA A*0201	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.389790	0.411532	-3.978257	24535.195648
HLA A*0219	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.373228	0.394899	-3.978329	23617.178156
HLA A*8001	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.365357	0.387024	-3.978333	23193.016179
HLA B*1517	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.488665	0.510101	-3.978565	30808.123907
HLA A*3002	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.584919	0.606197	-3.978722	38452.001792
HLA B*5701	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.417316	0.438531	-3.978785	26140.632511
HLA B*0801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.321229	0.342354	-3.978875	20952.179381
HLA B*3901	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.443919	0.464975	-3.978944	27791.968601
HLA B*5401	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.370545	0.391537	-3.979008	23471.718816
HLA A*0219	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.452939	0.473598	-3.979341	28375.203402
HLA A*0201	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.394484	0.415126	-3.979358	24801.834005
HLA A*2902	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.358553	0.379131	-3.979422	22832.481917
HLA B*2705	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.326748	0.347215	-3.979534	21220.135068
HLA A*3001	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.252779	0.273190	-3.979589	17896.961654
HLA B*4801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.417288	0.437367	-3.979921	26138.935551
HLA B*5101	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.428112	0.448098	-3.980014	26798.591913
HLA A*2603	1:305-313	9	AAFDVADVN	1.094624	-0.414757	-4.659912	0.679867	-3.980045	45699.575469
HLA B*4002	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.391606	0.411532	-3.980074	24638.012849
HLA B*4403	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.629893	0.649772	-3.980121	42647.423200
HLA A*2601	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.388049	0.407915	-3.980134	24437.037602
HLA A*3301	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.505831	0.525631	-3.980200	32050.188619
HLA B*0801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.325404	0.345166	-3.980238	21154.571775
HLA B*4801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.374607	0.394299	-3.980308	23692.296192
HLA B*5101	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.454086	0.473598	-3.980487	28450.213645
HLA B*1501	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.392104	0.411532	-3.980572	24666.286310
HLA B*4601	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.192806	0.211872	-3.980934	15588.572725
HLA A*0216	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.378298	0.397240	-3.981058	23894.513597
HLA B*2705	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.493905	0.512773	-3.981132	31182.045711
HLA A*2602	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.562944	0.581735	-3.981209	36554.783884
HLA B*5101	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.206292	0.225072	-3.981221	16080.235222
HLA A*6801	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.587449	0.606197	-3.981253	38676.694425
HLA A*2601	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.392820	0.411532	-3.981288	24707.019678
HLA A*2602	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.619177	0.637857	-3.981320	41607.995586
HLA A*3001	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.198506	0.217015	-3.981492	15794.511705
HLA B*4601	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.415011	0.433440	-3.981572	26002.269007
HLA B*1501	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.419012	0.437367	-3.981645	26242.935917
HLA A*6901	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.341357	0.359537	-3.981820	21946.094333
HLA A*0301	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.362373	0.380348	-3.982026	23034.213344
HLA A*3301	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.640621	0.658550	-3.982070	43713.999635
HLA B*4403	1:167-175	9	WNDLVRGPV	0.625194	0.047971	-4.655258	0.673165	-3.982092	45212.428594
HLA A*2501	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.508591	0.526478	-3.982113	32254.568375
HLA B*1517	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.194023	0.211872	-3.982151	15632.318200
HLA B*4001	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.329633	0.347463	-3.982170	21361.577026
HLA A*2902	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.329370	0.347179	-3.982191	21348.637805
HLA A*0201	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.394338	0.412011	-3.982327	24793.516540
HLA B*4402	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.397536	0.415126	-3.982410	24976.741411
HLA B*1502	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.585680	0.603125	-3.982555	38519.459720
HLA B*5701	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.416085	0.433440	-3.982645	26066.634452
HLA A*8001	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.457908	0.475212	-3.982696	28701.734591
HLA A*3002	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.447671	0.464975	-3.982696	28033.120123
HLA A*0219	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.416219	0.433440	-3.982779	26074.673695
HLA A*3101	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.374523	0.391537	-3.982986	23687.682425

HLA B*5301	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.592538	0.609548	-3.982990	39132.566663
HLA B*4403	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.649471	0.666384	-3.983087	44613.988841
HLA A*2501	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.449986	0.466843	-3.983142	28182.900069
HLA B*5801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.328402	0.345166	-3.983236	21301.107363
HLA A*2501	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.507236	0.523921	-3.983315	32154.042522
HLA B*0801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.280752	0.297408	-3.983344	19087.641783
HLA A*2601	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.391794	0.408334	-3.983459	24648.678271
HLA B*1517	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.198220	0.214632	-3.983588	15784.090664
HLA A*0211	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.507572	0.523921	-3.983651	32178.926969
HLA B*1501	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.195593	0.211872	-3.983721	15688.912563
HLA A*0201	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.378850	0.394899	-3.983952	23924.910582
HLA A*3002	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.566889	0.582728	-3.984161	36888.330983
HLA B*0802	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.487051	0.502859	-3.984192	30693.835138
HLA A*0301	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.347992	0.363771	-3.984221	22283.950613
HLA B*1517	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.326581	0.342354	-3.984227	21211.985934
HLA A*0216	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.451146	0.466843	-3.984303	28258.319186
HLA A*2402	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.546655	0.562255	-3.984400	35209.125713
HLA A*2601	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.325524	0.340987	-3.984537	21160.409219
HLA A*6802	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.437113	0.452486	-3.984627	27359.795843
HLA A*2301	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.510605	0.525631	-3.984974	32404.456616
HLA A*3101	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.365367	0.380348	-3.985019	23193.518071
HLA B*5801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.350405	0.365377	-3.985028	22408.103841
HLA B*1503	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.369596	0.384545	-3.985051	23420.475159
HLA A*0101	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.365616	0.380458	-3.985158	23206.822167
HLA A*3101	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.385901	0.400734	-3.985167	24316.503525
HLA A*0212	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.382494	0.397240	-3.985254	24126.502811
HLA B*4801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.365735	0.380458	-3.985278	23213.225914
HLA A*0101	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.372347	0.387024	-3.985323	23569.314354
HLA B*4403	1:427-435	9	LIEAALKDA	0.977888	-0.299401	-4.663810	0.678487	-3.985323	46111.575522
HLA B*5701	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.422713	0.437367	-3.985346	26467.496164
HLA A*0211	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.372493	0.387024	-3.985469	23577.221138
HLA A*3101	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.382758	0.397240	-3.985517	24141.125672
HLA A*3201	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.586486	0.600860	-3.985626	38591.002477
HLA A*3002	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.509329	0.523691	-3.985638	32309.405941
HLA A*0212	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.423084	0.437367	-3.985717	26490.129259
HLA A*0203	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.438584	0.452486	-3.986098	27452.609343
HLA B*1501	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.350457	0.364340	-3.986116	22410.770958
HLA B*0702	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.350013	0.363771	-3.986241	22387.868349
HLA B*2705	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.444807	0.458535	-3.986272	27848.859606
HLA B*4601	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.407382	0.421060	-3.986323	25549.503747
HLA A*6802	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.384012	0.397240	-3.986772	24210.967340
HLA A*2301	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.541996	0.555221	-3.986775	34833.427708
HLA A*6901	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.284380	0.297408	-3.986972	19247.746085
HLA B*3901	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.255610	0.268538	-3.987073	18014.011556
HLA B*5101	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.513673	0.526478	-3.987195	32634.215019
HLA A*0301	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.369062	0.381754	-3.987309	23391.731419
HLA B*4801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.398894	0.411532	-3.987362	25054.963815
HLA A*0250	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.570145	0.582728	-3.987418	37165.963169
HLA B*4601	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.379048	0.391537	-3.987511	23935.785267
HLA B*4002	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.610206	0.622672	-3.987535	40757.398995
HLA B*7301	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.379095	0.391537	-3.987558	23938.375206
HLA B*4001	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.369309	0.381582	-3.987727	23405.022594
HLA A*6901	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.368155	0.380348	-3.987808	23342.935369
HLA A*6901	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.240856	0.252948	-3.987908	17412.281160
HLA A*0211	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.504809	0.516619	-3.988189	31974.853531
HLA A*0101	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.396107	0.407915	-3.988193	24894.722561
HLA A*6801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-3.915849	-0.072551	-3.988400	8238.517363
HLA B*1509	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.491261	0.502859	-3.988403	30992.844211
HLA B*4402	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.335617	0.347179	-3.988439	21657.955138
HLA B*0803	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.441044	0.452486	-3.988558	27608.546357
HLA B*4002	1:180-188	9	GSVPDFALT	0.889299	-0.266865	-4.611135	0.622434	-3.988701	40844.586857
HLA B*5801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.352541	0.363771	-3.988769	22518.569080
HLA A*6802	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.427311	0.438531	-3.988780	26749.200187
HLA A*2601	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.386054	0.397240	-3.988814	24325.055752
HLA B*4601	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.396810	0.407915	-3.988895	24935.023776

HLA A*0203	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.347738	0.358727	-3.989011	22270.934616
HLA A*3301	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.629059	0.639976	-3.989083	42565.596969
HLA B*0803	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.502135	0.512773	-3.989362	31778.606534
HLA A*6802	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.401624	0.412011	-3.989613	25212.962706
HLA A*2301	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.540161	0.550534	-3.989627	34686.562657
HLA A*3101	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.397557	0.407915	-3.989642	24977.957533
HLA A*1101	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.463321	0.473598	-3.989723	29061.722905
HLA A*2403	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.354329	0.364577	-3.989752	22611.467451
HLA B*5301	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.602117	0.612321	-3.989796	40005.267995
HLA B*2705	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.463399	0.473598	-3.989801	29066.911651
HLA B*2705	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.247568	0.257713	-3.989855	17683.496868
HLA B*4402	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.432710	0.442758	-3.989952	27083.819919
HLA B*0803	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.513910	0.523921	-3.989990	32652.051187
HLA A*0101	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.405223	0.415126	-3.990097	25422.794823
HLA B*4501	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.584118	0.594015	-3.990103	38381.131997
HLA B*4601	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.390889	0.400734	-3.990155	24597.393250
HLA B*5101	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.493118	0.502859	-3.990259	31125.585266
HLA B*5301	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.586749	0.596390	-3.990359	38614.392144
HLA A*2902	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.377556	0.387024	-3.990532	23853.700225
HLA B*5301	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.552801	0.562255	-3.990546	35710.957420
HLA B*3901	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.507334	0.516619	-3.990715	32161.349244
HLA A*2403	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.338044	0.347179	-3.990866	21779.327614
HLA A*2902	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.424383	0.433440	-3.990944	26569.497612
HLA B*4001	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.399291	0.408334	-3.990956	25077.881323
HLA B*3501	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.398924	0.407915	-3.991010	25056.725956
HLA B*3501	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.428403	0.437367	-3.991036	26816.575143
HLA B*3801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.541578	0.550534	-3.991044	34799.900647
HLA B*3801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.573853	0.582728	-3.991125	37484.599887
HLA A*0202	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.574010	0.582728	-3.991283	37498.189114
HLA A*2601	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.406445	0.415126	-3.991319	25494.413453
HLA B*4001	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.412443	0.421060	-3.991383	25848.971033
HLA B*0702	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.443992	0.452486	-3.991506	27796.629887
HLA A*6802	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.399622	0.407915	-3.991707	25097.017888
HLA B*4403	1:194-202	9	PLYTLVNPC	0.850616	-0.173268	-4.669127	0.677348	-3.991778	46679.569898
HLA B*0803	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.501898	0.510101	-3.991797	31761.247484
HLA B*1502	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.586148	0.594015	-3.992133	38560.950866
HLA B*0702	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.465833	0.473598	-3.992235	29230.278757
HLA A*6802	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.407397	0.415126	-3.992271	25550.333081
HLA B*1503	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.516006	0.523691	-3.992315	32809.998405
HLA A*0212	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.444871	0.452486	-3.992385	27852.927702
HLA B*1517	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.440548	0.448098	-3.992450	27577.049551
HLA B*7301	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.604864	0.612321	-3.992543	40259.069422
HLA A*8001	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.445082	0.452486	-3.992597	27866.492317
HLA B*2705	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.440738	0.448098	-3.992640	27589.136490
HLA A*8001	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.389945	0.397240	-3.992704	24543.957570
HLA B*1517	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.466310	0.473598	-3.992712	29262.397301
HLA A*8001	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.430203	0.437367	-3.992836	26927.932934
HLA A*0250	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.357458	0.364577	-3.992881	22774.993535
HLA A*0201	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.387231	0.394299	-3.992932	24391.074702
HLA A*2902	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.245884	0.252948	-3.992936	17615.037379
HLA B*5701	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.414135	0.421060	-3.993075	25949.852227
HLA A*0219	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.384654	0.391537	-3.993117	24246.750929
HLA A*3101	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.290547	0.297408	-3.993139	19523.032578
HLA B*5301	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.575871	0.582728	-3.993143	37659.199752
HLA B*1501	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.296818	0.303652	-3.993166	19806.970486
HLA A*3301	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.631159	0.637857	-3.993302	42771.961596
HLA A*6801	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.594275	0.600860	-3.993415	39289.328217
HLA A*3101	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.297288	0.303652	-3.993636	19828.412787
HLA B*1801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.162437	0.168455	-3.993982	14535.732105
HLA A*1101	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.385584	0.391537	-3.994047	24298.750814
HLA A*6802	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.162536	0.168455	-3.994080	14539.035221
HLA A*3301	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.373322	0.379131	-3.994191	23622.289361
HLA A*0101	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.375989	0.381754	-3.994235	23767.781734
HLA A*0206	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.518407	0.523921	-3.994487	32991.904232
HLA B*3501	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.433020	0.438531	-3.994489	27103.167527

HLA B*5101	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.504609	0.510101	-3.994508	31960.153576
HLA A*3301	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.617262	0.622672	-3.994590	41424.947283
HLA A*2602	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.634697	0.639976	-3.994722	43121.860731
HLA B*5801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.354411	0.359537	-3.994874	22615.749250
HLA A*0201	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.359549	0.364577	-3.994972	22884.915017
HLA B*5801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.337405	0.342354	-3.995052	21747.303122
HLA A*0216	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.428495	0.433440	-3.995055	26822.233653
HLA A*6801	1:256-264	9	KKLSKRDPQ	0.617133	0.032639	-4.644915	0.649772	-3.995144	44148.444132
HLA B*4001	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.390074	0.394899	-3.995175	24551.261561
HLA B*5701	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.395978	0.400734	-3.995244	24887.316390
HLA B*4601	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.390149	0.394899	-3.995250	24555.512157
HLA A*0206	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.468885	0.473598	-3.995287	29436.416424
HLA A*0201	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.374461	0.379131	-3.995331	23684.350818
HLA A*2601	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.359862	0.364340	-3.995521	22901.386988
HLA B*1501	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.340690	0.345166	-3.995524	21912.402056
HLA A*0202	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.438393	0.442758	-3.995635	27440.582217
HLA A*2301	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.508443	0.512773	-3.995670	32243.577148
HLA A*0301	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.340977	0.345166	-3.995811	21926.869157
HLA B*4403	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.605524	0.609548	-3.995976	40320.316949
HLA A*0216	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.359841	0.363771	-3.996069	22900.271969
HLA B*5701	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.404495	0.408334	-3.996161	25380.194859
HLA A*6901	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.164674	0.168455	-3.996218	14610.787352
HLA A*3001	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.296101	0.299836	-3.996265	19774.315612
HLA A*2603	1:414-422	9	LAALTSVTD	1.356186	-0.689802	-4.662811	0.666384	-3.996427	46005.677442
HLA B*5701	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.411635	0.415126	-3.996509	25800.910784
HLA B*3501	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.461653	0.464975	-3.996678	28950.310315
HLA B*4001	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.383754	0.387024	-3.996730	24196.563974
HLA B*1501	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.411896	0.415126	-3.996770	25816.408824
HLA B*1502	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.361373	0.364577	-3.996795	22981.189525
HLA B*1517	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.377337	0.380458	-3.996879	23841.701977
HLA B*7301	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.579635	0.582728	-3.996907	37986.996968
HLA B*0801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.391465	0.394299	-3.997166	24630.016812
HLA B*0803	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.500034	0.502859	-3.997176	31625.282252
HLA A*6801	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.635033	0.637857	-3.997177	43155.233319
HLA A*1101	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.440052	0.442758	-3.997294	27545.588677
HLA A*2902	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.356918	0.359537	-3.997380	22746.672814
HLA B*3901	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.440212	0.442758	-3.997454	27555.723805
HLA B*4601	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.412803	0.415126	-3.997677	25870.375421
HLA A*3101	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.418773	0.421060	-3.997713	26228.458832
HLA A*2603	1:52-60	9	RDSEESYLA	0.919833	-0.281976	-4.635626	0.637857	-3.997769	43214.106628
HLA B*2705	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.378261	0.380458	-3.997803	23892.445420
HLA B*1502	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.521539	0.523691	-3.997848	33230.681386
HLA A*6802	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.418961	0.421060	-3.997901	26239.812733
HLA A*2301	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.524476	0.526478	-3.997998	33456.160791
HLA A*3201	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.579842	0.581735	-3.998107	38005.085752
HLA A*2601	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.378644	0.380458	-3.998186	23913.523355
HLA A*2403	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.385234	0.387024	-3.998210	24279.172127
HLA B*4801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.399049	0.400734	-3.998315	25063.911354
HLA A*3301	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.580114	0.581735	-3.998379	38028.943220
HLA A*1101	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.378996	0.380458	-3.998538	23932.936657
HLA A*8001	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.410594	0.412011	-3.998583	25739.150850
HLA A*3002	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.538937	0.540290	-3.998647	34588.934418
HLA A*2403	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.377852	0.379131	-3.998721	23869.965548
HLA A*2403	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.379294	0.380458	-3.998836	23949.385573
HLA B*4402	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.419978	0.421060	-3.998918	26301.351070
HLA B*1502	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.605115	0.606197	-3.998919	40282.380458
HLA A*2501	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.436359	0.437367	-3.998992	27312.324752
HLA B*1502	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.522961	0.523921	-3.999040	33339.623024
HLA B*4801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.407469	0.408334	-3.999135	25554.618399
HLA B*5701	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.396380	0.397240	-3.999140	24910.350076
HLA B*5701	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.390703	0.391537	-3.999167	24586.883032
HLA A*8001	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.432682	0.433440	-3.999242	27082.061730
HLA B*4402	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.411278	0.412011	-3.999267	25779.703334
HLA B*5101	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.267807	0.268538	-3.999269	18527.064508
HLA B*4001	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.411306	0.412011	-3.999295	25781.376973

HLA A*2601	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.380894	0.381582	-3.999313	24037.781061
HLA B*4403	1:448-456	9	FSPIRVAAT	0.935126	-0.269852	-4.664592	0.665274	-3.999318	46194.720077
HLA B*1509	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.451999	0.452486	-3.999513	28313.867108
HLA A*2402	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.562239	0.562720	-3.999519	36495.504803
HLA A*2403	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.436894	0.437367	-3.999527	27346.034054
HLA B*5701	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.407563	0.407915	-3.999649	25560.148903
HLA B*0801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.408014	0.408334	-3.999680	25586.711990
HLA A*3101	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.394608	0.394899	-3.999710	24808.946309
HLA B*3901	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.502574	0.502859	-3.999715	31810.771605
HLA A*0201	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.297156	0.297408	-3.999749	19822.406604
HLA A*0212	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.394653	0.394899	-3.999754	24811.496499
HLA A*2902	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.414898	0.415126	-3.999772	25995.517752
HLA A*6901	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.276638	0.276822	-3.999816	18907.683667
HLA B*5301	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.600747	0.600860	-3.999887	39879.291532
HLA B*4002	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.595865	0.595974	-3.999891	39433.489016
HLA B*5801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.347081	0.347179	-3.999902	22237.224834
HLA A*0202	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.397216	0.397240	-3.999976	24958.371659
HLA B*0702	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.465020	0.464975	-4.000045	29175.616063
HLA B*1501	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.364227	0.363771	-4.000456	23132.742771
HLA B*4002	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.640449	0.639976	-4.000473	43696.739427
HLA A*0250	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.562787	0.562255	-4.000531	36541.536544
HLA B*5301	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.594601	0.594015	-4.000586	39318.883905
HLA A*2403	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.326111	0.325371	-4.000741	21189.047447
HLA A*0206	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.409100	0.408334	-4.000765	25650.742604
HLA A*2501	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.453768	0.452989	-4.000779	28429.443043
HLA B*0802	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.448905	0.448098	-4.000807	28112.852735
HLA B*5801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.365627	0.364577	-4.001050	23207.449907
HLA B*3801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.541418	0.540290	-4.001128	34787.101076
HLA B*5801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.278003	0.276822	-4.001181	18967.206765
HLA B*4403	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.604441	0.603125	-4.001316	40219.885025
HLA A*6802	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.434761	0.433440	-4.001321	27212.034814
HLA A*0301	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.366746	0.365377	-4.001369	23267.288592
HLA A*0250	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.449504	0.448098	-4.001406	28151.661789
HLA A*0201	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.381754	0.380348	-4.001407	24085.423486
HLA A*3201	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.584165	0.582728	-4.001437	38385.284975
HLA A*0201	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.386056	0.384545	-4.001512	24325.187348
HLA A*0219	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.409499	0.407915	-4.001585	25674.343960
HLA B*0702	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.438971	0.437367	-4.001604	27477.125353
HLA B*1501	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.335982	0.334311	-4.001671	21676.123660
HLA A*2601	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.382043	0.380348	-4.001696	24101.455654
HLA A*0250	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.542137	0.540290	-4.001847	34844.736242
HLA A*8001	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.402606	0.400734	-4.001872	25270.042141
HLA A*3101	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.383488	0.381582	-4.001906	24181.776712
HLA A*0206	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.504811	0.502859	-4.001952	31975.026512
HLA B*1517	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.504921	0.502859	-4.002062	31983.157669
HLA B*2705	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.336400	0.334311	-4.002089	21697.006959
HLA B*1503	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.302017	0.299836	-4.002181	20045.526370
HLA B*4801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.440740	0.438531	-4.002209	27589.285745
HLA B*4001	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.402989	0.400734	-4.002255	25292.335393
HLA B*0802	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.460920	0.458535	-4.002385	28901.486724
HLA A*2601	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.366356	0.363771	-4.002584	23246.402978
HLA B*1801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.394176	0.391537	-4.002639	24784.263285
HLA A*2601	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.389703	0.387024	-4.002679	24530.285030
HLA A*0216	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.394390	0.391537	-4.002853	24796.467579
HLA B*4501	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.606031	0.603125	-4.002907	40367.460232
HLA A*0101	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.328301	0.325371	-4.002931	21296.152765
HLA A*2602	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.389977	0.387024	-4.002954	24545.816561
HLA B*5301	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.598934	0.595974	-4.002959	39713.085602
HLA B*4601	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.411424	0.408334	-4.003089	25788.351636
HLA A*0216	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.411029	0.407915	-4.003114	25764.924247
HLA B*1801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.478527	0.475212	-4.003315	30097.278331
HLA B*0702	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.441856	0.438531	-4.003325	27660.273028
HLA A*0203	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.424407	0.421060	-4.003347	26570.935031
HLA B*0802	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.476948	0.473598	-4.003350	29988.059965
HLA B*0801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.383714	0.380348	-4.003366	24194.338764

HLA B*4001	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.418695	0.415126	-4.003569	26223.776779
HLA A*2601	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.397891	0.394299	-4.003592	24997.153078
HLA A*3201	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.613200	0.609548	-4.003652	41039.277355
HLA B*5101	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.404483	0.400734	-4.003749	25379.508348
HLA B*5101	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.395351	0.391537	-4.003814	24851.394095
HLA A*0202	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.520637	0.516619	-4.004018	33161.719709
HLA B*5801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.362949	0.358727	-4.004222	23064.763659
HLA A*2902	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.349407	0.345166	-4.004240	22356.642247
HLA B*1502	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.520978	0.516619	-4.004358	33187.743092
HLA A*0250	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.520999	0.516619	-4.004379	33189.359010
HLA A*2902	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.425513	0.421060	-4.004454	26638.725639
HLA A*3301	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.363997	0.359537	-4.004459	23120.481755
HLA A*0216	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.425523	0.421060	-4.004463	26639.302096
HLA B*1501	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.345488	0.340987	-4.004501	22155.810211
HLA A*0212	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.438102	0.433440	-4.004662	27422.180527
HLA A*0216	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.463216	0.458535	-4.004681	29054.648835
HLA A*0216	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.405451	0.400734	-4.004717	25436.139170
HLA A*6801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.239829	0.235091	-4.004738	17371.165032
HLA B*3501	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.350062	0.345166	-4.004896	22390.411927
HLA A*6901	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.127575	0.122535	-4.005041	13414.523537
HLA B*4801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.438666	0.433440	-4.005226	27457.807880
HLA B*3901	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.387038	0.381582	-4.005456	24380.256955
HLA A*8001	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.448224	0.442758	-4.005466	28068.781964
HLA A*2402	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.545908	0.540290	-4.005618	35148.605951
HLA B*4801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.417633	0.412011	-4.005622	26159.730904
HLA A*2403	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.458127	0.452486	-4.005641	28716.178632
HLA B*4002	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.612241	0.606197	-4.006044	40948.793931
HLA A*2501	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.390621	0.384545	-4.006077	24582.228041
HLA B*5801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.353631	0.347463	-4.006168	22575.165939
HLA A*0101	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.364984	0.358727	-4.006257	23173.074765
HLA B*3901	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.023705	0.017415	-4.006289	10560.987288
HLA A*6802	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.443807	0.437367	-4.006439	27784.752667
HLA B*4601	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.348861	0.342354	-4.006508	22328.600155
HLA A*0301	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.366180	0.359537	-4.006642	23236.972857
HLA B*4403	1:413-421	9	ALAALTSVT	0.797068	-0.161181	-4.642615	0.635887	-4.006728	43915.239649
HLA A*0212	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.398271	0.391537	-4.006735	25019.070237
HLA B*0702	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.414863	0.407915	-4.006949	25993.408345
HLA A*0211	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.473866	0.466843	-4.007022	29775.965067
HLA B*4501	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.029005	0.021903	-4.007102	10690.670839
HLA A*2902	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.415437	0.408334	-4.007102	26027.742636
HLA B*1509	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.473988	0.466843	-4.007145	29784.342648
HLA B*1801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.465706	0.458535	-4.007171	29221.740845
HLA A*0203	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.418742	0.411532	-4.007210	26226.614287
HLA A*0203	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.404645	0.397240	-4.007405	25388.983839
HLA B*4001	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.401760	0.394299	-4.007461	25220.875109
HLA B*0801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.422736	0.415126	-4.007610	26468.928065
HLA A*2403	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.428699	0.421060	-4.007640	26834.860786
HLA A*0101	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.373045	0.365377	-4.007668	23607.214485
HLA A*6801	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.617288	0.609548	-4.007740	41427.412505
HLA A*2402	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.558309	0.550534	-4.007775	36166.683595
HLA A*0211	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.510666	0.502859	-4.007807	32409.014855
HLA A*0216	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.372446	0.364577	-4.007868	23574.670273
HLA A*2602	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.601939	0.594015	-4.007924	39988.823147
HLA B*4403	1:396-404	9	KAAAKELGP	0.601224	0.057326	-4.666517	0.658550	-4.007966	46399.849083
HLA B*4601	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.419555	0.411532	-4.008023	26275.751805
HLA B*4402	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.402357	0.394299	-4.008058	25255.555234
HLA B*4403	1:231-239	9	ALIRIGVAE	1.193914	-0.597940	-4.604149	0.595974	-4.008175	40192.913518
HLA A*3301	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.456306	0.448098	-4.008208	28596.033382
HLA B*0702	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.416705	0.408334	-4.008371	26103.889697
HLA A*8001	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.353781	0.345166	-4.008615	22582.983558
HLA A*2603	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.631331	0.622672	-4.008659	42788.856516
HLA A*3301	1:371-379	9	TRIVVLGDA	0.751953	-0.142405	-4.618251	0.609548	-4.008703	41519.402747
HLA A*0250	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.451532	0.442758	-4.008774	28283.401709
HLA A*0250	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.590807	0.581735	-4.009072	38976.852294
HLA A*0211	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.535603	0.526478	-4.009125	34324.424445

HLA A*0301	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.367911	0.358727	-4.009184	23329.805663
HLA A*6801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.519350	0.510101	-4.009249	33063.553421
HLA A*0301	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.356450	0.347179	-4.009272	22722.197652
HLA B*5801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.331504	0.321711	-4.009792	21453.764131
HLA B*4403	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.522606	0.512773	-4.009833	33312.399231
HLA B*4402	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.389113	0.379131	-4.009982	24496.998398
HLA A*3001	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.267708	0.257713	-4.009994	18522.855353
HLA A*0101	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.390424	0.380348	-4.010076	24571.059660
HLA A*0211	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.298963	0.288865	-4.010098	19905.043649
HLA A*2601	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.391883	0.381754	-4.010129	24653.745963
HLA B*0801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.410864	0.400734	-4.010130	25755.169117
HLA B*4001	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.389313	0.379131	-4.010182	24508.265702
HLA B*0702	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.401972	0.391537	-4.010435	25233.157891
HLA A*0101	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.389573	0.379131	-4.010442	24522.987279
HLA B*7301	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.604462	0.594015	-4.010447	40221.843338
HLA A*0202	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-3.938113	-0.072551	-4.010664	8671.870449
HLA A*0301	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.357893	0.347215	-4.010678	22797.798830
HLA A*0219	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.411438	0.400734	-4.010703	25789.188722
HLA A*2603	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.448247	0.437367	-4.010880	28070.300495
HLA A*2403	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.392557	0.381582	-4.010975	24692.054042
HLA A*2403	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.444476	0.433440	-4.011037	27827.624752
HLA A*3001	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.299001	0.287962	-4.011038	19906.766669
HLA A*0212	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.423079	0.412011	-4.011068	26489.842643
HLA A*2402	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.592881	0.581735	-4.011146	39163.487488
HLA A*2301	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.534858	0.523691	-4.011167	34265.610738
HLA A*6802	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.422856	0.411532	-4.011324	26476.231965
HLA A*0201	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.393107	0.381754	-4.011353	24723.331854
HLA B*7301	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.612225	0.600860	-4.011365	40947.243261
HLA A*3002	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.566614	0.555221	-4.011393	36864.989643
HLA A*3002	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.562174	0.550534	-4.011640	36489.976995
HLA A*3201	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.573994	0.562255	-4.011738	37496.769113
HLA B*7301	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.588871	0.577123	-4.011748	38803.489973
HLA A*8001	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.423286	0.411532	-4.011754	26502.456671
HLA A*0211	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.535448	0.523691	-4.011757	34312.171005
HLA B*4402	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.392311	0.380348	-4.011963	24678.031991
HLA B*4601	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.396582	0.384545	-4.012037	24921.942324
HLA A*2902	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.424069	0.412011	-4.012057	26550.243694
HLA B*5401	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.470694	0.458535	-4.012159	29559.292942
HLA A*1101	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.420081	0.407915	-4.012167	26307.612461
HLA A*0250	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.574922	0.562720	-4.012202	37576.981865
HLA A*2602	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.574539	0.562255	-4.012284	37543.860640
HLA B*4001	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.445820	0.433440	-4.012380	27913.869501
HLA A*2603	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.589573	0.577123	-4.012450	38866.307616
HLA B*1517	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.465504	0.452989	-4.012515	29208.148579
HLA A*3101	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.337939	0.325371	-4.012568	21774.026190
HLA A*2403	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.420953	0.408334	-4.012619	26360.466674
HLA B*4801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.433711	0.421060	-4.012651	27146.309616
HLA A*0212	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.413435	0.400734	-4.012700	25908.050955
HLA B*0702	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.465727	0.452989	-4.012738	29223.163657
HLA A*0301	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.355106	0.342354	-4.012753	22651.993476
HLA A*6801	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.652751	0.639976	-4.012775	44952.198347
HLA A*2603	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.652772	0.639976	-4.012796	44954.387078
HLA B*4501	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.652965	0.639976	-4.012989	44974.333759
HLA B*0702	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.393502	0.380458	-4.013044	24745.812149
HLA A*3002	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.421505	0.408334	-4.013171	26394.000678
HLA B*5701	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.424997	0.411532	-4.013464	26607.039737
HLA B*4001	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.398071	0.384545	-4.013527	25007.568098
HLA B*0801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.393990	0.380458	-4.013532	24773.673219
HLA B*4402	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.398250	0.384545	-4.013705	25017.852113
HLA A*0211	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.452314	0.438531	-4.013783	28334.399984
HLA B*4001	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.394402	0.380458	-4.013944	24797.138319
HLA A*3101	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.335798	0.321711	-4.014087	21666.978887
HLA A*2602	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.537868	0.523691	-4.014177	34503.898472
HLA A*2402	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.530836	0.516619	-4.014217	33949.717015
HLA A*2902	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.335942	0.321711	-4.014230	21674.130240

HLA B*2705	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.452911	0.438531	-4.014380	28373.361381
HLA A*3301	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.608461	0.594015	-4.014446	40593.901502
HLA A*2601	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.374379	0.359537	-4.014842	23679.866702
HLA A*2601	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.394181	0.379131	-4.015050	24784.531446
HLA B*1801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.482049	0.466843	-4.015206	30342.342238
HLA A*0216	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.402256	0.387024	-4.015232	25249.680838
HLA B*0803	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.473812	0.458535	-4.015277	29772.260350
HLA B*0801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.337037	0.321711	-4.015325	21728.839835
HLA B*4403	1:189-197	9	RASGDPLYT	0.798352	-0.175680	-4.638264	0.622672	-4.015592	43477.444648
HLA B*5801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.304473	0.288865	-4.015608	20159.171363
HLA A*8001	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.407291	0.391537	-4.015754	25544.113737
HLA A*3001	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.305753	0.289933	-4.015820	20218.696162
HLA B*5801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.356859	0.340987	-4.015872	22743.596598
HLA A*6901	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.345718	0.329580	-4.016138	22167.559652
HLA B*5101	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.469155	0.452989	-4.016166	29454.735613
HLA B*1503	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.542748	0.526478	-4.016270	34893.782329
HLA B*5101	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.313774	0.297408	-4.016366	20595.592374
HLA A*0216	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.395569	0.379131	-4.016438	24863.900466
HLA B*4402	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.346059	0.329580	-4.016479	22184.955460
HLA A*1101	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.403525	0.387024	-4.016501	25323.551592
HLA B*1502	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.481513	0.464975	-4.016538	30304.939404
HLA A*2403	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.411452	0.394899	-4.016553	25790.025835
HLA A*0212	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.425086	0.408334	-4.016751	26612.510063
HLA A*0101	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.381371	0.364577	-4.016794	24064.194034
HLA A*6801	1:168-176	9	NDLVRGPVT	1.090553	-0.440524	-4.666923	0.650029	-4.016894	46443.295532
HLA A*2501	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.459682	0.442758	-4.016924	28819.205599
HLA A*3001	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.301787	0.284825	-4.016963	20034.901668
HLA A*3301	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.617870	0.600860	-4.017010	41483.030999
HLA A*3002	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.470006	0.452989	-4.017016	29512.475695
HLA B*4801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.411969	0.394899	-4.017070	25820.738768
HLA B*5401	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.557411	0.540290	-4.017121	36092.019511
HLA A*0219	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.411438	0.394299	-4.017139	25789.188722
HLA A*6802	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.293968	0.276822	-4.017146	19677.418810
HLA B*2705	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.425556	0.408334	-4.017221	26641.319792
HLA A*6802	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.397731	0.380458	-4.017273	24987.959005
HLA B*0802	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.482355	0.464975	-4.017379	30363.689075
HLA A*3301	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.623624	0.606197	-4.017428	42036.289063
HLA A*6802	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.382807	0.365377	-4.017430	24143.868445
HLA B*4403	1:423-431	9	WTAPLIEAA	0.918370	-0.305704	-4.630205	0.612666	-4.017540	42678.119713
HLA A*0216	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.429080	0.411532	-4.017548	26858.389222
HLA B*5401	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.543194	0.525631	-4.017564	34929.667353
HLA B*5101	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.492793	0.475212	-4.017581	31102.356675
HLA B*1503	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.398060	0.380458	-4.017602	25006.891667
HLA B*0802	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.470128	0.452486	-4.017642	29520.779142
HLA B*1503	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.520545	0.502859	-4.017687	33154.723799
HLA B*3901	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.492911	0.475212	-4.017698	31110.770828
HLA A*2501	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.456278	0.438531	-4.017746	28594.177026
HLA A*1101	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.470328	0.452486	-4.017842	29534.357116
HLA A*8001	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.456381	0.438531	-4.017850	28600.984254
HLA A*0250	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.573153	0.555221	-4.017931	37424.217888
HLA B*4801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.397397	0.379131	-4.018266	24968.770520
HLA B*1501	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.398795	0.380348	-4.018447	25049.271589
HLA B*0702	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.397649	0.379131	-4.018518	24983.228080
HLA A*0212	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.433673	0.415126	-4.018547	27143.959981
HLA A*6801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.134163	0.115588	-4.018575	13619.564092
HLA A*8001	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.433943	0.415126	-4.018817	27160.852504
HLA A*0202	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.600595	0.581735	-4.018860	39865.270732
HLA B*4002	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.214934	0.196045	-4.018889	16403.397272
HLA B*0803	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.485759	0.466843	-4.018915	30602.643238
HLA A*0203	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.456325	0.437367	-4.018958	28597.271020
HLA A*0101	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.382741	0.363771	-4.018970	24140.211483
HLA B*0801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.403553	0.384545	-4.019008	25325.195617
HLA A*0201	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.377741	0.358727	-4.019014	23863.897028
HLA A*3101	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.197548	0.178488	-4.019059	15759.687956
HLA B*5401	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.543004	0.523921	-4.019083	34914.364490

HLA A*6901	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.400926	0.381754	-4.019173	25172.484632
HLA A*3101	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.430769	0.411532	-4.019237	26963.064020
HLA B*4402	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.366602	0.347215	-4.019388	23259.611578
HLA A*8001	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.427323	0.407915	-4.019408	26749.923748
HLA B*3901	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.467696	0.448098	-4.019598	29355.947252
HLA A*1101	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.478137	0.458535	-4.019602	30070.261856
HLA A*2403	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.354089	0.334311	-4.019778	22598.993689
HLA B*5301	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.317202	0.297408	-4.019794	20758.797209
HLA A*0206	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.156850	0.136944	-4.019905	14349.931731
HLA B*1801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.468272	0.448098	-4.020174	29394.882091
HLA B*5701	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.384576	0.364340	-4.020236	24242.422632
HLA B*0702	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.432005	0.411532	-4.020473	27039.899430
HLA B*7301	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.367852	0.347215	-4.020638	23326.650585
HLA B*1509	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.537278	0.516619	-4.020659	34457.078039
HLA A*8001	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.367956	0.347179	-4.020777	23332.203808
HLA B*4601	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.401229	0.380348	-4.020882	25190.058028
HLA B*5801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.368210	0.347215	-4.020995	23345.840051
HLA A*2403	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.418282	0.397240	-4.021041	26198.819942
HLA A*8001	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.385495	0.364340	-4.021154	24293.756093
HLA B*4601	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.318624	0.297408	-4.021216	20826.851708
HLA B*5101	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.433288	0.412011	-4.021277	27119.887948
HLA B*4002	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.561732	0.540290	-4.021442	36452.883396
HLA A*1101	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.415822	0.394299	-4.021523	26050.845265
HLA A*2501	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.495279	0.473598	-4.021681	31280.886509
HLA A*0206	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.534492	0.512773	-4.021719	34236.704725
HLA B*4601	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.366943	0.345166	-4.021777	23277.864365
HLA A*0201	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.343535	0.321711	-4.021824	22056.429710
HLA B*5301	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.603604	0.581735	-4.021869	40142.499266
HLA B*1509	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.548387	0.526478	-4.021909	35349.787836
HLA A*3002	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.298733	0.276822	-4.021910	19894.493406
HLA A*6901	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.369163	0.347215	-4.021949	23397.173559
HLA A*0301	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.369412	0.347463	-4.021949	23410.594475
HLA A*0216	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.430292	0.408334	-4.021958	26933.469235
HLA A*2301	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.524850	0.502859	-4.021991	33484.951237
HLA B*3901	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.443066	0.421060	-4.022007	27737.444572
HLA A*1101	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.419454	0.397240	-4.022214	26269.640113
HLA B*3901	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.356807	0.334311	-4.022497	22740.889871
HLA B*0702	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.455949	0.433440	-4.022509	28572.528439
HLA B*5701	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.403048	0.380348	-4.022700	25295.756343
HLA B*3901	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.423441	0.400734	-4.022707	26511.921134
HLA B*4402	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.382499	0.359537	-4.022962	24126.763856
HLA A*3101	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.365383	0.342354	-4.023029	23194.396408
HLA B*5701	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.404671	0.381582	-4.023089	25390.494751
HLA A*2902	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.475619	0.452486	-4.023133	29896.377046
HLA B*5801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.352719	0.329580	-4.023140	22527.829529
HLA A*0101	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.299973	0.276822	-4.023151	19951.401702
HLA B*4501	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.549648	0.526478	-4.023171	35452.632190
HLA B*5801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.357498	0.334311	-4.023187	22777.088204
HLA B*5401	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.533336	0.510101	-4.023235	34145.699238
HLA B*4601	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.403717	0.380458	-4.023259	25334.787888
HLA A*0301	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.344978	0.321711	-4.023266	22129.815748
HLA B*4001	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.403706	0.380348	-4.023358	25334.102605
HLA A*0211	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.017934	-0.005447	-4.023381	10421.594830
HLA B*1503	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.357724	0.334311	-4.023413	22788.920543
HLA B*4403	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.370890	0.347463	-4.023427	23490.392212
HLA A*2601	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.388157	0.364577	-4.023579	24443.119635
HLA B*1801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.404084	0.380458	-4.023626	25356.178022
HLA B*5701	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.404088	0.380458	-4.023631	25356.452372
HLA B*1502	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.606544	0.582728	-4.023816	40415.095916
HLA B*0803	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.488818	0.464975	-4.023843	30818.959267
HLA A*6901	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.020284	-0.003611	-4.023895	10478.127282
HLA B*1801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.276941	0.252948	-4.023993	18920.883485
HLA B*0801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.371261	0.347215	-4.024047	23510.479502
HLA A*0219	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.432414	0.408334	-4.024079	27065.364631
HLA A*2602	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.606835	0.582728	-4.024107	40442.216519

HLA A*6901	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.366471	0.342354	-4.024117	23252.566058
HLA A*0206	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.548044	0.523691	-4.024353	35321.878049
HLA B*1509	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.462017	0.437367	-4.024650	28974.596281
HLA A*3001	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.293284	0.268538	-4.024747	19646.465458
HLA B*1801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.463340	0.438531	-4.024809	29062.980698
HLA B*1517	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.425549	0.400734	-4.024814	26640.887415
HLA A*2501	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.489892	0.464975	-4.024916	30895.247842
HLA A*0201	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.390403	0.365377	-4.025026	24569.863349
HLA B*4801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.346937	0.321711	-4.025226	22229.887688
HLA B*5301	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.602394	0.577123	-4.025271	40030.814188
HLA A*0216	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.477792	0.452486	-4.025306	30046.357875
HLA B*7301	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.477794	0.452486	-4.025308	30046.520423
HLA A*8001	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.406898	0.381582	-4.025317	25521.046291
HLA B*1503	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.347113	0.321711	-4.025402	22238.909110
HLA A*3001	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-3.974055	-0.051442	-4.025497	9420.093269
HLA A*6802	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.020119	-0.005447	-4.025566	10474.160048
HLA B*0803	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.437684	0.412011	-4.025672	27395.786766
HLA A*6802	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.191984	0.166266	-4.025718	15559.084294
HLA A*0203	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.372979	0.347215	-4.025764	23603.638809
HLA B*3801	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.551420	0.525631	-4.025789	35597.540821
HLA A*2403	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.433708	0.407915	-4.025794	27146.162758
HLA A*0211	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.538585	0.512773	-4.025812	34560.877458
HLA B*4601	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.404955	0.379131	-4.025825	25407.120723
HLA A*3001	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.281838	0.255887	-4.025950	19135.408507
HLA B*0801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.390321	0.364340	-4.025980	24565.211581
HLA B*4403	1:68-76	9	LGLDWDEGP	0.726280	-0.086304	-4.666397	0.639976	-4.026421	46387.048929
HLA A*2601	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.385163	0.358727	-4.026436	24275.232018
HLA B*4001	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.391032	0.364577	-4.026455	24605.511809
HLA A*0219	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.413503	0.387024	-4.026479	25912.115905
HLA A*6901	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-3.890536	-0.136008	-4.026544	7772.052220
HLA B*3501	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.460004	0.433440	-4.026564	28840.573009
HLA A*0216	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.411118	0.384545	-4.026573	25770.221436
HLA A*0219	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.441903	0.415126	-4.026777	27663.265970
HLA A*3301	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.407178	0.380348	-4.026830	25537.481438
HLA B*4801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.418399	0.391537	-4.026863	26205.907537
HLA A*0201	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.391209	0.364340	-4.026868	24615.497316
HLA B*3801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.543629	0.516619	-4.027010	34964.643494
HLA B*0801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.392402	0.365377	-4.027025	24683.239252
HLA B*5801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.352444	0.325371	-4.027074	22513.574893
HLA A*0216	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.315050	0.287962	-4.027088	20656.182314
HLA A*0203	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.411654	0.384545	-4.027109	25802.027449
HLA B*3501	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.391923	0.364577	-4.027346	24656.013426
HLA A*0202	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.407904	0.380348	-4.027556	25580.207017
HLA A*0101	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.349439	0.321711	-4.027728	22358.335569
HLA A*0203	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.406896	0.379131	-4.027765	25520.908225
HLA A*0101	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.368809	0.340987	-4.027822	23378.068370
HLA B*5401	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.544487	0.516619	-4.027867	35033.753222
HLA B*4001	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.373106	0.345166	-4.027940	23610.535242
HLA A*0212	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.392287	0.364340	-4.027947	24676.696973
HLA B*5701	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.422929	0.394899	-4.028030	26480.672575
HLA B*0803	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.501634	0.473598	-4.028036	31742.008932
HLA B*5301	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.583310	0.555221	-4.028088	38309.771061
HLA A*0216	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.423122	0.394899	-4.028223	26492.422296
HLA A*2403	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.301475	0.273190	-4.028285	20020.491435
HLA A*0301	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.313671	0.285370	-4.028301	20590.690483
HLA A*1101	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.409922	0.381582	-4.028340	25699.357300
HLA A*3101	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.286189	0.257713	-4.028476	19328.092007
HLA A*2403	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.387229	0.358727	-4.028502	24390.942749
HLA B*5401	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.502137	0.473598	-4.028539	31778.778453
HLA B*4402	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.410338	0.381754	-4.028585	25723.977515
HLA B*2705	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.443722	0.415126	-4.028596	27779.341947
HLA B*4002	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.640952	0.612321	-4.028631	43747.357149
HLA A*6901	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.392978	0.364340	-4.028637	24715.976671
HLA B*3501	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.413197	0.384545	-4.028653	25893.898694
HLA B*1801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.502266	0.473598	-4.028668	31788.235441

HLA B*0702	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.443962	0.415126	-4.028836	27794.675059
HLA B*5401	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.541613	0.512773	-4.028840	34802.724715
HLA A*0101	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.358464	0.329580	-4.028884	22827.788594
HLA A*2902	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.410481	0.381582	-4.028900	25732.467912
HLA A*2403	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.429649	0.400734	-4.028914	26893.575069
HLA A*6901	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.376475	0.347463	-4.029012	23794.412923
HLA A*0219	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.481551	0.452486	-4.029065	30307.562660
HLA B*4801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.444244	0.415126	-4.029118	27812.724851
HLA B*5101	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.350976	0.321711	-4.029265	22437.580974
HLA B*1801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.441283	0.412011	-4.029272	27623.785197
HLA A*6802	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.423671	0.394299	-4.029373	26525.980663
HLA A*3101	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.388244	0.358727	-4.029517	24448.012804
HLA A*0201	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.376792	0.347215	-4.029578	23811.797164
HLA A*2902	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.317618	0.287962	-4.029656	20778.684323
HLA A*2402	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.555306	0.525631	-4.029675	35917.495408
HLA A*6802	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.276222	0.246392	-4.029830	18889.587273
HLA A*2403	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.441431	0.411532	-4.029899	27633.201623
HLA A*2402	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.532767	0.502859	-4.029909	34101.025171
HLA B*1509	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.488475	0.458535	-4.029940	30794.626713
HLA B*4001	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.394343	0.364340	-4.030002	24793.784801
HLA B*0802	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.442183	0.412011	-4.030172	27681.080673
HLA B*1517	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.488811	0.458535	-4.030276	30818.459090
HLA A*2601	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.395689	0.365377	-4.030312	24870.761471
HLA A*0201	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.394127	0.363771	-4.030355	24781.447762
HLA B*5101	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.495519	0.464975	-4.030543	31298.152337
HLA B*4002	1:313-321	9	NSSPARFDQ	0.598070	0.005055	-4.633692	0.603125	-4.030567	43022.130475
HLA A*0219	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.451811	0.421060	-4.030751	28301.615769
HLA B*4002	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.624792	0.594015	-4.030777	42149.464740
HLA B*0702	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.428030	0.397240	-4.030789	26793.518183
HLA A*0219	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.442907	0.412011	-4.030895	27727.242607
HLA A*0250	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.581491	0.550534	-4.030957	38149.693688
HLA B*2705	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.483980	0.452989	-4.030991	30477.572933
HLA A*2403	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.443120	0.412011	-4.031109	27740.896086
HLA B*4402	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.411637	0.380458	-4.031179	25801.050364
HLA B*1502	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.299863	0.268538	-4.031325	19946.329408
HLA B*0702	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.395696	0.364340	-4.031356	24871.165118
HLA B*1502	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.581987	0.550534	-4.031453	38193.265916
HLA B*0801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.335305	0.303652	-4.031653	21642.377513
HLA A*3301	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.608778	0.577123	-4.031655	40623.559479
HLA B*5301	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.594434	0.562720	-4.031714	39303.784338
HLA A*0202	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.329264	0.297408	-4.031857	21343.441218
HLA A*2403	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.377159	0.345166	-4.031993	23831.901439
HLA A*2902	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.259576	0.227561	-4.032016	18179.266978
HLA B*2705	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.484636	0.452486	-4.032150	30523.609268
HLA A*6901	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.379360	0.347179	-4.032181	23953.013626
HLA A*0212	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.379454	0.347215	-4.032240	23958.197513
HLA A*8001	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.411635	0.379131	-4.032504	25800.910784
HLA B*5701	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.397919	0.365377	-4.032542	24998.775913
HLA B*7301	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.549176	0.516619	-4.032557	35414.102385
HLA A*0212	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.412941	0.380348	-4.032594	25878.634135
HLA A*0201	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.392402	0.359537	-4.032865	24683.239252
HLA A*0101	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.397214	0.364340	-4.032873	24958.236637
HLA B*1501	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.414638	0.381754	-4.032884	25979.912190
HLA A*0203	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.448024	0.415126	-4.032898	28055.877766
HLA A*0212	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.427271	0.394299	-4.032972	26746.740227
HLA B*0801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.367300	0.334311	-4.032989	23297.013698
HLA B*5101	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.491565	0.458535	-4.033029	31014.480912
HLA B*1501	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.398419	0.365377	-4.033042	25027.598765
HLA A*8001	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.413508	0.380458	-4.033050	25912.396270
HLA A*2403	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.398541	0.365377	-4.033165	25034.640376
HLA A*8001	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.454234	0.421060	-4.033174	28459.911785
HLA A*0301	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.367545	0.334311	-4.033234	23310.124949
HLA A*0212	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.391989	0.358727	-4.033262	24659.748525
HLA B*4402	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.430551	0.397240	-4.033310	26949.501784
HLA B*3501	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.485914	0.452486	-4.033428	30613.571945

HLA B*1501	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.380617	0.347179	-4.033438	24022.441034
HLA B*5101	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.500356	0.466843	-4.033513	31648.730171
HLA B*0702	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.415350	0.381754	-4.033596	26022.533291
HLA B*4403	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.646097	0.612321	-4.033776	44268.743344
HLA A*2902	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.212316	0.178488	-4.033828	16304.837577
HLA B*0702	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.245799	0.211872	-4.033927	17611.607079
HLA B*3501	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.442296	0.408334	-4.033961	27688.269682
HLA A*0101	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.381176	0.347215	-4.033962	24053.391135
HLA A*2501	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.445496	0.411532	-4.033964	27893.037768
HLA B*4601	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.355757	0.321711	-4.034046	22685.963825
HLA B*5701	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.331464	0.297408	-4.034056	21451.791159
HLA A*0216	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.449224	0.415126	-4.034098	28133.544234
HLA A*3001	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.182708	0.148579	-4.034129	15230.293298
HLA B*1503	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.415965	0.381754	-4.034212	26059.443547
HLA A*0206	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.399629	0.365377	-4.034252	25097.425207
HLA B*0801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.413430	0.379131	-4.034299	25907.770637
HLA A*0212	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.413573	0.379131	-4.034442	25916.321696
HLA B*5401	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.560959	0.526478	-4.034481	36388.060308
HLA A*3201	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.589773	0.555221	-4.034552	38884.184031
HLA A*3101	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.214807	0.180214	-4.034593	16398.605982
HLA A*0101	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.381982	0.347179	-4.034803	24098.065851
HLA A*0101	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.382299	0.347463	-4.034836	24115.671941
HLA A*0203	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.429221	0.394299	-4.034922	26867.108691
HLA A*3101	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.400339	0.365377	-4.034962	25138.462556
HLA B*2705	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.435790	0.400734	-4.035056	27276.591040
HLA B*4402	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.430010	0.394899	-4.035112	26915.990059
HLA A*6802	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.262924	0.227561	-4.035364	18319.954209
HLA A*6802	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.394911	0.359537	-4.035374	24826.265913
HLA B*0802	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.488508	0.452989	-4.035518	30796.959139
HLA A*3001	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.247397	0.211872	-4.035524	17676.514647
HLA A*0212	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.382706	0.347179	-4.035527	24138.252625
HLA B*3801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.562073	0.526478	-4.035595	36481.489493
HLA A*2602	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.598372	0.562720	-4.035652	39661.771213
HLA B*1509	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.447218	0.411532	-4.035686	28003.865776
HLA B*1517	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.488252	0.452486	-4.035766	30778.804205
HLA A*3201	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.250413	0.214632	-4.035781	17799.728423
HLA B*4601	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.401187	0.365377	-4.035810	25187.605190
HLA A*0301	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.339478	0.303652	-4.035826	21851.318821
HLA A*3001	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.271072	0.235091	-4.035982	18666.908462
HLA B*4601	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.394832	0.358727	-4.036104	24821.699883
HLA B*0803	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.484211	0.448098	-4.036112	30493.735486
HLA A*3101	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.396020	0.359537	-4.036483	24889.739985
HLA B*0802	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.479265	0.442758	-4.036507	30148.448183
HLA A*0101	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.396046	0.359537	-4.036509	24891.221187
HLA A*0211	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.546672	0.510101	-4.036571	35210.459081
HLA B*3901	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.423686	0.387024	-4.036662	26526.841692
HLA A*3201	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.577034	0.540290	-4.036744	37760.182289
HLA A*0203	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.402145	0.365377	-4.036769	25243.261549
HLA B*4801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.418392	0.381582	-4.036810	26205.482227
HLA A*8001	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.417213	0.380348	-4.036865	26134.410863
HLA A*2601	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.384343	0.347463	-4.036880	24229.442375
HLA A*3201	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.428547	0.391537	-4.037010	26825.426160
HLA B*1801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.424132	0.387024	-4.037108	26554.122092
HLA A*6901	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.371518	0.334311	-4.037207	23524.347200
HLA B*3801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.561149	0.523921	-4.037228	36404.009088
HLA A*0101	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.371572	0.334311	-4.037261	23527.274457
HLA B*1517	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.384442	0.347179	-4.037263	24234.948301
HLA A*2603	1:207-215	9	MKITHVLRG	1.118769	-0.512572	-4.643496	0.606197	-4.037300	44004.421297
HLA B*5301	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.587919	0.550534	-4.037385	38718.564398
HLA A*3001	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.307189	0.269593	-4.037596	20285.638471
HLA A*0301	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.363015	0.325371	-4.037644	23068.257702
HLA A*8001	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.432560	0.394899	-4.037661	27074.444232
HLA B*5401	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.372023	0.334311	-4.037712	23551.724903
HLA B*3501	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.452876	0.415126	-4.037750	28371.059024
HLA B*0802	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.476507	0.438531	-4.037976	29957.575839

HLA A*3001	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.299012	0.261006	-4.038006	19907.305143
HLA A*0250	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.561962	0.523921	-4.038041	36472.214714
HLA B*4601	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.402655	0.364577	-4.038078	25272.913175
HLA B*2705	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.446060	0.407915	-4.038145	27929.276867
HLA A*2402	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.418528	0.380348	-4.038181	26213.706105
HLA A*0301	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.367777	0.329580	-4.038197	23322.612707
HLA B*0803	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.476894	0.438531	-4.038363	29984.328859
HLA B*0803	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.481344	0.442758	-4.038586	30293.137565
HLA B*4001	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.402528	0.363771	-4.038757	25265.531176
HLA B*5101	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.481572	0.442758	-4.038814	30309.038340
HLA A*6802	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.336259	0.297408	-4.038851	21689.965398
HLA B*0801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.450390	0.411532	-4.038858	28209.136488
HLA A*2403	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.433203	0.394299	-4.038905	27114.606701
HLA B*1801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.454215	0.415126	-4.039089	28458.680092
HLA A*3001	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.285489	0.246392	-4.039097	19296.957386
HLA B*4403	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.621827	0.582728	-4.039099	41862.678637
HLA B*2705	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.476490	0.437367	-4.039123	29956.441390
HLA B*3501	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.460194	0.421060	-4.039134	28853.213747
HLA A*0211	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.360980	0.321711	-4.039269	22960.436512
HLA B*0803	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.492349	0.452989	-4.039360	31070.571730
HLA B*4801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.421190	0.381754	-4.039437	26374.873937
HLA B*2705	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.430995	0.391537	-4.039458	26977.070907
HLA A*2501	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.434524	0.394899	-4.039625	27197.170252
HLA B*0801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.403466	0.363771	-4.039694	25320.126883
HLA A*2603	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.640665	0.600860	-4.039805	43718.493136
HLA A*2603	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.602618	0.562720	-4.039898	40051.392891
HLA B*5801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.337354	0.297408	-4.039946	21744.714965
HLA B*4002	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.640818	0.600860	-4.039958	43733.869132
HLA B*4501	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.622736	0.582728	-4.040008	41950.415287
HLA B*5401	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.339882	0.299836	-4.040045	21871.660956
HLA B*5701	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.385215	0.345166	-4.040049	24278.121369
HLA A*8001	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.405463	0.365377	-4.040086	25436.827213
HLA B*0802	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.477515	0.437367	-4.040148	30027.183395
HLA A*3002	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.553015	0.512773	-4.040242	35728.542249
HLA B*4601	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.404864	0.364340	-4.040523	25401.760750
HLA A*1101	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.448874	0.408334	-4.040540	28110.875668
HLA B*1502	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.478013	0.437367	-4.040646	30061.641222
HLA B*4501	1:221-229	9	STPRQLALH	0.899770	-0.287449	-4.652981	0.612321	-4.040660	44976.036934
HLA B*5401	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.455824	0.415126	-4.040698	28564.337180
HLA B*1503	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.207054	0.166266	-4.040788	16108.445440
HLA A*0219	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.478304	0.437367	-4.040937	30081.814126
HLA A*2902	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.405651	0.364577	-4.041074	25447.838429
HLA A*6901	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.386275	0.345166	-4.041109	24337.428908
HLA A*3101	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-3.737603	-0.303590	-4.041193	5465.161902
HLA A*3101	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.386369	0.345166	-4.041203	24342.695990
HLA B*4601	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.423129	0.381754	-4.041375	26492.852263
HLA A*2601	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.363092	0.321711	-4.041381	23072.376361
HLA A*0211	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.436300	0.394899	-4.041401	27308.631086
HLA A*1101	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.479949	0.438531	-4.041418	30195.947593
HLA A*1101	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.489730	0.448098	-4.041631	30883.717343
HLA B*5701	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.423469	0.381754	-4.041716	26513.642308
HLA B*0702	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.406382	0.364577	-4.041804	25490.689832
HLA B*4801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.426385	0.384545	-4.041840	26692.245087
HLA B*2705	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.297840	0.255887	-4.041953	19853.637154
HLA B*3901	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.495232	0.452989	-4.042243	31277.502170
HLA A*0216	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.331128	0.288865	-4.042262	21435.202167
HLA B*1801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.485033	0.442758	-4.042275	30551.528888
HLA A*2602	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.479718	0.437367	-4.042351	30179.942876
HLA B*0802	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.450317	0.407915	-4.042402	28204.406027
HLA A*2601	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.387581	0.345166	-4.042415	24410.743627
HLA A*0212	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.424247	0.381754	-4.042494	26561.162113
HLA A*2402	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.555445	0.512773	-4.042672	35928.961508
HLA A*0202	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.331562	0.288865	-4.042697	21456.665889
HLA A*2601	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.389921	0.347215	-4.042707	24542.629805
HLA B*5101	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.440026	0.397240	-4.042786	27543.949522

HLA A*3001	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.136438	0.093574	-4.042864	13691.073729
HLA B*0702	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.289739	0.246392	-4.043347	19486.733964
HLA A*0203	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.258014	0.214632	-4.043382	18113.983181
HLA A*8001	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.384482	0.340987	-4.043495	24237.177246
HLA B*1509	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.437867	0.394299	-4.043568	27407.349443
HLA A*3301	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.567274	0.523691	-4.043583	36921.073638
HLA B*1501	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.223975	0.180214	-4.043761	16748.450015
HLA B*4001	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.390955	0.347179	-4.043776	24601.119469
HLA B*1502	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.424313	0.380458	-4.043855	26565.185820
HLA B*5301	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.584430	0.540290	-4.044140	38408.757745
HLA B*5701	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.385457	0.340987	-4.044470	24291.653359
HLA B*4002	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.606762	0.562255	-4.044507	40435.434663
HLA B*5701	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.408320	0.363771	-4.044548	25604.713085
HLA B*4403	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.568581	0.523921	-4.044660	37032.295664
HLA A*6801	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.606934	0.562255	-4.044678	40451.406655
HLA B*4402	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.379024	0.334311	-4.044713	23934.490402
HLA B*4801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.403478	0.358727	-4.044751	25320.811788
HLA B*4002	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.621900	0.577123	-4.044777	41869.699871
HLA A*3301	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.561412	0.516619	-4.044793	36426.073237
HLA A*3201	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.498084	0.452989	-4.045095	31483.596495
HLA A*0216	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.224045	0.178924	-4.045121	16751.168453
HLA A*0101	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.390391	0.345166	-4.045225	24569.198757
HLA A*3301	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.429832	0.384545	-4.045287	26904.925782
HLA B*1801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.424498	0.379131	-4.045368	26576.541709
HLA A*0211	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.503946	0.458535	-4.045411	31911.432699
HLA B*4801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.442869	0.397240	-4.045629	27724.842689
HLA A*2403	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.430537	0.384545	-4.045992	26948.627035
HLA A*3201	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.386996	0.340987	-4.046009	24377.882970
HLA A*6801	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.512879	0.466843	-4.046036	32574.596493
HLA B*1801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.446866	0.400734	-4.046131	27981.150322
HLA B*0801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.371633	0.325371	-4.046262	23530.583968
HLA A*2902	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.428016	0.381754	-4.046262	26792.648498
HLA A*0250	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.484814	0.438531	-4.046283	30536.161679
HLA A*2601	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.388760	0.342354	-4.046407	24477.127555
HLA B*1509	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.485042	0.438531	-4.046511	30552.190017
HLA B*3501	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.458056	0.411532	-4.046524	28711.518470
HLA A*0201	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.314949	0.268381	-4.046568	20651.377723
HLA A*0301	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.299551	0.252948	-4.046603	19931.982882
HLA A*0201	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.393842	0.347179	-4.046664	24765.231219
HLA A*3301	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.570709	0.523921	-4.046789	37214.249807
HLA A*0212	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.344205	0.297408	-4.046797	22090.462949
HLA B*1502	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.587172	0.540290	-4.046882	38652.012382
HLA B*4002	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.609711	0.562720	-4.046991	40710.901513
HLA B*4601	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.410808	0.363771	-4.047037	25751.825351
HLA B*2705	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.459109	0.412011	-4.047097	28781.188971
HLA A*0201	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.394592	0.347463	-4.047129	24808.006831
HLA B*4002	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.434235	0.387024	-4.047211	27179.078829
HLA B*1801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.512226	0.464975	-4.047250	32525.642776
HLA A*2601	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.381623	0.334311	-4.047312	24078.127821
HLA B*4601	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.406990	0.359537	-4.047453	25526.431434
HLA B*1501	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.406997	0.359537	-4.047460	25526.845723
HLA B*5701	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.412215	0.364577	-4.047638	25835.410105
HLA B*4501	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.481114	0.433440	-4.047674	30277.081335
HLA A*0101	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.390055	0.342354	-4.047701	24550.199027
HLA A*0201	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.393022	0.345166	-4.047856	24718.517305
HLA A*0216	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.412279	0.364340	-4.047938	25839.184082
HLA A*1101	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.481419	0.433440	-4.047980	30298.382259
HLA B*5301	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.445348	0.397240	-4.048108	27883.532799
HLA B*4402	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.429691	0.381582	-4.048109	26896.194039
HLA A*1101	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.448849	0.400734	-4.048114	28109.202874
HLA B*0702	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.351777	0.303652	-4.048125	22479.011403
HLA B*1503	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.273302	0.225072	-4.048231	18762.990517
HLA A*3101	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.244349	0.196045	-4.048304	17552.919269
HLA A*0212	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.413827	0.365377	-4.048450	25931.468199
HLA B*1501	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.395957	0.347463	-4.048494	24886.104681

HLA A*2601	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.395706	0.347179	-4.048527	24871.703325
HLA A*0216	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.395771	0.347179	-4.048592	24875.471099
HLA B*1801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.338564	0.289933	-4.048631	21805.382234
HLA A*2501	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.501136	0.452486	-4.048651	31705.625002
HLA B*5401	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.501766	0.452989	-4.048777	31751.626751
HLA A*6901	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.336769	0.287962	-4.048806	21715.443197
HLA A*2301	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.501832	0.452989	-4.048842	31756.436753
HLA B*4402	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.394009	0.345166	-4.048843	24774.745424
HLA B*4001	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.244923	0.196045	-4.048877	17576.104649
HLA B*4002	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.645479	0.596390	-4.049089	44205.802526
HLA A*0202	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.589392	0.540290	-4.049102	38850.120781
HLA B*4001	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.414518	0.365377	-4.049141	25972.745208
HLA A*0203	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.228086	0.178924	-4.049162	16907.765671
HLA B*1517	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.352905	0.303652	-4.049253	22537.459558
HLA A*0206	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.461355	0.412011	-4.049343	28930.426664
HLA B*4001	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.431267	0.381754	-4.049514	26994.005604
HLA B*1501	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.318210	0.268538	-4.049673	20807.031057
HLA B*0702	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.450411	0.400734	-4.049677	28210.509996
HLA A*2403	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.431472	0.381754	-4.049718	27006.713602
HLA A*3002	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.525186	0.475212	-4.049973	33510.865692
HLA A*0201	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.390964	0.340987	-4.049977	24601.651832
HLA A*3301	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.465248	0.415126	-4.050122	29190.930256
HLA B*0801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.391150	0.340987	-4.050163	24612.168364
HLA B*1517	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.458641	0.408334	-4.050307	28750.220738
HLA A*2301	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.488844	0.438531	-4.050313	30820.793320
HLA A*3002	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.498636	0.448098	-4.050538	31523.647798
HLA A*2902	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.319162	0.268538	-4.050624	20852.669346
HLA B*4001	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.409558	0.358727	-4.050831	25677.816578
HLA A*2301	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.499005	0.448098	-4.050907	31550.433864
HLA A*0211	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.319620	0.268381	-4.051239	20874.679026
HLA B*1503	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.524859	0.473598	-4.051261	33485.675844
HLA A*3101	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.328177	0.276822	-4.051354	21290.047519
HLA A*0219	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.435957	0.384545	-4.051412	27287.070049
HLA B*5301	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.575418	0.523921	-4.051497	37619.899977
HLA A*3001	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-3.942144	-0.109399	-4.051543	8752.749463
HLA B*1517	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.446003	0.394299	-4.051705	27925.650839
HLA A*0216	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.349115	0.297408	-4.051707	22341.649854
HLA B*7301	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.510278	0.458535	-4.051743	32380.098448
HLA B*4403	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.628866	0.577123	-4.051743	42546.718593
HLA B*4001	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.377145	0.325371	-4.051774	23831.127884
HLA A*1101	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.472851	0.421060	-4.051791	29706.457743
HLA B*3901	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.321490	0.269593	-4.051897	20964.764895
HLA B*4403	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.645916	0.594015	-4.051901	44250.306532
HLA A*3101	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.386308	0.334311	-4.051997	24339.272257
HLA A*3001	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.218284	0.166266	-4.052019	16530.430682
HLA B*1517	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.485594	0.433440	-4.052155	30591.056448
HLA B*1517	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.473347	0.421060	-4.052287	29740.386628
HLA B*5401	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.439364	0.387024	-4.052340	27501.960820
HLA A*0203	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.394716	0.342354	-4.052363	24815.120905
HLA B*5101	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.446687	0.394299	-4.052388	27969.648193
HLA B*5101	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.485879	0.433440	-4.052439	30611.087805
HLA B*1509	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.447380	0.394899	-4.052481	28014.321076
HLA A*2902	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.416844	0.364340	-4.052503	26112.222957
HLA B*3801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.565291	0.512773	-4.052518	36752.878271
HLA B*1501	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.377972	0.325371	-4.052601	23876.552284
HLA B*4402	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.418113	0.365377	-4.052736	26188.617174
HLA A*0219	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.417328	0.364577	-4.052751	26141.339610
HLA A*1101	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.490160	0.437367	-4.052792	30914.307663
HLA A*0211	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.340840	0.287962	-4.052878	21919.990164
HLA A*0301	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.341790	0.288865	-4.052924	21967.950782
HLA A*3301	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.635675	0.582728	-4.052947	43219.016361
HLA B*0802	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.450211	0.397240	-4.052971	28197.540641
HLA B*1517	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.491513	0.438531	-4.052982	31010.789864
HLA A*3101	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.400224	0.347179	-4.053045	25131.799621
HLA A*0203	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.306115	0.252948	-4.053167	20235.547840

HLA B*2705	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.434766	0.381582	-4.053184	27212.329243
HLA B*1517	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.461216	0.407915	-4.053302	28921.194024
HLA A*0202	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.465323	0.412011	-4.053312	29195.984123
HLA A*6801	1:32-40	9	AYARHTGGT	0.723455	-0.146332	-4.630438	0.577123	-4.053315	42700.983341
HLA A*6901	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.378705	0.325371	-4.053334	23916.887199
HLA B*4001	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.395783	0.342354	-4.053429	24876.143976
HLA B*5801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.353269	0.299836	-4.053433	22556.365884
HLA A*3002	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.468572	0.415126	-4.053446	29415.244091
HLA B*4403	1:110-118	9	AFSTPEEVE	1.155223	-0.554363	-4.654311	0.600860	-4.053451	45113.964495
HLA A*0211	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.527314	0.473598	-4.053716	33675.517673
HLA A*0201	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.396091	0.342354	-4.053737	24893.779835
HLA B*5701	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.401018	0.347179	-4.053839	25177.796226
HLA A*0201	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.383500	0.329580	-4.053920	24182.430825
HLA A*2403	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.401147	0.347215	-4.053932	25185.288840
HLA B*3901	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.492636	0.438531	-4.054105	31091.085278
HLA B*5401	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.521203	0.466843	-4.054360	33204.983602
HLA B*1503	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.497128	0.442758	-4.054370	31414.351389
HLA B*4002	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-3.900056	-0.154364	-4.054420	7944.303423
HLA B*2705	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.401603	0.347179	-4.054424	25211.735142
HLA A*2902	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.339807	0.285370	-4.054437	21867.874940
HLA A*2301	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.469660	0.415126	-4.054534	29489.015119
HLA A*3001	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.282096	0.227561	-4.054536	19146.799144
HLA A*3101	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.436291	0.381754	-4.054537	27308.040146
HLA B*4801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.351982	0.297408	-4.054574	22489.593873
HLA B*4501	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.594864	0.540290	-4.054574	39342.714734
HLA A*0219	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.418479	0.363771	-4.054708	26210.728196
HLA A*6802	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.419092	0.364340	-4.054752	26247.763388
HLA B*1501	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.286064	0.231300	-4.054764	19322.550971
HLA B*0802	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.446398	0.391537	-4.054861	27951.042922
HLA B*3901	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.307865	0.252948	-4.054917	20317.269105
HLA B*4601	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.402491	0.347179	-4.055312	25263.344331
HLA B*4501	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.528921	0.473598	-4.055323	33800.360191
HLA B*5801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.308328	0.252948	-4.055380	20338.933740
HLA B*1509	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.528994	0.473598	-4.055396	33806.029209
HLA A*2902	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.450385	0.394899	-4.055486	28208.831273
HLA A*0201	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.389942	0.334311	-4.055631	24543.824790
HLA B*0803	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.493122	0.437367	-4.055755	31125.922040
HLA A*0203	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.234268	0.178488	-4.055779	17150.141801
HLA B*5801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.359432	0.303652	-4.055780	22878.725611
HLA B*0702	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.450691	0.394899	-4.055792	28228.677115
HLA A*0219	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.353429	0.297408	-4.056021	22564.665276
HLA A*2403	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.447559	0.391537	-4.056022	28025.841576
HLA B*0702	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.415585	0.359537	-4.056047	26036.615002
HLA B*5701	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.333014	0.276822	-4.056192	21528.522259
HLA B*0802	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.437853	0.381582	-4.056271	27406.459833
HLA A*0216	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.436648	0.380348	-4.056300	27330.504868
HLA B*0803	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.443337	0.387024	-4.056313	27754.706439
HLA A*0211	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.149891	0.093574	-4.056317	14121.819635
HLA A*0206	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.403649	0.347215	-4.056435	25330.813506
HLA B*2705	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.453780	0.397240	-4.056540	28430.212054
HLA B*5701	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.390889	0.334311	-4.056578	24597.393250
HLA B*0803	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.464501	0.407915	-4.056586	29140.754964
HLA B*4801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.416179	0.359537	-4.056641	26072.275767
HLA B*5101	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.495258	0.438531	-4.056727	31279.363511
HLA A*3201	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.531943	0.475212	-4.056730	34036.333161
HLA A*3201	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.464663	0.407915	-4.056748	29151.634724
HLA A*6802	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.438534	0.381754	-4.056781	27449.490693
HLA A*0216	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.468850	0.412011	-4.056838	29434.027805
HLA B*3901	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.509404	0.452486	-4.056918	32314.999714
HLA B*2705	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.436154	0.379131	-4.057023	27299.472949
HLA A*2602	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.612255	0.555221	-4.057034	40950.123123
HLA B*0801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.310041	0.252948	-4.057093	20419.304994
HLA A*2501	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.465018	0.407915	-4.057103	29175.458227
HLA B*2705	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.468688	0.411532	-4.057155	29423.042652
HLA B*0802	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.490597	0.433440	-4.057157	30945.430513

HLA B*5701	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.404434	0.347215	-4.057219	25376.625205
HLA A*2403	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.325785	0.268538	-4.057247	21173.119811
HLA A*2501	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.416841	0.359537	-4.057304	26112.081693
HLA B*0802	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.444370	0.387024	-4.057346	27820.851080
HLA A*0216	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.494861	0.437367	-4.057494	31250.778757
HLA A*2501	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.444638	0.387024	-4.057614	27838.014252
HLA A*3101	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.421571	0.363771	-4.057800	26397.999062
HLA B*5701	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.416541	0.358727	-4.057814	26094.006228
HLA B*4002	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.640578	0.582728	-4.057850	43709.743060
HLA B*2705	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.452178	0.394299	-4.057879	28325.510793
HLA A*2301	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.533155	0.475212	-4.057943	34131.478417
HLA B*1509	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.449673	0.391537	-4.058137	28162.629335
HLA B*4501	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.654623	0.596390	-4.058233	45146.436361
HLA A*0301	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.238471	0.180214	-4.058257	17316.931695
HLA B*0702	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.311234	0.252948	-4.058287	20475.498993
HLA A*0206	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.438687	0.380348	-4.058339	27459.144806
HLA B*0702	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.442949	0.384545	-4.058404	27729.942762
HLA B*4801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.438981	0.380348	-4.058633	27477.719952
HLA A*0212	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.443261	0.384545	-4.058717	27749.902058
HLA B*4402	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.401196	0.342354	-4.058842	25188.150245
HLA A*3002	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.239239	0.180214	-4.059026	17347.593044
HLA B*7301	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.470565	0.411532	-4.059033	29550.499063
HLA A*0219	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.441058	0.381754	-4.059304	27609.442526
HLA A*6802	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.327836	0.268381	-4.059455	21273.353432
HLA B*1502	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.614736	0.555221	-4.059515	41184.734255
HLA B*2705	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.348403	0.288865	-4.059538	22305.057501
HLA B*4402	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.418308	0.358727	-4.059581	26200.379049
HLA A*8001	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.441349	0.381754	-4.059595	27627.969879
HLA B*1502	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.454074	0.394299	-4.059775	28449.444093
HLA B*5301	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.576411	0.516619	-4.059792	37706.087298
HLA A*2501	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.440308	0.380458	-4.059850	27561.836493
HLA B*5101	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.480921	0.421060	-4.059862	30263.653070
HLA B*5701	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.348735	0.288865	-4.059869	22322.078164
HLA A*2602	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.600169	0.540290	-4.059879	39826.254166
HLA B*0802	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.471444	0.411532	-4.059911	29610.349071
HLA B*7301	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.328461	0.268381	-4.060080	21303.988474
HLA B*0801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.441915	0.381754	-4.060162	27664.014256
HLA A*0301	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.348309	0.287962	-4.060347	22300.231308
HLA A*0203	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.287909	0.227561	-4.060348	19404.783753
HLA B*4601	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.407596	0.347215	-4.060382	25562.084862
HLA A*0219	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.407632	0.347179	-4.060453	25564.159267
HLA A*2301	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.525446	0.464975	-4.060471	33530.994932
HLA A*2601	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.385859	0.325371	-4.060488	24314.135748
HLA B*4601	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.394810	0.334311	-4.060500	24820.491368
HLA B*3501	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.419372	0.358727	-4.060645	26264.666530
HLA A*3001	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.136339	0.075603	-4.060736	13687.963261
HLA B*1501	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.172267	0.111406	-4.060861	14868.499943
HLA A*0101	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.364699	0.303652	-4.061047	23157.910713
HLA B*5801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.349111	0.287962	-4.061148	22341.408124
HLA A*2403	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.425490	0.364340	-4.061150	26637.284553
HLA A*3301	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.623878	0.562720	-4.061158	42060.856699
HLA A*2501	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.476366	0.415126	-4.061240	29947.853387
HLA A*2402	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.499802	0.438531	-4.061271	31608.348949
HLA A*3201	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.612056	0.550534	-4.061521	40931.296924
HLA A*6801	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.585448	0.523921	-4.061527	38498.835029
HLA B*5301	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.528407	0.466843	-4.061563	33760.338396
HLA A*3101	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.350523	0.288865	-4.061657	22414.165929
HLA B*1503	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.335392	0.273594	-4.061798	21646.710013
HLA B*4801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.319535	0.257713	-4.061822	20870.613953
HLA B*1503	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.473847	0.412011	-4.061836	29774.676418
HLA B*0702	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.420589	0.358727	-4.061862	26338.371822
HLA A*6901	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.199540	0.137558	-4.061982	15832.152972
HLA A*8001	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.425786	0.363771	-4.062015	26655.447942
HLA A*0212	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.396333	0.334311	-4.062022	24907.654977
HLA B*0802	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.483083	0.421060	-4.062023	30414.653698

HLA B*5701	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.421674	0.359537	-4.062137	26404.283461
HLA B*4001	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.421778	0.359537	-4.062240	26410.569356
HLA A*0203	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.444006	0.381754	-4.062253	27797.532162
HLA A*2601	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.351155	0.288865	-4.062289	22446.808118
HLA A*2501	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.470638	0.408334	-4.062303	29555.455291
HLA A*2403	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.409802	0.347463	-4.062339	25692.267714
HLA A*3001	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.302203	0.239809	-4.062394	20054.095283
HLA A*2602	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.612969	0.550534	-4.062435	41017.525364
HLA B*0702	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.456738	0.394299	-4.062439	28624.512606
HLA A*8001	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.421996	0.359537	-4.062459	26423.860377
HLA B*2705	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.496397	0.433440	-4.062958	31361.541950
HLA A*2601	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.315908	0.252948	-4.062960	20697.010505
HLA B*4601	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.404046	0.340987	-4.063059	25353.983331
HLA A*2601	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.392980	0.329580	-4.063400	24716.110382
HLA A*2602	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.589096	0.525631	-4.063465	38823.647774
HLA B*1503	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.500988	0.437367	-4.063621	31694.820836
HLA A*0206	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.484951	0.421060	-4.063891	30545.744622
HLA B*1801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.405026	0.340987	-4.064039	25411.244549
HLA B*5301	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.576825	0.512773	-4.064052	37742.005888
HLA B*3801	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.574295	0.510101	-4.064194	37522.743336
HLA B*4002	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.614793	0.550534	-4.064259	41190.081918
HLA A*0250	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.590783	0.526478	-4.064305	38974.743746
HLA B*2705	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.386082	0.321711	-4.064371	24326.634953
HLA A*0301	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.361793	0.297408	-4.064385	23003.454602
HLA A*0216	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.458738	0.394299	-4.064439	28756.598401
HLA A*6802	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.428239	0.363771	-4.064467	26806.421836
HLA B*1503	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.498019	0.433440	-4.064579	31478.827818
HLA B*3901	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.476138	0.411532	-4.064606	29932.142096
HLA A*2402	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.588342	0.523691	-4.064651	38756.286127
HLA B*5801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.276706	0.211872	-4.064834	18910.650265
HLA A*2501	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.429266	0.364340	-4.064925	26869.870447
HLA B*4403	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.627649	0.562720	-4.064929	42427.655867
HLA A*2501	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.406299	0.340987	-4.065312	25485.863726
HLA B*3501	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.445696	0.380348	-4.065348	27905.867068
HLA A*2403	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.387116	0.321711	-4.065404	24384.609862
HLA A*3002	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.568409	0.502859	-4.065550	37017.673686
HLA B*1509	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.365409	0.299836	-4.065573	23195.776719
HLA B*4501	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.628166	0.562255	-4.065911	42478.182290
HLA B*3901	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.503357	0.437367	-4.065989	31868.130140
HLA B*5301	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.568858	0.502859	-4.065999	37055.943403
HLA A*6901	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.291076	0.225072	-4.066004	19546.810971
HLA B*1501	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.395661	0.329580	-4.066081	24869.146947
HLA B*1517	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.481398	0.415126	-4.066272	30296.907097
HLA B*5101	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.203849	0.137558	-4.066291	15990.017274
HLA B*3501	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.445505	0.379131	-4.066374	27893.641368
HLA B*0802	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.451045	0.384545	-4.066501	28251.746353
HLA B*4501	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.629378	0.562720	-4.066658	42596.925914
HLA B*5701	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.388526	0.321711	-4.066814	24463.889281
HLA B*2705	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.431178	0.364340	-4.066838	26988.456860
HLA B*5801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.351812	0.284825	-4.066988	22480.835612
HLA B*3901	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.396589	0.329580	-4.067009	24922.346802
HLA B*1502	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.542276	0.475212	-4.067064	34855.859881
HLA A*3301	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.629364	0.562255	-4.067109	42595.543269
HLA A*0250	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.590856	0.523691	-4.067165	38981.280615
HLA B*5801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.352545	0.285370	-4.067176	22518.812727
HLA B*3801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.570068	0.502859	-4.067209	37159.328658
HLA B*1517	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.431004	0.363771	-4.067233	26977.654685
HLA A*0219	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.446414	0.379131	-4.067284	27952.101426
HLA A*2501	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.479596	0.412011	-4.067585	30171.454023
HLA B*4801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.432052	0.364340	-4.067712	27042.825246
HLA A*1101	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.412883	0.345166	-4.067717	25875.134358
HLA B*5101	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.520245	0.452486	-4.067759	33131.773234
HLA B*1517	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.414974	0.347215	-4.067759	26000.018394
HLA A*2902	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.408870	0.340987	-4.067883	25637.146976
HLA A*0201	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.393333	0.325371	-4.067962	24736.175235

HLA A*2902	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.341162	0.273190	-4.067972	21936.242292
HLA B*5801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.357914	0.289933	-4.067981	22798.908859
HLA A*6801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.532981	0.464975	-4.068006	34117.817236
HLA A*1101	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.479563	0.411532	-4.068031	30169.168970
HLA A*2602	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.521177	0.452989	-4.068188	33203.007673
HLA B*0802	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.433699	0.365377	-4.068322	27145.575333
HLA B*1517	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.433706	0.365377	-4.068329	27146.015900
HLA A*3201	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.581174	0.512773	-4.068401	38121.841802
HLA B*4801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.433034	0.364577	-4.068457	27104.047292
HLA B*1517	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.505828	0.437367	-4.068461	32050.015231
HLA A*0301	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.368332	0.299836	-4.068495	23352.408492
HLA B*7301	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.239091	0.170588	-4.068503	17341.681592
HLA A*0219	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.433967	0.365377	-4.068590	27162.321916
HLA B*1509	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.521652	0.452989	-4.068663	33239.311673
HLA B*3501	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.428241	0.359537	-4.068704	26806.566857
HLA A*1101	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.321854	0.252948	-4.068906	20982.351911
HLA A*0101	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.368881	0.299836	-4.069045	23381.989354
HLA B*4001	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.337539	0.268381	-4.069158	21754.010234
HLA A*0211	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.477129	0.407915	-4.069215	30000.554437
HLA A*6801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.481290	0.412011	-4.069279	30289.368501
HLA A*0212	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.428932	0.359537	-4.069394	26849.236824
HLA B*5101	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.464374	0.394899	-4.069475	29132.243201
HLA B*5401	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.481048	0.411532	-4.069516	30272.495404
HLA B*4402	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.456560	0.387024	-4.069536	28612.746012
HLA A*2902	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.428291	0.358727	-4.069564	26809.612461
HLA A*2601	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.373266	0.303652	-4.069614	23619.222505
HLA A*0212	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.338044	0.268381	-4.069663	21779.327614
HLA B*0702	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.416896	0.347179	-4.069717	26115.330955
HLA A*0101	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.355116	0.285370	-4.069746	22652.483660
HLA A*0202	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.593485	0.523691	-4.069794	39217.975980
HLA B*4801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.433607	0.363771	-4.069836	27139.848610
HLA A*0211	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.434301	0.364340	-4.069960	27183.196144
HLA A*2402	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.535011	0.464975	-4.070036	34277.662112
HLA A*3002	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.507506	0.437367	-4.070139	32174.052974
HLA A*8001	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.327986	0.257713	-4.070273	21280.720242
HLA B*4403	1:308-316	9	DVADVNSSP	0.667764	-0.071374	-4.666676	0.596390	-4.070286	46416.921450
HLA A*0219	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.429017	0.358727	-4.070290	26854.466384
HLA A*2301	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.543939	0.473598	-4.070341	34989.620850
HLA A*0216	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.435762	0.365377	-4.070385	27274.820337
HLA A*6801	1:238-246	9	AERIPKFAH	0.768090	-0.186355	-4.652140	0.581735	-4.070405	44889.014328
HLA A*0212	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.250768	0.180214	-4.070554	17814.274842
HLA A*2403	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.326466	0.255887	-4.070579	21206.363709
HLA B*2705	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-3.666094	-0.404745	-4.070839	4635.473543
HLA B*4801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.436258	0.365377	-4.070881	27305.971955
HLA B*5301	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.317334	0.246392	-4.070942	20765.087118
HLA B*4403	1:451-459	9	IRVAATGTT	0.799130	-0.236875	-4.633337	0.562255	-4.071082	42987.000337
HLA B*4402	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.412173	0.340987	-4.071186	25832.894427
HLA A*0211	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.462821	0.391537	-4.071284	29028.254183
HLA A*2402	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.508709	0.437367	-4.071342	32263.294237
HLA B*5101	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.486741	0.415126	-4.071615	30671.924329
HLA A*0206	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.505224	0.433440	-4.071785	32005.485728
HLA B*1517	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.436164	0.364340	-4.071823	27300.063703
HLA B*5301	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.597505	0.525631	-4.071874	39582.675412
HLA B*5101	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.479796	0.407915	-4.071881	30185.331272
HLA A*0211	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.456520	0.384545	-4.071975	28610.114672
HLA A*0211	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.472717	0.400734	-4.071983	29697.298763
HLA B*3801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.509425	0.437367	-4.072058	32316.573138
HLA A*2403	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.414614	0.342354	-4.072260	25978.506744
HLA B*0802	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.466611	0.394299	-4.072312	29282.667528
HLA A*2603	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.655060	0.582728	-4.072333	45191.887347
HLA B*1801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.505868	0.433440	-4.072429	32052.962946
HLA A*0206	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.524930	0.452486	-4.072444	33491.110899
HLA A*2301	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.530979	0.458535	-4.072444	33960.922381
HLA A*3001	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.195621	0.123142	-4.072479	15689.931100
HLA B*1801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.525169	0.452486	-4.072683	33509.596685

HLA A*0216	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.341115	0.268381	-4.072734	21933.868968
HLA B*5801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.341287	0.268538	-4.072749	21942.532844
HLA B*0801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.419971	0.347179	-4.072792	26300.924211
HLA B*0802	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.481142	0.408334	-4.072808	30279.046946
HLA B*0803	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.473572	0.400734	-4.072838	29755.836290
HLA A*3002	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.452037	0.379131	-4.072906	28316.318013
HLA A*3002	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.420234	0.347215	-4.073020	26316.864970
HLA B*1502	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.583173	0.510101	-4.073073	38297.752353
HLA A*0203	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.420253	0.347179	-4.073074	26318.003965
HLA B*3501	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.398447	0.325371	-4.073077	25029.223577
HLA A*0216	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.454995	0.381754	-4.073241	28509.840179
HLA B*1502	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.269355	0.196045	-4.073310	18593.233539
HLA A*6802	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.420697	0.347215	-4.073482	26344.927071
HLA B*3501	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.455406	0.381754	-4.073652	28536.844098
HLA A*6901	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.347294	0.273594	-4.073701	22248.174913
HLA A*2301	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.540615	0.466843	-4.073771	34722.798109
HLA B*1509	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.432567	0.358727	-4.073840	27074.883645
HLA A*6802	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.377523	0.303652	-4.073871	23851.893651
HLA B*1502	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.522016	0.448098	-4.073918	33267.195616
HLA A*2501	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.507555	0.433440	-4.074116	32177.708401
HLA B*3901	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.395936	0.321711	-4.074224	24884.893031
HLA B*1509	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.482357	0.407915	-4.074442	30363.853340
HLA A*0211	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.185871	0.111406	-4.074465	15341.600651
HLA B*2705	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.270664	0.196045	-4.074618	18649.345182
HLA B*4402	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.439232	0.364577	-4.074655	27493.630258
HLA A*2602	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.533200	0.458535	-4.074665	34134.986900
HLA A*0212	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.417112	0.342354	-4.074758	26128.332046
HLA B*5801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.343145	0.268381	-4.074764	22036.631010
HLA B*4402	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.439155	0.364340	-4.074814	27488.722359
HLA A*0301	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.343371	0.268538	-4.074833	22048.078693
HLA B*3501	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.309989	0.235091	-4.074899	20416.874883
HLA B*1801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.469263	0.394299	-4.074964	29462.066481
HLA B*1503	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.439643	0.364577	-4.075066	27519.671644
HLA A*8001	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.422426	0.347215	-4.075212	26450.033209
HLA B*1502	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.456802	0.381582	-4.075220	28628.694008
HLA A*0250	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.462419	0.387024	-4.075395	29001.412822
HLA A*0202	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.439761	0.364340	-4.075420	27527.116570
HLA A*0212	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.423042	0.347463	-4.075579	26487.549828
HLA A*0101	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.373002	0.297408	-4.075595	23604.915774
HLA A*0101	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.364563	0.288865	-4.075698	23150.645512
HLA A*2501	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.457363	0.381582	-4.075781	28665.733805
HLA B*3901	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.440423	0.364577	-4.075846	27569.143679
HLA B*4801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.421035	0.345166	-4.075869	26365.458399
HLA B*4002	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.246490	0.170588	-4.075901	17639.640758
HLA B*4002	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.631227	0.555221	-4.076006	42778.672477
HLA A*2603	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.599751	0.523691	-4.076060	39787.921525
HLA B*4001	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.397837	0.321711	-4.076125	24994.042940
HLA A*0202	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.588925	0.512773	-4.076152	38808.318492
HLA A*3201	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.541211	0.464975	-4.076236	34770.543914
HLA A*2501	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.497645	0.421060	-4.076585	31451.762242
HLA B*5301	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.603144	0.526478	-4.076666	40099.957196
HLA B*1503	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.515221	0.438531	-4.076690	32750.767450
HLA B*7301	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.602326	0.525631	-4.076695	40024.534375
HLA A*2603	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.589562	0.512773	-4.076788	38865.256318
HLA A*2601	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.364765	0.287962	-4.076803	23161.418867
HLA A*2403	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.350403	0.273594	-4.076809	22407.982616
HLA A*6901	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.376872	0.299836	-4.077036	23816.177419
HLA B*1801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.530030	0.452989	-4.077041	33886.778605
HLA B*0702	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.418068	0.340987	-4.077081	26185.925440
HLA B*5101	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.514632	0.437367	-4.077265	32706.325947
HLA A*0206	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.435999	0.358727	-4.077272	27289.727338
HLA B*0802	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.492399	0.415126	-4.077273	31074.101786
HLA B*5401	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.552543	0.475212	-4.077331	35689.712587
HLA A*0206	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.257603	0.180214	-4.077389	18096.842234
HLA A*1101	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.489481	0.412011	-4.077469	30866.012207

HLA B*4601	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.425095	0.347463	-4.077632	26613.085952
HLA A*0212	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.366555	0.288865	-4.077690	23257.095076
HLA A*2602	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.590466	0.512773	-4.077693	38946.289517
HLA B*5801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.350920	0.273190	-4.077730	22434.667928
HLA A*6901	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.381402	0.303652	-4.077750	24065.886493
HLA A*6901	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.347351	0.269593	-4.077758	22251.063744
HLA B*7301	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.312851	0.235091	-4.077760	20551.850880
HLA A*0301	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.367751	0.289933	-4.077818	23321.224848
HLA A*0301	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.354723	0.276822	-4.077901	22632.027482
HLA B*7301	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.493073	0.415126	-4.077947	31122.386097
HLA B*3901	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.511610	0.433440	-4.078171	32479.573881
HLA B*4601	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.367056	0.288865	-4.078191	23283.909821
HLA B*0702	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.425422	0.347215	-4.078207	26633.105843
HLA B*3801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.516998	0.438531	-4.078467	32884.988320
HLA A*6801	1:123-131	9	AAGRNPKLG	1.153018	-0.570290	-4.661261	0.582728	-4.078533	45841.705843
HLA B*0803	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.486931	0.408334	-4.078597	30685.367743
HLA B*0802	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.479345	0.400734	-4.078611	30153.994085
HLA B*3901	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.473565	0.394899	-4.078666	29755.353367
HLA B*5801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.352287	0.273594	-4.078693	22505.416043
HLA A*1101	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.493825	0.415126	-4.078699	31176.310731
HLA A*1101	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.473643	0.394899	-4.078744	29760.665955
HLA A*0206	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.162207	0.083388	-4.078819	14528.027751
HLA A*0203	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.413209	0.334311	-4.078898	25894.599119
HLA A*2902	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.444431	0.365377	-4.079055	27824.764556
HLA A*2602	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.075482	-0.003611	-4.079093	11898.233027
HLA A*6901	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.363924	0.284825	-4.079099	23116.604624
HLA B*3801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.521894	0.442758	-4.079136	33257.838396
HLA B*7301	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.603092	0.523921	-4.079171	40095.184881
HLA B*7301	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.473537	0.394299	-4.079238	29753.421751
HLA B*1517	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.490867	0.411532	-4.079335	30964.688808
HLA A*2403	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.443167	0.363771	-4.079396	27743.897752
HLA B*4001	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.420486	0.340987	-4.079499	26332.103111
HLA B*0803	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.304600	0.225072	-4.079528	20165.061403
HLA A*0203	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.439194	0.359537	-4.079657	27491.250561
HLA B*0802	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.458890	0.379131	-4.079759	28766.712230
HLA A*3301	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.635015	0.555221	-4.079793	43153.365640
HLA A*0219	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.460483	0.380348	-4.080136	28872.419537
HLA A*6802	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.422520	0.342354	-4.080166	26455.757498
HLA A*0301	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.348573	0.268381	-4.080191	22313.747281
HLA B*4501	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.630809	0.550534	-4.080275	42737.498143
HLA B*1801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.445677	0.365377	-4.080300	27904.659353
HLA A*2501	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.481107	0.400734	-4.080373	30276.589952
HLA B*3901	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.488722	0.408334	-4.080387	30812.124212
HLA A*3201	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.357381	0.276822	-4.080558	22770.927961
HLA A*2301	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.517947	0.437367	-4.080580	32956.940194
HLA B*1502	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.547475	0.466843	-4.080632	35275.665145
HLA A*0211	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.514289	0.433440	-4.080849	32680.503257
HLA B*5701	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.428316	0.347463	-4.080853	26811.207916
HLA A*0212	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.444688	0.363771	-4.080916	27841.177044
HLA A*0250	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.583822	0.502859	-4.080963	38354.978566
HLA B*4001	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.428272	0.347215	-4.081057	26808.452190
HLA A*3101	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.410705	0.329580	-4.081125	25745.696242
HLA B*4601	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.406508	0.325371	-4.081138	25498.137618
HLA A*8001	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.423549	0.342354	-4.081195	26518.519576
HLA A*3201	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.604911	0.523691	-4.081220	40263.425599
HLA B*5101	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.489577	0.408334	-4.081242	30872.859216
HLA A*3301	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.631817	0.550534	-4.081283	42836.800331
HLA B*3801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.533907	0.452486	-4.081421	34190.616796
HLA A*2403	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.440980	0.359537	-4.081443	27604.513953
HLA A*3101	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.003612	-0.077849	-4.081461	10083.509786
HLA A*6802	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.197087	0.115588	-4.081499	15742.986212
HLA B*4002	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.524319	0.442758	-4.081561	33444.036383
HLA A*0202	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.428805	0.347215	-4.081591	26841.394394
HLA A*3101	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.354933	0.273190	-4.081743	22642.926978
HLA B*1509	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.546893	0.464975	-4.081917	35228.369194

HLA B*4501	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.598645	0.516619	-4.082025	39686.668655
HLA B*4002	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.598851	0.516619	-4.082232	39705.566795
HLA B*7301	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.490185	0.407915	-4.082271	30916.147391
HLA A*3201	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.606238	0.523921	-4.082317	40386.682554
HLA B*0803	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.476732	0.394299	-4.082433	29973.138327
HLA A*6801	1:318-326	9	RFDQKKADA	0.655618	-0.061603	-4.676478	0.594015	-4.082464	47476.466049
HLA A*6802	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.430071	0.347463	-4.082608	26919.776251
HLA A*3201	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.592884	0.510101	-4.082783	39163.699359
HLA B*1503	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.494534	0.411532	-4.083002	31227.287799
HLA A*0101	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.336005	0.252948	-4.083057	21677.296346
HLA A*2403	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.424045	0.340987	-4.083058	26548.807395
HLA A*3301	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.470299	0.387024	-4.083275	29532.439847
HLA B*1502	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.372157	0.288865	-4.083291	23558.988519
HLA B*4001	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.412913	0.329580	-4.083333	25876.954183
HLA A*0206	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.467964	0.384545	-4.083419	29374.057451
HLA A*6801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.463782	0.380348	-4.083434	29092.554505
HLA B*4801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.430687	0.347179	-4.083508	26957.959152
HLA B*3901	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.468150	0.384545	-4.083605	29386.614056
HLA A*2301	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.526450	0.442758	-4.083692	33608.541824
HLA B*0803	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.504903	0.421060	-4.083843	31981.773496
HLA B*1502	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.596683	0.512773	-4.083910	39507.798063
HLA A*0201	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.383801	0.299836	-4.083964	24199.182131
HLA B*5801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.353612	0.269593	-4.084020	22574.188927
HLA B*3801	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.549002	0.464975	-4.084027	35399.927832
HLA B*1503	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.484772	0.400734	-4.084038	30533.188273
HLA A*3201	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.542584	0.458535	-4.084048	34880.570826
HLA A*3002	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.464630	0.380458	-4.084172	29149.426908
HLA B*1501	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.301207	0.217015	-4.084192	20008.148057
HLA B*4601	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.413820	0.329580	-4.084240	25931.047343
HLA A*0301	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.369079	0.284825	-4.084254	23392.617262
HLA A*0216	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.429446	0.345166	-4.084280	26881.065731
HLA A*0250	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.597280	0.512773	-4.084507	39562.123512
HLA B*3501	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.448355	0.363771	-4.084584	28077.286796
HLA B*4501	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.597451	0.512773	-4.084678	39577.750547
HLA B*3901	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.479007	0.394299	-4.084708	30130.512546
HLA A*0101	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.353415	0.268381	-4.085034	22563.932854
HLA B*7301	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.611642	0.526478	-4.085164	40892.343126
HLA A*0201	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.374076	0.288865	-4.085211	23663.346864
HLA B*0801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.249718	0.164416	-4.085302	17771.248044
HLA B*0802	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.465744	0.380348	-4.085396	29224.270337
HLA A*0250	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.595541	0.510101	-4.085440	39404.060352
HLA A*0212	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.426561	0.340987	-4.085574	26703.077441
HLA B*0803	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.477181	0.391537	-4.085644	30004.125243
HLA B*2705	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.451344	0.365377	-4.085967	28271.163552
HLA A*0216	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.433328	0.347215	-4.086113	27122.382227
HLA A*3201	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.588974	0.502859	-4.086115	38812.727666
HLA A*0212	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.343951	0.257713	-4.086238	22077.559968
HLA B*0801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.243701	0.157454	-4.086247	17526.730046
HLA A*0301	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.359486	0.273190	-4.086296	22881.572530
HLA A*2601	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.383726	0.297408	-4.086318	24194.993217
HLA B*1801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.433565	0.347215	-4.086351	27137.205914
HLA A*1101	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.445153	0.358727	-4.086426	27871.015323
HLA A*8001	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.321591	0.235091	-4.086500	20969.642396
HLA A*2601	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.371971	0.285370	-4.086601	23548.922001
HLA A*6801	1:9-17	9	VRFCPSPTG	0.945473	-0.382753	-4.649358	0.562720	-4.086638	44602.405221
HLA B*4403	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.626939	0.540290	-4.086649	42358.394729
HLA A*0219	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.451024	0.364340	-4.086684	28250.370837
HLA B*4001	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.421125	0.334311	-4.086814	26370.879056
HLA A*2402	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.535037	0.448098	-4.086939	34279.701995
HLA B*1503	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.450822	0.363771	-4.087051	28237.230396
HLA B*1801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.468664	0.381582	-4.087082	29421.450941
HLA B*4402	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.450862	0.363771	-4.087091	28239.827440
HLA A*3301	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.390753	0.303652	-4.087101	24589.676449
HLA B*4801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.434648	0.347463	-4.087185	27204.969455
HLA B*3901	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.502323	0.415126	-4.087197	31792.363009

HLA B*5801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.344952	0.257713	-4.087239	22128.498869
HLA A*0203	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.304428	0.217015	-4.087413	20157.099351
HLA A*2603	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.642721	0.555221	-4.087500	43925.931896
HLA A*2602	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.614083	0.526478	-4.087605	41122.841061
HLA B*3801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.546237	0.458535	-4.087702	35175.237044
HLA A*2902	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.451480	0.363771	-4.087708	28280.035688
HLA A*1101	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.452067	0.364340	-4.087727	28318.309528
HLA B*1509	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.469320	0.381582	-4.087738	29465.892005
HLA B*0803	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.521220	0.433440	-4.087780	33206.241073
HLA A*6901	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.377918	0.289933	-4.087985	23873.581570
HLA B*0801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.417680	0.329580	-4.088100	26162.561482
HLA A*2603	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.628420	0.540290	-4.088129	42503.008186
HLA A*3101	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.356702	0.268538	-4.088164	22735.354389
HLA B*0803	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.430565	0.342354	-4.088211	26950.376561
HLA B*5101	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.472809	0.384545	-4.088264	29703.565128
HLA B*5701	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.392014	0.303652	-4.088363	24661.216040
HLA A*0211	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.467640	0.379131	-4.088509	29352.136001
HLA A*3201	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.615187	0.526478	-4.088710	41227.535010
HLA A*3201	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.473382	0.384545	-4.088837	29742.800109
HLA B*3901	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.500850	0.412011	-4.088838	31684.705988
HLA A*3301	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.500892	0.412011	-4.088881	31687.791532
HLA A*0211	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.436178	0.347215	-4.088963	27300.949860
HLA A*2301	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.476081	0.387024	-4.089057	29928.256039
HLA A*0216	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.410869	0.321711	-4.089158	25755.447784
HLA B*2705	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.431533	0.342354	-4.089179	27010.512556
HLA A*0216	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.430177	0.340987	-4.089190	26926.330534
HLA B*0801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.357801	0.268381	-4.089420	22792.989329
HLA B*1517	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.257932	0.168455	-4.089476	18110.553693
HLA B*3801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.564720	0.475212	-4.089508	36704.594569
HLA B*3801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.563132	0.473598	-4.089534	36570.607894
HLA A*6801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.542598	0.452989	-4.089608	34881.703045
HLA A*0201	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.342786	0.252948	-4.089838	22018.398550
HLA B*1517	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.448569	0.358727	-4.089842	28091.112645
HLA A*0212	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.419428	0.329580	-4.089848	26268.076885
HLA B*7301	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.613557	0.523691	-4.089866	41073.037961
HLA A*2501	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.471700	0.381754	-4.089946	29627.814789
HLA B*1503	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.321389	0.231300	-4.090089	20959.888529
HLA B*1503	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.498606	0.408334	-4.090271	31521.430864
HLA B*5301	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.538409	0.448098	-4.090310	34546.857514
HLA B*5701	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.415747	0.325371	-4.090376	26046.335825
HLA A*0203	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.315449	0.225072	-4.090378	20675.188154
HLA A*0219	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.435875	0.345166	-4.090709	27281.903837
HLA A*0101	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.378686	0.287962	-4.090723	23915.852120
HLA B*0803	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.487986	0.397240	-4.090746	30759.994335
HLA B*5101	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.502292	0.411532	-4.090760	31790.127177
HLA B*4801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.390656	0.299836	-4.090820	24584.222929
HLA B*2705	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.485797	0.394899	-4.090898	30605.292263
HLA A*6901	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.318628	0.227561	-4.091068	20827.077051
HLA A*0301	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.364725	0.273594	-4.091132	23159.288853
HLA B*1501	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.337535	0.246392	-4.091142	21753.774862
HLA B*4002	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.615107	0.523921	-4.091187	41219.952470
HLA B*4402	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.412913	0.321711	-4.091202	25876.954183
HLA B*5401	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.556196	0.464975	-4.091221	35991.214321
HLA B*1517	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.471681	0.380348	-4.091333	29626.532551
HLA A*8001	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.438920	0.347463	-4.091456	27473.855287
HLA B*1509	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.499877	0.408334	-4.091543	31613.821348
HLA B*2705	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.473497	0.381754	-4.091743	29750.685511
HLA A*3002	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.483358	0.391537	-4.091821	30433.910961
HLA B*4402	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.113746	0.021903	-4.091843	12994.099354
HLA A*0212	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.270830	0.178924	-4.091906	18656.509811
HLA B*4001	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.376769	0.284825	-4.091944	23810.509007
HLA B*3501	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.215112	0.123142	-4.091971	16410.142942
HLA A*3001	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.270574	0.178488	-4.092086	18645.511722
HLA B*4601	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.365790	0.273594	-4.092196	23216.114456
HLA B*5301	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.602460	0.510101	-4.092359	40036.878391

HLA A*2301	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.544924	0.452486	-4.092438	35069.023306
HLA A*3301	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.632804	0.540290	-4.092514	42934.242774
HLA B*5801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.353539	0.261006	-4.092533	22570.403405
HLA B*7301	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.545647	0.452989	-4.092658	35127.505631
HLA B*2705	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.390276	0.297408	-4.092868	24562.686705
HLA A*6802	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.440099	0.347179	-4.092920	27548.569210
HLA A*2501	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.490216	0.397240	-4.092976	30918.321755
HLA A*0219	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.435461	0.342354	-4.093107	27255.939994
HLA B*3901	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.474876	0.381754	-4.093123	29845.312103
HLA A*0301	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.289225	0.196045	-4.093179	19463.660421
HLA B*0802	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.457020	0.363771	-4.093249	28643.101292
HLA B*2705	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.438553	0.345166	-4.093387	27450.678708
HLA B*5701	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.423112	0.329580	-4.093532	26491.849018
HLA B*5401	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.487892	0.394299	-4.093593	30753.338728
HLA B*4801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.436037	0.342354	-4.093683	27292.089591
HLA B*1509	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.362286	0.268538	-4.093749	23029.603142
HLA B*0803	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.475332	0.381582	-4.093750	29876.651753
HLA B*5801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.349738	0.255887	-4.093851	22373.702274
HLA A*0201	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.397595	0.303652	-4.093943	24980.119674
HLA B*0802	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.488942	0.394899	-4.094044	30827.797073
HLA A*0203	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.441692	0.347463	-4.094229	27649.800280
HLA B*1503	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.347271	0.252948	-4.094323	22246.971343
HLA A*3101	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.367925	0.273594	-4.094332	23330.562945
HLA B*0702	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.379706	0.285370	-4.094336	23972.069926
HLA A*8001	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.458916	0.364577	-4.094339	28768.424153
HLA A*8001	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.453275	0.358727	-4.094548	28397.163354
HLA B*5301	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.568193	0.473598	-4.094595	36999.254211
HLA A*0212	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.416341	0.321711	-4.094630	26082.009904
HLA A*3002	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.568317	0.473598	-4.094719	37009.864311
HLA B*1503	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.460150	0.365377	-4.094773	28850.248138
HLA B*1517	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.454396	0.359537	-4.094858	28470.537351
HLA A*2602	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.618848	0.523921	-4.094927	41576.494267
HLA B*0803	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.475456	0.380458	-4.094999	29885.219338
HLA A*3201	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.611635	0.516619	-4.095016	40891.679463
HLA A*0301	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.206466	0.111406	-4.095060	16086.673940
HLA A*6901	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.380547	0.285370	-4.095177	24018.542588
HLA B*3901	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.492739	0.397240	-4.095499	31098.486929
HLA A*0202	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.474792	0.379131	-4.095661	29839.500116
HLA B*0802	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.476201	0.380458	-4.095743	29936.514514
HLA B*1509	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.570979	0.475212	-4.095767	37237.409382
HLA B*1501	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.383749	0.287962	-4.095787	24196.302174
HLA B*0802	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.460558	0.364577	-4.095981	28877.418260
HLA B*4801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.437038	0.340987	-4.096051	27355.059823
HLA A*0101	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.380955	0.284825	-4.096131	24041.162384
HLA B*4801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.430447	0.334311	-4.096137	26943.087619
HLA A*0203	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.441330	0.345166	-4.096164	27626.774191
HLA A*2402	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.483196	0.387024	-4.096172	30422.552639
HLA A*6802	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.430508	0.334311	-4.096198	26946.877623
HLA B*4402	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.396173	0.299836	-4.096337	24898.493822
HLA A*0212	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.369614	0.273190	-4.096424	23421.488799
HLA B*3901	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.488294	0.391537	-4.096757	30781.801530
HLA A*0301	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.366417	0.269593	-4.096824	23249.672980
HLA A*0219	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.444135	0.347215	-4.096921	27805.804379
HLA A*3002	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.332105	0.235091	-4.097014	21483.496711
HLA B*4501	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.652272	0.555221	-4.097050	44902.615685
HLA A*0203	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.293118	0.196045	-4.097072	19638.920658
HLA A*0211	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.505518	0.408334	-4.097184	32027.136313
HLA B*1509	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.518264	0.421060	-4.097204	32981.018593
HLA A*0219	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.418928	0.321711	-4.097216	26237.825446
HLA A*0212	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.311883	0.214632	-4.097251	20506.094398
HLA B*4601	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.401067	0.303652	-4.097415	25180.656779
HLA A*8001	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.422898	0.325371	-4.097528	26478.810293
HLA B*0802	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.438715	0.340987	-4.097728	27460.927475
HLA B*5101	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.484800	0.387024	-4.097776	30535.170511
HLA A*6901	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.366431	0.268538	-4.097893	23250.427662

HLA A*2501	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.440369	0.342354	-4.098015	27565.713534
HLA B*4402	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.423467	0.325371	-4.098096	26513.498873
HLA A*2902	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.445338	0.347215	-4.098124	27882.929418
HLA A*0203	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.427762	0.329580	-4.098182	26776.998982
HLA B*4001	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.387207	0.288865	-4.098342	24389.755208
HLA A*2403	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.428138	0.329580	-4.098558	26800.186711
HLA B*7301	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.480350	0.381754	-4.098597	30223.894518
HLA A*2602	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.573933	0.475212	-4.098720	37491.495297
HLA A*6802	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.384097	0.285370	-4.098727	24215.683030
HLA B*0803	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.462523	0.363771	-4.098751	29008.316999
HLA A*8001	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.277252	0.178488	-4.098763	18934.399815
HLA A*3101	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.265121	0.166266	-4.098856	18412.855812
HLA B*1501	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.384233	0.285370	-4.098863	24223.282464
HLA B*1517	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.384242	0.285370	-4.098873	24223.806651
HLA B*1502	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.625478	0.526478	-4.099000	42216.100346
HLA B*5701	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.367601	0.268538	-4.099063	23313.151670
HLA B*3501	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.441441	0.342354	-4.099087	27633.799600
HLA B*3901	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.446558	0.347215	-4.099343	27961.327233
HLA B*2705	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.480010	0.380348	-4.099662	30200.195166
HLA A*3002	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.311573	0.211872	-4.099700	20491.456114
HLA B*0803	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.514853	0.415126	-4.099727	32722.962311
HLA B*2705	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.484314	0.384545	-4.099769	30500.994930
HLA A*2601	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.399641	0.299836	-4.099805	25098.104088
HLA B*0803	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.511350	0.411532	-4.099817	32460.075827
HLA A*2501	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.478976	0.379131	-4.099845	30128.393585
HLA A*0219	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.459419	0.359537	-4.099881	28801.749113
HLA A*2301	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.533364	0.433440	-4.099925	34147.916003
HLA A*2601	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.389876	0.289933	-4.099943	24540.107249
HLA A*1101	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.314904	0.214632	-4.100273	20649.255121
HLA B*0702	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.389383	0.288865	-4.100518	24512.243635
HLA B*4601	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.369119	0.268538	-4.100581	23394.768736
HLA A*2501	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.494908	0.394299	-4.100609	31254.160205
HLA B*4402	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.374208	0.273594	-4.100614	23670.516851
HLA A*0202	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.425997	0.325371	-4.100627	26668.429374
HLA B*4501	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.624576	0.523921	-4.100655	42128.491758
HLA B*4403	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.655885	0.555221	-4.100664	45277.782441
HLA A*0101	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.361699	0.261006	-4.100693	22998.477295
HLA B*1503	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.206974	0.106226	-4.100748	16105.482786
HLA B*3501	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.465133	0.364340	-4.100792	29183.193216
HLA A*0211	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.512426	0.411532	-4.100893	32540.602826
HLA A*2402	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.576174	0.475212	-4.100962	37685.490365
HLA A*6802	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.446292	0.345166	-4.101126	27944.239208
HLA B*3501	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.404904	0.303652	-4.101252	25404.097010
HLA B*4002	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.628074	0.526478	-4.101596	42469.220948
HLA B*2705	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.442615	0.340987	-4.101628	27708.648682
HLA A*2603	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.627395	0.525631	-4.101764	42402.873985
HLA A*2603	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.560393	0.458535	-4.101858	36340.649077
HLA B*0801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.449408	0.347463	-4.101945	28145.418289
HLA A*0206	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.513478	0.411532	-4.101946	32619.564867
HLA B*0702	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.449701	0.347463	-4.102238	28164.457675
HLA B*4403	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.628742	0.526478	-4.102264	42534.521171
HLA A*0219	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.268563	0.166266	-4.102298	18559.366490
HLA A*2403	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.337410	0.235091	-4.102319	21747.538424
HLA B*0801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.281011	0.178488	-4.102522	19099.003986
HLA A*2501	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.482902	0.380348	-4.102554	30401.986764
HLA B*0802	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.466968	0.364340	-4.102627	29306.756661
HLA A*2603	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.569556	0.466843	-4.102712	37115.530419
HLA B*5101	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.447918	0.345166	-4.102752	28049.048534
HLA B*5401	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.545523	0.442758	-4.102765	35117.435171
HLA A*1101	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.483130	0.380348	-4.102782	30417.944674
HLA B*1517	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.467541	0.364577	-4.102964	29345.467503
HLA A*0203	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.400461	0.297408	-4.103053	25145.535358
HLA A*0212	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.448233	0.345166	-4.103067	28069.389366
HLA B*5401	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.524138	0.421060	-4.103078	33430.107787
HLA A*2902	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.445477	0.342354	-4.103123	27891.830608

HLA A*2403	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.400642	0.297408	-4.103234	25156.012201
HLA B*1503	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.498178	0.394899	-4.103280	31490.410142
HLA B*3501	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.432874	0.329580	-4.103295	27094.078293
HLA A*2603	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.653895	0.550534	-4.103361	45070.786277
HLA A*0101	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.393297	0.289933	-4.103364	24734.168017
HLA B*0802	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.450550	0.347179	-4.103371	28219.515761
HLA A*0101	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.330982	0.227561	-4.103421	21428.013725
HLA A*3002	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.515522	0.412011	-4.103511	32773.454091
HLA A*0201	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.393518	0.289933	-4.103585	24746.749272
HLA B*0803	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.488191	0.384545	-4.103646	30774.475252
HLA A*0216	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.463371	0.359537	-4.103833	29065.024727
HLA A*2601	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.377443	0.273594	-4.103849	23847.506827
HLA B*5401	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.537328	0.433440	-4.103888	34460.992849
HLA A*2602	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.568865	0.464975	-4.103889	37056.544814
HLA A*1101	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.468467	0.364577	-4.103890	29408.083969
HLA A*0203	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.391918	0.287962	-4.103956	24655.746655
HLA B*5401	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.542692	0.438531	-4.104161	34889.252108
HLA B*0801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.377772	0.273594	-4.104178	23865.575400
HLA A*3201	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.546954	0.442758	-4.104196	35233.324664
HLA A*6801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.468789	0.364577	-4.104211	29429.887991
HLA B*4601	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.404053	0.299836	-4.104217	25354.394821
HLA A*3002	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.446870	0.342354	-4.104516	27981.453074
HLA B*2705	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.468312	0.363771	-4.104540	29397.585608
HLA A*1101	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.426261	0.321711	-4.104549	26684.592873
HLA A*6802	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.434138	0.329580	-4.104559	27173.051030
HLA A*2602	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.621179	0.516619	-4.104559	41800.218882
HLA A*3101	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.032252	-0.072551	-4.104803	10770.898822
HLA A*2403	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.344694	0.239809	-4.104885	22115.334387
HLA A*6801	1:442-450	9	LKPRKAFSP	0.427282	0.127939	-4.660185	0.555221	-4.104963	45728.263107
HLA B*4001	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.408651	0.303652	-4.104999	25624.251667
HLA B*3901	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.450181	0.345166	-4.105015	28195.557618
HLA A*6801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.393894	0.288865	-4.105029	24768.178892
HLA B*1801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.513419	0.408334	-4.105085	32615.153460
HLA B*3901	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.484244	0.379131	-4.105113	30496.045121
HLA A*0212	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.430506	0.325371	-4.105135	26946.731843
HLA B*4501	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.580497	0.475212	-4.105285	38062.492386
HLA A*0211	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.526353	0.421060	-4.105294	33601.088093
HLA A*0216	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.464200	0.358727	-4.105473	29120.582972
HLA A*6901	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.340589	0.235091	-4.105498	21907.305271
HLA A*0301	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.366530	0.261006	-4.105524	23255.711116
HLA B*0702	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.485876	0.380348	-4.105529	30610.922203
HLA B*5701	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.390920	0.285370	-4.105550	24599.123210
HLA A*2403	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.390393	0.284825	-4.105569	24569.331674
HLA A*2402	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.572417	0.466843	-4.105574	37360.901258
HLA A*6801	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.656137	0.550534	-4.105603	45303.999441
HLA A*0206	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.499926	0.394299	-4.105628	31617.413125
HLA A*3101	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.361568	0.255887	-4.105680	22991.510874
HLA A*0202	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.539186	0.433440	-4.105747	34608.775070
HLA A*0301	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.363494	0.257713	-4.105781	23093.730286
HLA B*1801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.503260	0.397240	-4.106020	31861.062399
HLA B*0702	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.451379	0.345166	-4.106213	28273.457803
HLA B*5101	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.486880	0.380348	-4.106532	30681.715863
HLA A*2501	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.470309	0.363771	-4.106537	29533.078923
HLA B*1509	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.491099	0.384545	-4.106555	30981.277288
HLA A*0203	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.380171	0.273594	-4.106577	23997.761559
HLA B*2705	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.431984	0.325371	-4.106613	27038.582916
HLA A*0250	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.573529	0.466843	-4.106685	37456.625651
HLA A*6802	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.321403	0.214632	-4.106771	20960.568884
HLA B*1801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.491623	0.384545	-4.107079	31018.675819
HLA A*0206	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.522258	0.415126	-4.107132	33285.737881
HLA B*4001	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.364908	0.257713	-4.107195	23169.063471
HLA B*5801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.353676	0.246392	-4.107283	22577.486512
HLA B*1801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.489060	0.381754	-4.107306	30836.136949
HLA B*0801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.319183	0.211872	-4.107310	20853.684667
HLA A*2602	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.617506	0.510101	-4.107406	41448.260696

HLA B*3801	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.560491	0.452989	-4.107502	36348.907168
HLA A*3101	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.319418	0.211872	-4.107545	20864.969331
HLA A*0219	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.455061	0.347463	-4.107597	28514.159088
HLA A*3101	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.455063	0.347463	-4.107600	28514.313347
HLA B*4002	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.499200	0.391537	-4.107664	31564.603846
HLA A*0211	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.454851	0.347179	-4.107673	28500.433392
HLA B*5801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.353647	0.245974	-4.107673	22576.020860
HLA A*0250	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.324772	0.217015	-4.107758	21123.808759
HLA A*2501	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.473163	0.365377	-4.107787	29727.839684
HLA A*0211	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.560306	0.452486	-4.107820	36333.375647
HLA B*3501	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.455068	0.347215	-4.107853	28514.621867
HLA A*0202	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.442279	0.334311	-4.107969	27687.221168
HLA B*4402	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.381240	0.273190	-4.108050	24056.904799
HLA A*6801	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.634554	0.526478	-4.108076	43107.632725
HLA A*0201	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.392924	0.284825	-4.108099	24712.901517
HLA A*0101	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.376858	0.268538	-4.108320	23815.404374
HLA A*0301	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.364279	0.255887	-4.108392	23135.496138
HLA A*6901	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.260178	0.151627	-4.108550	18204.461462
HLA B*1501	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.385391	0.276822	-4.108569	24287.974014
HLA A*0201	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.385410	0.276822	-4.108588	24289.025198
HLA B*0803	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.488997	0.380348	-4.108649	30831.633136
HLA B*1503	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.523938	0.415126	-4.108812	33414.738801
HLA A*0219	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.438572	0.329580	-4.108992	27451.866775
HLA A*0201	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.397369	0.287962	-4.109407	24967.149633
HLA A*6901	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.321293	0.211872	-4.109420	20955.240027
HLA B*0801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.305483	0.196045	-4.109438	20206.121270
HLA A*2403	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.031650	-0.077849	-4.109500	10755.992188
HLA B*1503	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.507036	0.397240	-4.109796	32139.260188
HLA B*7301	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.585008	0.475212	-4.109796	38459.907405
HLA A*0219	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.450876	0.340987	-4.109889	28240.744101
HLA A*3001	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.289015	0.178924	-4.110091	19454.291311
HLA A*2601	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.378667	0.268538	-4.110129	23914.817085
HLA B*4001	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.379727	0.269593	-4.110134	23973.237130
HLA A*3301	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.501679	0.391537	-4.110142	31745.271794
HLA B*5101	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.356563	0.246392	-4.110171	22728.098798
HLA A*2402	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.494734	0.384545	-4.110189	31241.650675
HLA A*2902	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.399086	0.288865	-4.110221	25066.080936
HLA A*0250	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.568797	0.458535	-4.110262	37050.731588
HLA A*0206	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.322195	0.211872	-4.110323	20998.817637
HLA B*4002	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.636102	0.525631	-4.110472	43261.590753
HLA B*4403	1:480-488	9	LRAARQLVG	0.999712	-0.449178	-4.661009	0.550534	-4.110475	45815.177677
HLA B*1509	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.525602	0.415126	-4.110475	33542.969402
HLA A*3002	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.549028	0.438531	-4.110497	35402.034501
HLA A*2902	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.440085	0.329580	-4.110505	27547.675017
HLA B*0801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.132223	0.021584	-4.110639	13558.839914
HLA A*6802	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.436049	0.325371	-4.110678	27292.827837
HLA A*0206	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.275118	0.164416	-4.110702	18841.618713
HLA B*4801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.440341	0.329580	-4.110761	27563.924063
HLA A*3001	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.279249	0.168455	-4.110793	19021.668363
HLA A*2902	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.408541	0.297408	-4.111133	25617.737150
HLA A*3201	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.475781	0.364577	-4.111203	29907.538919
HLA B*4403	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.584839	0.473598	-4.111241	38444.929726
HLA A*0301	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.328278	0.217015	-4.111263	21295.000697
HLA A*0212	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.357733	0.246392	-4.111341	22789.413690
HLA A*3001	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.308791	0.197447	-4.111344	20360.621476
HLA B*4801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.436718	0.325371	-4.111348	27334.940878
HLA B*1503	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.242399	0.131008	-4.111391	17474.279697
HLA A*2301	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.505734	0.394299	-4.111435	32043.080501
HLA B*4002	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-3.960795	-0.150664	-4.111459	9136.812432
HLA A*1101	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.458754	0.347215	-4.111539	28757.687412
HLA A*3002	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.519488	0.407915	-4.111573	33074.108445
HLA A*2601	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.396401	0.284825	-4.111576	24911.562965
HLA A*3002	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.506568	0.394899	-4.111670	32104.678709
HLA B*3501	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.452681	0.340987	-4.111694	28358.322688
HLA B*3501	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.458902	0.347179	-4.111723	28767.490364

HLA B*0802	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.493522	0.381754	-4.111768	31154.561131
HLA B*3901	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.351594	0.239809	-4.111785	22469.527905
HLA A*6801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.512621	0.400734	-4.111886	32555.217515
HLA B*1801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.260495	0.148579	-4.111916	18217.761675
HLA B*5401	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.564422	0.452486	-4.111936	36679.385121
HLA B*4801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.343253	0.231300	-4.111953	22042.115616
HLA A*2403	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.380408	0.268381	-4.112027	24010.877490
HLA B*4001	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.385326	0.273190	-4.112135	24284.295225
HLA B*3801	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.560313	0.448098	-4.112215	36333.965330
HLA B*5101	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.446748	0.334311	-4.112437	27973.582600
HLA A*2501	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.397956	0.285370	-4.112587	25000.939856
HLA B*1509	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.130601	0.017995	-4.112606	13508.321504
HLA A*2403	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.401551	0.288865	-4.112686	25208.734681
HLA A*0203	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.438057	0.325371	-4.112687	27419.362003
HLA B*3501	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.386002	0.273190	-4.112812	24322.160815
HLA B*1509	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.499926	0.387024	-4.112902	31617.413125
HLA B*0801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.412887	0.299836	-4.113051	25875.414322
HLA B*5801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.352886	0.239809	-4.113077	22536.484178
HLA A*3201	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.472804	0.359537	-4.113266	29703.243744
HLA A*0212	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.413195	0.299836	-4.113359	25893.758611
HLA A*6801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.508330	0.394899	-4.113432	32235.205395
HLA A*0216	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.413400	0.299836	-4.113563	25905.948645
HLA B*1801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.399018	0.285370	-4.113649	25062.148708
HLA A*2301	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.498493	0.384545	-4.113948	31513.246609
HLA A*6801	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.551392	0.437367	-4.114025	35595.229951
HLA B*0803	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.478617	0.364577	-4.114039	30103.466239
HLA B*1517	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.509087	0.394899	-4.114188	32291.407554
HLA B*4001	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.402183	0.287962	-4.114221	25245.446656
HLA B*3801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.508671	0.394299	-4.114372	32260.501704
HLA B*1501	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.293357	0.178924	-4.114433	19649.760576
HLA A*8001	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.402425	0.287962	-4.114463	25259.517807
HLA B*4501	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.515217	0.400734	-4.114483	32750.413096
HLA B*4402	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.375596	0.261006	-4.114590	23746.318393
HLA A*6901	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.382988	0.268381	-4.114607	24153.927945
HLA B*4801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.370503	0.255887	-4.114615	23469.433299
HLA B*3501	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.399507	0.284825	-4.114682	25090.365937
HLA B*1501	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.387875	0.273190	-4.114685	24427.256637
HLA B*3501	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.462215	0.347463	-4.114752	28987.766219
HLA B*3801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.535815	0.421060	-4.114755	34341.140734
HLA A*0250	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.478710	0.363771	-4.114939	30109.981200
HLA B*1509	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.457330	0.342354	-4.114976	28663.562789
HLA A*0219	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.449300	0.334311	-4.114989	28138.415035
HLA A*3301	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.618018	0.502859	-4.115160	41497.171780
HLA A*0101	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.329979	0.214632	-4.115347	21378.571656
HLA A*0219	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.383803	0.268381	-4.115422	24199.313046
HLA A*0201	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.388730	0.273190	-4.115540	24475.406174
HLA A*2501	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.480118	0.364577	-4.115541	30207.711568
HLA A*3001	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.286180	0.170588	-4.115591	19327.673760
HLA B*1801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.536724	0.421060	-4.115664	34413.113593
HLA A*6901	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.376686	0.261006	-4.115680	23806.001006
HLA B*4402	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.392590	0.276822	-4.115768	24693.924251
HLA B*1501	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.340894	0.225072	-4.115823	21922.717782
HLA B*5701	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.368839	0.252948	-4.115891	23379.712574
HLA A*2301	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.527467	0.411532	-4.115935	33687.361509
HLA A*6801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.475553	0.359537	-4.116015	29891.848778
HLA B*7301	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.581287	0.464975	-4.116311	38131.742364
HLA A*3101	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.280839	0.164416	-4.116423	19091.462860
HLA A*0216	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.463902	0.347463	-4.116439	29100.582375
HLA A*3301	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.591707	0.475212	-4.116494	39057.695570
HLA B*0802	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.458949	0.342354	-4.116595	28770.603111
HLA B*4801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.420333	0.303652	-4.116681	26322.845244
HLA B*3501	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.451019	0.334311	-4.116709	28250.065176
HLA B*4601	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.406664	0.289933	-4.116730	25507.243422
HLA A*0201	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.402101	0.285370	-4.116731	25240.666981
HLA B*0801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.385462	0.268538	-4.116924	24291.916191

HLA B*3801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.464184	0.347179	-4.117005	29119.480219
HLA B*1509	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.517834	0.400734	-4.117100	32948.383222
HLA B*0802	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.438821	0.321711	-4.117110	27467.613514
HLA A*0212	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.401948	0.284825	-4.117124	25231.792842
HLA B*0802	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.475896	0.358727	-4.117169	29915.467997
HLA A*2402	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.575866	0.458535	-4.117331	37658.792290
HLA B*0801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.394265	0.276822	-4.117443	24789.358853
HLA A*0101	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.391089	0.273594	-4.117495	24608.706731
HLA B*0702	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.439227	0.321711	-4.117516	27493.332785
HLA B*1801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.421228	0.303652	-4.117576	26377.156998
HLA A*2603	1:274-282	9	GFIPEGLLN	1.010665	-0.486744	-4.641504	0.523921	-4.117583	43803.009580
HLA A*2602	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.565700	0.448098	-4.117602	36787.490805
HLA A*1101	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.394451	0.276822	-4.117628	24799.955624
HLA A*3101	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.417523	0.299836	-4.117686	26153.080251
HLA A*0202	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.512172	0.394299	-4.117873	32521.595945
HLA A*2402	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.591537	0.473598	-4.117939	39042.485091
HLA A*8001	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.403365	0.285370	-4.117995	25314.237468
HLA B*2705	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.482608	0.364577	-4.118031	30381.434791
HLA A*8001	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.452469	0.334311	-4.118158	28344.518664
HLA A*0203	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.421919	0.303652	-4.118267	26419.143443
HLA B*5301	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.519082	0.400734	-4.118347	33043.168510
HLA B*4403	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.519089	0.400734	-4.118354	33043.704794
HLA A*2501	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.465835	0.347463	-4.118372	29230.436890
HLA B*4501	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.644053	0.525631	-4.118422	44060.877474
HLA B*1801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.498792	0.380348	-4.118444	31534.905411
HLA A*1101	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.465713	0.347179	-4.118534	29222.215108
HLA A*3301	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.631387	0.512773	-4.118614	42794.412468
HLA B*1502	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.621526	0.502859	-4.118667	41833.700197
HLA A*0250	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.592270	0.473598	-4.118672	39108.439978
HLA A*0202	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.539788	0.421060	-4.118728	34656.739063
HLA B*4001	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.418582	0.299836	-4.118746	26216.968012
HLA B*0801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.346376	0.227561	-4.118815	22201.163828
HLA A*2601	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.388500	0.269593	-4.118907	24462.433509
HLA B*0702	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.461270	0.342354	-4.118916	28924.792838
HLA B*4001	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.387565	0.268538	-4.119027	24409.819228
HLA A*3101	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.407065	0.287962	-4.119103	25530.850862
HLA A*3101	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.403992	0.284825	-4.119168	25350.828796
HLA A*2501	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.466376	0.347179	-4.119197	29266.830214
HLA B*5701	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.387579	0.268381	-4.119198	24410.611568
HLA B*4402	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.387581	0.268381	-4.119200	24410.743627
HLA A*0211	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.534382	0.415126	-4.119256	34228.000643
HLA A*0212	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.407328	0.287962	-4.119366	25546.324886
HLA A*6901	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.375324	0.255887	-4.119436	23731.421134
HLA B*0803	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.466895	0.347179	-4.119716	29301.842137
HLA B*4001	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.359540	0.239809	-4.119731	22884.419803
HLA B*4601	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.354994	0.235091	-4.119903	22646.112091
HLA A*2402	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.572897	0.452989	-4.119907	37402.156159
HLA B*5701	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.419771	0.299836	-4.119935	26288.832759
HLA A*6901	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.334600	0.214632	-4.119968	21607.281142
HLA B*5101	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.499116	0.379131	-4.119985	31558.457049
HLA A*1101	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.454337	0.334311	-4.120026	28466.687050
HLA A*0203	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.355412	0.235091	-4.120321	22667.929900
HLA A*3002	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.465537	0.345166	-4.120371	29210.360842
HLA B*1801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.484145	0.363771	-4.120373	30489.116739
HLA B*5301	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.563172	0.442758	-4.120414	36573.971379
HLA A*2301	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.541500	0.421060	-4.120441	34793.688502
HLA A*2403	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.366922	0.246392	-4.120530	23276.731016
HLA A*2601	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.393765	0.273190	-4.120575	24760.810368
HLA A*0101	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.376510	0.255887	-4.120623	23796.343879
HLA B*4501	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.501113	0.380458	-4.120655	31703.909809
HLA A*0250	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.408677	0.287962	-4.120715	25625.776580
HLA A*0301	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.367216	0.246392	-4.120823	23292.476906
HLA A*0301	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.366830	0.245974	-4.120856	23271.820477
HLA B*0803	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.468112	0.347215	-4.120897	29384.070512
HLA A*3301	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.559615	0.438531	-4.121084	36275.633076

HLA B*1503	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.462156	0.340987	-4.121169	28983.845969
HLA A*6801	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.515677	0.394299	-4.121378	32785.158030
HLA A*0211	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.533566	0.412011	-4.121555	34163.807033
HLA B*1501	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.421432	0.299836	-4.121596	26389.574602
HLA A*3002	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.518990	0.397240	-4.121750	33036.197610
HLA A*3001	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.293858	0.171999	-4.121858	19672.416171
HLA B*1501	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.377765	0.255887	-4.121878	23865.188073
HLA B*4501	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.645653	0.523691	-4.121962	44223.503057
HLA B*4501	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.353307	0.231300	-4.122006	22558.318407
HLA A*0101	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.395224	0.273190	-4.122034	24844.135218
HLA B*4001	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.407453	0.285370	-4.122083	25553.650683
HLA B*1509	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.564915	0.442758	-4.122158	36721.079396
HLA A*2601	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.399035	0.276822	-4.122212	25063.097810
HLA A*0202	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.463202	0.340987	-4.122215	29053.705756
HLA B*5101	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.486055	0.363771	-4.122284	30623.510519
HLA B*5401	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.530211	0.407915	-4.122297	33900.897472
HLA B*1509	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.486976	0.364577	-4.122399	30688.521990
HLA B*5101	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.502931	0.380458	-4.122473	31836.940460
HLA B*5801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.357571	0.235091	-4.122480	22780.908392
HLA A*2603	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.463538	0.340987	-4.122551	29076.190810
HLA B*1509	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.444283	0.321711	-4.122572	27815.282852
HLA A*0201	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.392198	0.269593	-4.122605	24671.624563
HLA A*0201	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.380356	0.257713	-4.122643	24008.019944
HLA A*0206	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.380408	0.257713	-4.122695	24010.877490
HLA A*0206	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.560430	0.437367	-4.123063	36343.794796
HLA A*3001	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.260027	0.136944	-4.123083	18198.159570
HLA A*0301	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.337786	0.214632	-4.123154	21766.370857
HLA A*1101	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.465516	0.342354	-4.123162	29208.938654
HLA A*2403	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.376205	0.252948	-4.123257	23779.614136
HLA A*2902	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.457586	0.334311	-4.123275	28680.470044
HLA A*8001	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.426965	0.303652	-4.123314	26727.936243
HLA A*1101	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.488747	0.365377	-4.123371	30813.957858
HLA A*0203	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.400261	0.276822	-4.123439	25133.975079
HLA B*1502	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.510464	0.387024	-4.123440	32393.940052
HLA B*1501	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.413522	0.289933	-4.123589	25913.237382
HLA B*4001	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.421005	0.297408	-4.123597	26363.604219
HLA A*2602	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.590447	0.466843	-4.123604	38944.603993
HLA A*2402	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.449088	0.325371	-4.123718	28124.718057
HLA B*0802	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.470995	0.347215	-4.123780	29579.768830
HLA B*1801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.453503	0.329580	-4.123923	28412.068938
HLA A*0219	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.412044	0.287962	-4.124081	25825.209150
HLA B*0802	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.469289	0.345166	-4.124123	29463.819785
HLA A*0211	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.561565	0.437367	-4.124198	36438.884455
HLA A*8001	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.392844	0.268538	-4.124306	24708.356337
HLA B*1509	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.504656	0.380348	-4.124308	31963.611781
HLA A*3101	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.339106	0.214632	-4.124475	21832.649114
HLA A*0201	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.398147	0.273594	-4.124553	25011.897694
HLA A*6901	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.397790	0.273190	-4.124599	24991.338786
HLA B*4402	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.320651	0.196045	-4.124606	20924.314081
HLA B*4002	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.599878	0.475212	-4.124666	39799.546628
HLA A*0206	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.471852	0.347179	-4.124674	29638.235029
HLA A*2603	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.634796	0.510101	-4.124695	43131.659792
HLA B*0802	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.472191	0.347463	-4.124728	29661.332922
HLA A*0206	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.470086	0.345166	-4.124919	29517.904608
HLA B*5101	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.472113	0.347179	-4.124934	29656.038065
HLA B*3901	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.505368	0.380348	-4.125020	32016.049384
HLA A*1101	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.466044	0.340987	-4.125057	29244.514153
HLA A*2603	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.628023	0.502859	-4.125164	42464.166665
HLA A*8001	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.425065	0.299836	-4.125228	26611.214358
HLA A*0211	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.489025	0.363771	-4.125253	30833.634749
HLA B*1517	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.398924	0.273594	-4.125331	25056.725956
HLA B*0801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.410185	0.284825	-4.125361	25714.933454
HLA A*2603	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.578364	0.452989	-4.125375	37875.981061
HLA A*2301	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.516918	0.391537	-4.125381	32878.940136
HLA B*5801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.352978	0.227561	-4.125417	22541.239555

HLA A*0101	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.395055	0.269593	-4.125462	24834.460013
HLA B*4002	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.649173	0.523691	-4.125482	44583.347063
HLA B*2705	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.429193	0.303652	-4.125541	26865.364571
HLA A*0211	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.505894	0.380348	-4.125546	32054.870436
HLA B*4501	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.635698	0.510101	-4.125598	43221.354525
HLA B*0702	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.425636	0.299836	-4.125799	26646.220546
HLA B*1501	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.386820	0.261006	-4.125814	24367.993853
HLA A*0206	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.489652	0.363771	-4.125881	30878.204278
HLA B*3801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.537483	0.411532	-4.125951	34473.299436
HLA B*4601	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.394362	0.268381	-4.125981	24794.857878
HLA B*5101	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.507821	0.381754	-4.126067	32197.385210
HLA B*4601	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.411175	0.284825	-4.126350	25773.567590
HLA B*0803	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.491802	0.365377	-4.126425	31031.431818
HLA A*6801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.411807	0.285370	-4.126437	25811.102141
HLA A*6901	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.384242	0.257713	-4.126529	24223.806651
HLA A*8001	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.448242	0.321711	-4.126531	28069.996782
HLA B*0803	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.521431	0.394899	-4.126532	33222.412797
HLA A*2601	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.387691	0.261006	-4.126685	24416.951209
HLA B*1501	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.411518	0.284825	-4.126693	25793.932724
HLA A*2902	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.474160	0.347463	-4.126696	29796.107461
HLA B*0802	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.486250	0.359537	-4.126713	30637.264200
HLA A*0250	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.524081	0.397240	-4.126841	33425.767593
HLA A*0301	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.338726	0.211872	-4.126853	21813.523318
HLA A*2902	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.403680	0.276822	-4.126857	25332.595048
HLA A*2601	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.395381	0.268381	-4.127000	24853.141919
HLA A*0301	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.362183	0.235091	-4.127092	23024.121940
HLA B*1509	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.539214	0.412011	-4.127203	34611.021898
HLA B*4601	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.415249	0.287962	-4.127286	26016.480498
HLA B*5701	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.415399	0.287962	-4.127437	26025.489819
HLA A*2403	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.427405	0.299836	-4.127568	26754.989222
HLA B*1503	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.491936	0.364340	-4.127595	31041.002260
HLA B*4501	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.475442	0.347215	-4.128228	29884.249300
HLA A*2603	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.644883	0.516619	-4.128263	44145.100524
HLA B*1509	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.417154	0.288865	-4.128289	26130.876495
HLA B*1501	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.276930	0.148579	-4.128351	18920.371693
HLA B*4501	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.475837	0.347463	-4.128374	29911.422286
HLA B*5701	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.402174	0.273594	-4.128580	25244.900361
HLA A*0201	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.389684	0.261006	-4.128678	24529.223404
HLA B*2705	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.397259	0.268538	-4.128721	24960.802173
HLA A*0211	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.523043	0.394299	-4.128744	33345.936350
HLA B*5801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.360054	0.231300	-4.128754	22911.548546
HLA A*0201	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.384771	0.255887	-4.128884	24253.310428
HLA A*0301	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.368726	0.239809	-4.128918	23373.642242
HLA B*1517	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.381884	0.252948	-4.128936	24092.591023
HLA B*7301	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.602545	0.473598	-4.128947	40044.676573
HLA A*1101	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.454461	0.325371	-4.129091	28474.850306
HLA B*3901	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.488665	0.359537	-4.129128	30808.123907
HLA B*4501	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.582177	0.452989	-4.129188	38210.005911
HLA B*1801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.414161	0.284825	-4.129336	25951.396517
HLA B*5401	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.526588	0.397240	-4.129348	33619.270827
HLA B*5701	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.419362	0.289933	-4.129429	26264.098180
HLA B*4001	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.403034	0.273594	-4.129440	25294.935273
HLA A*0201	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.398013	0.268538	-4.129475	25004.186123
HLA A*0219	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.454875	0.325371	-4.129504	28501.975275
HLA A*6802	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.429512	0.299836	-4.129676	26885.137900
HLA B*5801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.354754	0.225072	-4.129682	22633.619216
HLA A*0219	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.418554	0.288865	-4.129689	26215.266097
HLA B*5401	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.567223	0.437367	-4.129856	36916.679644
HLA A*2602	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.632799	0.502859	-4.129940	42933.778238
HLA B*0803	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.464414	0.334311	-4.130103	29134.922562
HLA A*6901	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.361455	0.231300	-4.130154	22985.541336
HLA B*3901	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.495568	0.365377	-4.130191	31301.708250
HLA B*0702	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.459821	0.329580	-4.130241	28828.405681
HLA B*5401	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.342158	0.211872	-4.130286	21986.617244
HLA B*4601	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.383397	0.252948	-4.130449	24176.675242

HLA B*4601	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.415852	0.285370	-4.130483	26052.677448
HLA B*5101	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.472851	0.342354	-4.130497	29706.457743
HLA B*4402	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.427966	0.297408	-4.130558	26789.604820
HLA B*1801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.495267	0.364577	-4.130690	31280.040390
HLA B*0801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.370500	0.239809	-4.130692	23469.306332
HLA A*3201	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.388408	0.257713	-4.130695	24457.272830
HLA B*1503	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.490486	0.359537	-4.130949	30937.563180
HLA A*2501	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.489720	0.358727	-4.130993	30883.049041
HLA A*2902	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.434691	0.303652	-4.131039	27207.618749
HLA B*4601	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.407899	0.276822	-4.131077	25579.930246
HLA A*1101	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.490632	0.359537	-4.131094	30947.941785
HLA A*3301	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.495676	0.364577	-4.131099	31309.498802
HLA A*0216	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.404366	0.273190	-4.131176	25372.644260
HLA A*1101	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.512980	0.381754	-4.131227	32582.175048
HLA A*6901	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.371179	0.239809	-4.131371	23506.028305
HLA B*2705	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.491019	0.359537	-4.131482	30975.579233
HLA B*5101	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.491069	0.359537	-4.131531	30979.098496
HLA A*2301	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.539520	0.407915	-4.131605	34635.371893
HLA B*4403	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.648238	0.516619	-4.131618	44487.456329
HLA A*0216	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.474103	0.342354	-4.131749	29792.239065
HLA B*1503	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.512130	0.380348	-4.131782	32518.429211
HLA A*2501	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.435454	0.303652	-4.131802	27255.497643
HLA A*8001	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.461409	0.329580	-4.131829	28934.026627
HLA A*0212	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.400374	0.268538	-4.131836	25140.502583
HLA B*5301	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.607061	0.475212	-4.131848	40463.225613
HLA A*2403	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.435602	0.303652	-4.131950	27264.788527
HLA A*6901	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.377981	0.245974	-4.132007	23877.068967
HLA B*1509	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.497478	0.365377	-4.132101	31439.683873
HLA A*0216	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.461801	0.329580	-4.132221	28960.178928
HLA B*1501	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.367599	0.235091	-4.132508	23313.025549
HLA A*0301	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.311474	0.178924	-4.132550	20486.800669
HLA A*0206	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.514355	0.381754	-4.132601	32685.453973
HLA B*1503	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.379036	0.246392	-4.132644	23935.137826
HLA A*0101	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.379057	0.246392	-4.132665	23936.303232
HLA A*3001	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.299647	0.166895	-4.132752	19936.404395
HLA B*5701	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.390565	0.257713	-4.132851	24579.036558
HLA B*0702	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.467191	0.334311	-4.132880	29321.822431
HLA B*1502	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.256137	0.123142	-4.132995	18035.854440
HLA B*1517	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.154623	0.021584	-4.133039	14276.525427
HLA A*2301	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.541472	0.408334	-4.133138	34791.429815
HLA A*6801	1:421-429	9	TDWTAPLIE	1.238956	-0.726183	-4.645975	0.512773	-4.133202	44256.291668
HLA B*4002	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.512383	0.379131	-4.133252	32537.434241
HLA A*0212	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.386291	0.252948	-4.133343	24338.350565
HLA A*0219	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.406720	0.273190	-4.133530	25510.555429
HLA A*8001	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.410425	0.276822	-4.133603	25729.127094
HLA B*1509	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.567093	0.433440	-4.133654	36905.696945
HLA B*1517	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.468044	0.334311	-4.133733	29379.460902
HLA B*5301	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.598880	0.464975	-4.133904	39708.144512
HLA A*3101	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.365263	0.231300	-4.133963	23187.997856
HLA A*2902	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.257105	0.123142	-4.133963	18076.098926
HLA B*4501	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.592691	0.458535	-4.134156	39146.329767
HLA A*3301	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.599277	0.464975	-4.134301	39744.465128
HLA A*2501	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.481542	0.347215	-4.134327	30306.906824
HLA A*0301	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.365670	0.231300	-4.134369	23209.709913
HLA A*0101	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.392101	0.257713	-4.134388	24666.152869
HLA A*0202	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.549552	0.415126	-4.134426	35444.769475
HLA B*5701	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.419280	0.284825	-4.134456	26259.125646
HLA B*5701	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.404187	0.269593	-4.134595	25362.214401
HLA B*5401	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.515066	0.380458	-4.134608	32739.075788
HLA A*2301	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.546679	0.412011	-4.134667	35211.030540
HLA B*1502	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.573216	0.438531	-4.134685	37429.684731
HLA B*1503	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.380669	0.245974	-4.134695	24025.300296
HLA A*0212	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.218256	0.083388	-4.134868	16529.357583
HLA B*3501	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.420295	0.285370	-4.134925	26320.566884
HLA B*5801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.351960	0.217015	-4.134946	22488.498904

HLA B*5801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.315172	0.180214	-4.134959	20661.994009
HLA A*8001	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.387973	0.252948	-4.135025	24432.807515
HLA A*2902	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.419858	0.284825	-4.135034	26294.095414
HLA B*4002	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.593574	0.458535	-4.135039	39226.039075
HLA B*0801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.425015	0.289933	-4.135082	26608.191291
HLA B*0802	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.424000	0.288865	-4.135135	26546.078639
HLA A*0219	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.434980	0.299836	-4.135143	27225.729169
HLA B*4501	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.573933	0.438531	-4.135402	37491.495297
HLA B*4403	1:382-390	9	LLKFFNDDQ	0.635696	-0.110065	-4.661183	0.525631	-4.135552	45833.522622
HLA A*0219	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.393309	0.257713	-4.135596	24734.837071
HLA B*1517	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.360733	0.225072	-4.135662	22947.397806
HLA A*2601	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.382154	0.246392	-4.135761	24107.584585
HLA B*3801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.569250	0.433440	-4.135811	37089.436778
HLA B*4001	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.382250	0.246392	-4.135858	24112.932372
HLA B*4402	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.424740	0.288865	-4.135875	26591.354779
HLA B*0803	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.515019	0.379131	-4.135889	32735.533684
HLA B*0803	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.424816	0.288865	-4.135951	26595.958578
HLA A*0101	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.375763	0.239809	-4.135954	23755.441157
HLA A*0101	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.381968	0.245974	-4.135994	24097.283657
HLA B*5801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.350743	0.214632	-4.136112	22425.567094
HLA B*0801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.424158	0.287962	-4.136195	26555.702343
HLA A*0101	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.348077	0.211872	-4.136204	22288.290969
HLA A*0216	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.470593	0.334311	-4.136282	29552.417504
HLA B*3901	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.500854	0.364340	-4.136514	31685.048811
HLA A*6901	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.315050	0.178488	-4.136562	20656.182314
HLA A*0211	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.495366	0.358727	-4.136639	31287.148502
HLA B*5301	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.406262	0.269593	-4.136669	25483.657810
HLA B*1801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.483957	0.347179	-4.136778	30475.924175
HLA A*6802	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.376604	0.239809	-4.136796	23801.493859
HLA A*2601	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.376628	0.239809	-4.136819	23802.781528
HLA B*5701	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.410044	0.273190	-4.136854	25706.587912
HLA B*4801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.405456	0.268538	-4.136918	25436.414385
HLA A*0301	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.230497	0.093574	-4.136923	17001.873941
HLA A*2403	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.382945	0.245974	-4.136972	24151.575998
HLA B*5101	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.425842	0.288865	-4.136977	26658.909039
HLA B*4001	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.382953	0.245974	-4.136979	24151.967973
HLA A*0212	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.440635	0.303652	-4.136983	27582.570088
HLA A*0203	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.436840	0.299836	-4.137004	27342.631668
HLA A*0301	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.362169	0.225072	-4.137097	23023.374604
HLA A*0202	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.521704	0.384545	-4.137159	33243.267970
HLA A*0301	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.364725	0.227561	-4.137165	23159.288853
HLA B*4403	1:113-121	9	TPEEVEARH	0.935903	-0.412212	-4.660899	0.523691	-4.137208	45803.529972
HLA A*3101	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.383601	0.246392	-4.137209	24188.056923
HLA A*0250	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.570707	0.433440	-4.137267	37214.048483
HLA A*0216	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.441062	0.303652	-4.137410	27609.741256
HLA A*0202	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.364981	0.227561	-4.137421	23172.949401
HLA B*4002	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.647742	0.510101	-4.137641	44436.703465
HLA B*3801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.524699	0.387024	-4.137675	33473.359652
HLA B*4601	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.410942	0.273190	-4.137752	25759.767503
HLA A*2603	1:379-387	9	AWELLKFFN	1.049111	-0.522633	-4.664259	0.526478	-4.137781	46159.246723
HLA B*0702	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.411381	0.273190	-4.138191	25785.840540
HLA A*1101	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.467933	0.329580	-4.138354	29371.991689
HLA A*2403	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.369755	0.231300	-4.138455	23429.092492
HLA A*2602	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.533545	0.394899	-4.138646	34162.143672
HLA B*0702	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.464052	0.325371	-4.138681	29110.659699
HLA B*5301	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.520282	0.381582	-4.138700	33134.641185
HLA B*3801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.546653	0.407915	-4.138738	35208.935237
HLA B*4002	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.605648	0.466843	-4.138805	40331.879414
HLA B*4402	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.426853	0.287962	-4.138890	26720.996576
HLA B*5401	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.518118	0.379131	-4.138988	32969.958182
HLA B*0803	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.521175	0.381754	-4.139422	33202.828049
HLA A*2403	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.400510	0.261006	-4.139504	25148.392246
HLA A*2601	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.395452	0.255887	-4.139565	24857.175829
HLA B*1502	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.598186	0.458535	-4.139651	39644.824138
HLA B*0803	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.461555	0.321711	-4.139843	28943.733107

HLA A*6801	1:342-350	9	VRLRDHLDT	0.718655	-0.178365	-4.680169	0.540290	-4.139879	47881.685014
HLA A*3101	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.365059	0.225072	-4.139987	23177.086752
HLA B*1517	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.521744	0.381754	-4.139990	33246.325431
HLA A*2301	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.540744	0.400734	-4.140010	34733.131203
HLA B*7301	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.548575	0.408334	-4.140240	35365.090222
HLA A*2501	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.485428	0.345166	-4.140262	30579.308615
HLA A*0216	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.465861	0.325371	-4.140491	29232.176409
HLA A*2402	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.583256	0.442758	-4.140498	38305.004570
HLA A*0212	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.430438	0.289933	-4.140505	26942.504589
HLA B*0803	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.499268	0.358727	-4.140541	31569.556304
HLA B*5101	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.499541	0.358727	-4.140814	31589.373906
HLA B*1502	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.614417	0.473598	-4.140819	41154.443940
HLA A*0203	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.409370	0.268538	-4.140833	25666.705852
HLA A*3201	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.614438	0.473598	-4.140840	41156.447758
HLA A*2601	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.355529	0.214632	-4.140897	22674.062279
HLA A*3101	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.368569	0.227561	-4.141008	23365.171707
HLA A*0216	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.292638	0.151627	-4.141011	19617.258759
HLA A*0216	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.358053	0.217015	-4.141038	22806.187055
HLA B*1801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.486224	0.345166	-4.141058	30635.441068
HLA B*1501	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.381230	0.239809	-4.141422	24056.384224
HLA A*2403	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.411088	0.269593	-4.141495	25768.409117
HLA B*3901	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.505302	0.363771	-4.141530	32011.200060
HLA A*8001	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.369163	0.227561	-4.141603	23397.173559
HLA A*2403	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.431542	0.289933	-4.141609	27011.097058
HLA B*0702	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.411464	0.269593	-4.141871	25790.723451
HLA B*4501	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.489053	0.347179	-4.141874	30835.636493
HLA B*4402	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.397771	0.255887	-4.141883	24990.257207
HLA B*0803	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.467259	0.325371	-4.141888	29326.422998
HLA B*3801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.539217	0.397240	-4.141977	34611.209141
HLA A*3301	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.608820	0.466843	-4.141977	40627.515513
HLA A*2602	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.615603	0.473598	-4.142005	41267.031359
HLA A*2403	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.430215	0.287962	-4.142252	26928.661330
HLA A*0301	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.308523	0.166266	-4.142258	20348.068395
HLA A*2601	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.388382	0.245974	-4.142408	24455.817451
HLA B*0702	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.400181	0.257713	-4.142468	25129.352455
HLA B*0802	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.472200	0.329580	-4.142620	29661.974787
HLA B*3501	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.442651	0.299836	-4.142814	27710.897284
HLA A*2402	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.576254	0.433440	-4.142814	37692.422729
HLA B*0803	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.483905	0.340987	-4.142918	30472.297221
HLA A*8001	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.411503	0.268381	-4.143122	25793.095484
HLA B*0802	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.447023	0.303652	-4.143371	27991.294280
HLA A*6901	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.340904	0.197447	-4.143457	21923.192186
HLA A*8001	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.432334	0.288865	-4.143469	27060.386788
HLA A*3001	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.274583	0.131008	-4.143575	18818.392756
HLA A*0101	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.378698	0.235091	-4.143607	23916.499039
HLA B*4801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.431587	0.287962	-4.143624	27013.873614
HLA A*3101	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.413223	0.269593	-4.143631	25895.439654
HLA A*0212	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.413254	0.269593	-4.143661	25897.260907
HLA A*0216	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.401377	0.257713	-4.143664	25198.644843
HLA B*5101	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.508258	0.364577	-4.143680	32229.799793
HLA A*2301	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.538615	0.394899	-4.143717	34563.308160
HLA B*1801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.339818	0.196045	-4.143773	21868.466462
HLA B*4402	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.447629	0.303652	-4.143977	28030.390446
HLA B*5801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.322545	0.178488	-4.144057	21015.751051
HLA A*3002	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.544816	0.400734	-4.144081	35060.297294
HLA A*2402	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.596577	0.452486	-4.144091	39498.181257
HLA B*4001	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.421024	0.276822	-4.144201	26364.745237
HLA A*2602	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.524568	0.380348	-4.144220	33463.220307
HLA A*0212	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.417849	0.273594	-4.144256	26172.754099
HLA A*2601	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.401974	0.257713	-4.144261	25233.294400
HLA A*0211	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.485273	0.340987	-4.144286	30568.392140
HLA B*4403	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.609311	0.464975	-4.144336	40673.477676
HLA A*3002	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.255756	0.111406	-4.144350	18020.054705
HLA B*3501	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.281358	0.136944	-4.144414	19114.301987
HLA B*3801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.526196	0.381582	-4.144614	33588.911163

HLA B*1801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.503408	0.358727	-4.144681	31871.923233
HLA A*0211	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.510102	0.365377	-4.144725	32366.963157
HLA A*8001	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.369814	0.225072	-4.144743	23432.261426
HLA A*0219	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.429609	0.284825	-4.144784	26891.101831
HLA B*0803	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.509153	0.364340	-4.144812	32296.299327
HLA B*0702	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.432839	0.287962	-4.144877	27091.879743
HLA A*0201	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.391413	0.246392	-4.145021	24627.085582
HLA B*2705	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.376595	0.231300	-4.145294	23800.978811
HLA B*5301	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.598339	0.452989	-4.145350	39658.767406
HLA A*0202	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.556965	0.411532	-4.145433	36054.940344
HLA B*0801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.401351	0.255887	-4.145464	25197.145347
HLA B*2705	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.422379	0.276822	-4.145557	26447.171529
HLA A*6801	1:42-50	9	VFRIEDTDA	0.672491	-0.155872	-4.662194	0.516619	-4.145574	45940.267069
HLA B*5401	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.385424	0.239809	-4.145615	24289.813617
HLA A*6802	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.418843	0.273190	-4.145653	26232.715969
HLA B*5101	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.510102	0.364340	-4.145762	32366.963157
HLA A*3001	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.303244	0.157454	-4.145790	20102.214182
HLA A*2301	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.543096	0.397240	-4.145856	34921.731698
HLA A*0101	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.239484	0.093574	-4.145910	17357.356040
HLA B*0801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.419132	0.273190	-4.145942	26250.177456
HLA B*5701	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.392355	0.246392	-4.145963	24680.568724
HLA B*1517	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.471364	0.325371	-4.145993	29604.903156
HLA B*5301	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.604669	0.458535	-4.146134	40240.996320
HLA A*2301	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.526727	0.380458	-4.146269	33630.003254
HLA B*4402	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.386632	0.239809	-4.146823	24357.449883
HLA A*2402	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.415298	0.268381	-4.146917	26019.436337
HLA A*2603	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.558454	0.411532	-4.146922	36178.816410
HLA A*2501	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.399874	0.252948	-4.146926	25111.549706
HLA B*5101	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.472296	0.325371	-4.146926	29668.554705
HLA B*5301	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.468822	0.321711	-4.147110	29432.117049
HLA B*1801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.481546	0.334311	-4.147236	30307.234740
HLA B*4403	1:30-38	9	NWAYARHTG	1.030515	-0.520414	-4.657361	0.510101	-4.147260	45431.871252
HLA B*5701	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.372394	0.225072	-4.147322	23571.864640
HLA B*0702	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.343429	0.196045	-4.147384	22051.060836
HLA B*4001	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.400362	0.252948	-4.147414	25139.822556
HLA A*3101	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.408437	0.261006	-4.147431	25611.639955
HLA A*0201	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.382598	0.235091	-4.147507	24132.246450
HLA A*2402	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.539160	0.391537	-4.147624	34606.715605
HLA A*1101	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.416179	0.268538	-4.147641	26072.275767
HLA A*0101	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.379269	0.231300	-4.147968	23947.960417
HLA B*5301	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.555931	0.407915	-4.148016	35969.218987
HLA B*4402	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.405858	0.257713	-4.148144	25459.956272
HLA B*4403	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.581707	0.433440	-4.148268	38168.685890
HLA A*2403	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.433720	0.285370	-4.148350	27146.897056
HLA A*0250	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.600898	0.452486	-4.148412	39893.101446
HLA B*4402	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.394484	0.245974	-4.148510	24801.834005
HLA B*1501	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.327152	0.178488	-4.148664	21239.889613
HLA A*8001	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.438642	0.289933	-4.148709	27456.322483
HLA B*3801	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.560747	0.412011	-4.148736	36370.347637
HLA B*4402	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.376459	0.227561	-4.148898	23793.511864
HLA A*0211	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.401896	0.252948	-4.148948	25228.789995
HLA B*3501	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.426082	0.276822	-4.149260	26673.623716
HLA B*0803	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.508836	0.359537	-4.149298	32272.720819
HLA A*2602	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.587851	0.438531	-4.149320	38712.490444
HLA A*6802	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.439258	0.289933	-4.149325	27495.266419
HLA A*6802	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.434155	0.284825	-4.149330	27174.080072
HLA A*1101	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.446922	0.297408	-4.149514	27984.783556
HLA B*1501	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.407239	0.257713	-4.149526	25541.073719
HLA A*3101	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.439509	0.289933	-4.149576	27511.186885
HLA B*5301	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.583025	0.433440	-4.149586	38284.701822
HLA B*4601	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.410676	0.261006	-4.149670	25744.024920
HLA B*1502	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.557625	0.407915	-4.149710	36109.791983
HLA A*0216	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.434801	0.284825	-4.149976	27214.537568
HLA A*6802	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.385079	0.235091	-4.149988	24270.504731
HLA A*0203	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.435440	0.285370	-4.150070	27254.612962

HLA A*0203	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.396535	0.246392	-4.150143	24919.245971
HLA A*0202	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.602648	0.452486	-4.150162	40054.209747
HLA A*0212	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.427048	0.276822	-4.150225	26732.997553
HLA A*0201	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.396659	0.245974	-4.150685	24926.391945
HLA B*5701	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.406595	0.255887	-4.150708	25503.241986
HLA A*0203	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.440752	0.289933	-4.150819	27590.032030
HLA B*0802	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.485204	0.334311	-4.150894	30563.596739
HLA B*3901	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.439777	0.288865	-4.150912	27528.159020
HLA B*5301	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.542457	0.391537	-4.150920	34870.382514
HLA B*4601	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.406866	0.255887	-4.150978	25519.113440
HLA B*3501	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.378559	0.227561	-4.150998	23908.866506
HLA B*5301	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.545297	0.394299	-4.150998	35099.201689
HLA B*4403	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.542616	0.391537	-4.151080	34883.212727
HLA B*5301	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.589618	0.438531	-4.151087	38870.302807
HLA A*2601	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.386293	0.235091	-4.151203	24338.482233
HLA A*0216	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.244873	0.093574	-4.151300	17574.107982
HLA B*4402	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.436786	0.285370	-4.151416	27339.229706
HLA A*1101	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.436831	0.285370	-4.151461	27342.039992
HLA A*0203	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.424769	0.273190	-4.151579	26593.081110
HLA A*6801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.363536	0.211872	-4.151664	23095.979216
HLA B*1503	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.332016	0.180214	-4.151802	21479.080678
HLA A*2301	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.531057	0.379131	-4.151926	33966.985841
HLA A*0219	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.455585	0.303652	-4.151933	28548.579479
HLA B*4001	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.407881	0.255887	-4.151993	25578.823194
HLA B*4601	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.366645	0.214632	-4.152013	23261.876663
HLA B*4801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.437449	0.285370	-4.152079	27380.969958
HLA B*3501	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.420495	0.268381	-4.152114	26332.672932
HLA B*4601	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.421775	0.269593	-4.152183	26410.426478
HLA A*0203	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.413266	0.261006	-4.152260	25897.961423
HLA B*5301	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.377337	0.225072	-4.152266	23841.701977
HLA B*4801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.421860	0.269593	-4.152267	26415.570568
HLA B*2705	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.481997	0.329580	-4.152418	30338.731181
HLA B*1801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.516819	0.364340	-4.152479	32871.470385
HLA A*0216	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.367364	0.214632	-4.152732	23300.416872
HLA B*4001	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.377972	0.225072	-4.152900	23876.552284
HLA A*2902	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.408806	0.255887	-4.152919	25633.402508
HLA A*0206	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.493937	0.340987	-4.152951	31184.407481
HLA B*1502	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.605543	0.452486	-4.153057	40322.062015
HLA B*4601	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.399528	0.246392	-4.153136	25091.587592
HLA B*4801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.443243	0.289933	-4.153310	27748.701093
HLA B*1801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.380899	0.227561	-4.153338	24038.041146
HLA A*0216	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.443283	0.289933	-4.153350	27751.253206
HLA A*2902	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.421768	0.268381	-4.153387	26409.997849
HLA A*2402	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.561316	0.407915	-4.153401	36417.994631
HLA A*0201	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.381033	0.227561	-4.153472	24045.454748
HLA A*3201	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.565059	0.411532	-4.153527	36733.199471
HLA B*5301	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.606036	0.452486	-4.153550	40367.897002
HLA A*3201	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.421954	0.268381	-4.153573	26421.287399
HLA A*2402	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.561979	0.408334	-4.153644	36473.595915
HLA B*1502	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.406598	0.252948	-4.153650	25503.379956
HLA A*0219	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.388791	0.235091	-4.153700	24478.849057
HLA B*0803	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.498925	0.345166	-4.153759	31544.631130
HLA B*0801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.368416	0.214632	-4.153784	23356.956957
HLA B*7301	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.565848	0.412011	-4.153837	36800.030966
HLA B*0702	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.430727	0.276822	-4.153905	26960.438538
HLA A*2301	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.535730	0.381754	-4.153977	34334.453242
HLA B*4001	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.389099	0.235091	-4.154008	24496.203255
HLA B*1502	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.517902	0.363771	-4.154131	32953.552793
HLA A*2902	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.453980	0.299836	-4.154143	28443.288425
HLA B*4801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.427792	0.273594	-4.154199	26778.882236
HLA A*1101	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.501663	0.347463	-4.154199	31744.069648
HLA A*0211	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.536047	0.381754	-4.154294	34359.538055
HLA B*5401	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.536146	0.381754	-4.154392	34367.345956
HLA A*2301	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.479768	0.325371	-4.154397	30183.371744
HLA A*0250	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.555207	0.400734	-4.154473	35909.335329

HLA A*0201	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.366382	0.211872	-4.154509	23247.786385
HLA A*2301	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.536122	0.381582	-4.154541	34365.486771
HLA A*0219	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.366429	0.211872	-4.154556	23250.301880
HLA A*2902	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.424153	0.269593	-4.154560	26555.415018
HLA B*5101	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.495902	0.340987	-4.154915	31325.763594
HLA A*8001	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.410808	0.255887	-4.154921	25751.825351
HLA B*4601	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.412753	0.257713	-4.155040	25867.436514
HLA B*1517	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.502527	0.347463	-4.155064	31807.329936
HLA B*5801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.352592	0.197447	-4.155146	22521.249345
HLA B*0702	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.401279	0.245974	-4.155305	25192.919975
HLA A*6802	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.333867	0.178488	-4.155379	21570.841289
HLA B*5701	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.416442	0.261006	-4.155436	26088.077943
HLA B*0802	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.380544	0.225072	-4.155473	24018.412651
HLA A*0219	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.432296	0.276822	-4.155474	27058.044590
HLA A*2902	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.416482	0.261006	-4.155476	26090.477325
HLA A*0212	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.440853	0.285370	-4.155483	27596.450914
HLA B*4403	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.502948	0.347179	-4.155769	31838.146123
HLA A*2501	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.455641	0.299836	-4.155805	28552.286391
HLA B*4001	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.372878	0.217015	-4.155863	23598.148645
HLA B*1501	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.425551	0.269593	-4.155958	26641.031540
HLA A*0219	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.336174	0.180214	-4.155961	21685.741558
HLA A*6802	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.424611	0.268538	-4.156074	26583.443860
HLA B*4402	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.391234	0.235091	-4.156144	24616.962198
HLA A*3201	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.550530	0.394299	-4.156231	35524.628248
HLA A*3201	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.594998	0.438531	-4.156467	39354.848469
HLA B*0702	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.446457	0.289933	-4.156524	27954.823479
HLA A*6802	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.430147	0.273594	-4.156553	26924.436910
HLA A*2501	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.425293	0.268538	-4.156755	26625.182503
HLA A*0201	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.396690	0.239809	-4.156881	24928.145044
HLA B*5301	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.502071	0.345166	-4.156905	31773.965067
HLA A*2402	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.568466	0.411532	-4.156933	37022.480275
HLA B*1502	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.552014	0.394899	-4.157116	35646.296603
HLA B*1502	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.522580	0.365377	-4.157203	33310.416910
HLA B*4402	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.425807	0.268538	-4.157270	26656.745801
HLA B*7301	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.590741	0.433440	-4.157301	38970.948648
HLA A*2301	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.521915	0.364577	-4.157338	33259.457727
HLA A*3002	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.609906	0.452486	-4.157420	40729.185659
HLA B*4601	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.382511	0.225072	-4.157439	24127.416480
HLA B*0702	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.454908	0.297408	-4.157500	28504.134052
HLA A*2603	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.631169	0.473598	-4.157571	42772.887172
HLA B*1517	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.425972	0.268381	-4.157590	26666.842415
HLA A*3001	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.280282	0.122535	-4.157748	19067.000546
HLA B*5301	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.569847	0.412011	-4.157836	37140.436844
HLA B*0803	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.461557	0.303652	-4.157905	28943.889690
HLA B*1517	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.487528	0.329580	-4.157948	30727.561854
HLA B*4801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.322463	0.164416	-4.158046	21011.772177
HLA A*0250	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.566041	0.407915	-4.158126	36816.359482
HLA B*5101	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.457990	0.299836	-4.158154	28707.169668
HLA B*4801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.435233	0.276822	-4.158411	27241.640940
HLA A*2403	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.435247	0.276822	-4.158425	27242.525200
HLA B*3501	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.324819	0.166266	-4.158554	21126.094432
HLA B*4801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.443414	0.284825	-4.158590	27759.661827
HLA A*2603	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.570665	0.412011	-4.158653	37210.424830
HLA A*8001	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.456165	0.297408	-4.158757	28586.752806
HLA B*0803	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.444215	0.285370	-4.158846	27810.919344
HLA B*4601	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.404876	0.245974	-4.158902	25402.447863
HLA B*4001	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.289974	0.131008	-4.158966	19497.278923
HLA A*0206	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.153537	-0.005447	-4.158984	14240.887679
HLA A*2402	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.559756	0.400734	-4.159022	36287.409816
HLA A*6802	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.428669	0.269593	-4.159076	26832.973595
HLA A*0219	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.337593	0.178488	-4.159105	21756.717199
HLA B*4501	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.601894	0.442758	-4.159136	39984.712991
HLA A*2902	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.296224	0.136944	-4.159279	19779.879191
HLA A*0219	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.449368	0.289933	-4.159435	28142.829927
HLA A*0202	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.394665	0.235091	-4.159574	24812.167646

HLA A*0201	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.390927	0.231300	-4.159626	24599.522449
HLA B*5801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.355717	0.196045	-4.159672	22683.877535
HLA B*1801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.459513	0.299836	-4.159676	28807.982358
HLA A*3002	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.387351	0.227561	-4.159790	24397.805234
HLA B*3501	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.447796	0.287962	-4.159834	28041.159047
HLA B*4402	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.406285	0.246392	-4.159893	25485.036485
HLA B*4501	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.626744	0.466843	-4.159901	42339.379199
HLA A*0101	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.384997	0.225072	-4.159925	24265.909640
HLA B*5301	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.581099	0.421060	-4.160039	38115.242855
HLA A*0203	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.444899	0.284825	-4.160074	27854.735936
HLA B*4002	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.489741	0.329580	-4.160162	30884.552742
HLA B*1501	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.406248	0.245974	-4.160274	25482.830641
HLA A*3101	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.400207	0.239809	-4.160398	25130.847917
HLA A*3301	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.613428	0.452989	-4.160438	41060.818747
HLA A*0212	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.416397	0.255887	-4.160510	26085.396543
HLA A*6801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.575711	0.415126	-4.160585	37645.348517
HLA B*0802	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.486010	0.325371	-4.160640	30620.362955
HLA A*0203	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.416668	0.255887	-4.160780	26101.630289
HLA B*5401	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.429214	0.268381	-4.160833	26866.672650
HLA A*2403	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.283980	0.123142	-4.160839	19230.052433
HLA B*7301	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.627722	0.466843	-4.160878	42434.771860
HLA B*3801	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.545464	0.384545	-4.160919	35112.685956
HLA A*6801	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.636251	0.475212	-4.161038	43276.337812
HLA B*1801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.418940	0.257713	-4.161226	26238.535174
HLA A*3001	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.276958	0.115588	-4.161370	18921.600018
HLA A*6802	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.449593	0.287962	-4.161631	28157.449684
HLA A*3001	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.299276	0.137558	-4.161718	19919.370785
HLA B*3801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.570263	0.408334	-4.161928	37176.017716
HLA B*1502	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.509216	0.347215	-4.162002	32301.017095
HLA B*0801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.393333	0.231300	-4.162032	24736.175235
HLA A*2601	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.387118	0.225072	-4.162047	24384.741780
HLA A*0301	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.340594	0.178488	-4.162105	21907.542305
HLA B*0803	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.435748	0.273594	-4.162154	27273.935029
HLA B*1517	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.430732	0.268538	-4.162194	26960.730246
HLA A*2501	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.450225	0.287962	-4.162263	28198.455929
HLA A*0250	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.599803	0.437367	-4.162436	39792.657268
HLA A*2501	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.492119	0.329580	-4.162539	31054.103438
HLA A*0212	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.320026	0.157454	-4.162572	20894.225010
HLA B*1509	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.541731	0.379131	-4.162600	34812.139933
HLA A*2602	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.615305	0.452486	-4.162819	41238.688338
HLA B*3901	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.503923	0.340987	-4.162936	31909.706373
HLA A*0250	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.090435	-0.072551	-4.162985	12315.005011
HLA B*0801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.432611	0.269593	-4.163019	27077.666758
HLA B*5701	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.409039	0.245974	-4.163065	25647.134898
HLA A*6801	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.621620	0.458535	-4.163085	41842.753804
HLA B*4402	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.394390	0.231300	-4.163089	24796.467579
HLA A*0219	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.416099	0.252948	-4.163151	26067.480572
HLA B*3801	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.554968	0.391537	-4.163431	35889.525712
HLA B*4601	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.403292	0.239809	-4.163483	25309.992460
HLA B*4801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.436713	0.273190	-4.163523	27334.645122
HLA B*4402	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.334114	0.170588	-4.163525	21583.097836
HLA A*0219	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.432205	0.268538	-4.163667	27052.336332
HLA B*5101	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.510887	0.347215	-4.163672	32425.499988
HLA A*3301	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.637289	0.473598	-4.163691	43379.942755
HLA B*0801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.398783	0.235091	-4.163693	25048.594030
HLA B*5701	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.395109	0.231300	-4.163808	24837.550293
HLA B*3901	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.506317	0.342354	-4.163963	32086.100032
HLA A*0219	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.437627	0.273594	-4.164034	27392.230001
HLA B*7301	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.452955	0.288865	-4.164090	28376.277969
HLA A*3002	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.522841	0.358727	-4.164114	33330.425746
HLA B*3801	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.579402	0.415126	-4.164276	37966.657376
HLA A*0101	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.361765	0.197447	-4.164318	23001.961297
HLA B*0801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.425391	0.261006	-4.164385	26631.232841
HLA B*0801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.410458	0.245974	-4.164484	25731.075852
HLA A*0212	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.425598	0.261006	-4.164592	26643.914196

HLA A*2601	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.395915	0.231300	-4.164614	24883.681440
HLA A*3002	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.545020	0.380348	-4.164672	35076.802670
HLA B*4501	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.454654	0.289933	-4.164721	28487.484862
HLA A*2601	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.392299	0.227561	-4.164738	24677.364473
HLA B*4001	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.425774	0.261006	-4.164768	26654.726937
HLA B*3501	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.438469	0.273594	-4.164875	27445.333044
HLA A*2902	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.455016	0.289933	-4.165083	28511.228329
HLA B*1517	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.396399	0.231300	-4.165098	24911.428197
HLA A*3201	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.258686	0.093574	-4.165112	18142.031341
HLA A*0202	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.602481	0.437367	-4.165114	40038.827794
HLA A*1101	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.528919	0.363771	-4.165148	33800.177336
HLA B*7301	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.552317	0.387024	-4.165294	35671.181970
HLA A*0250	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.556887	0.391537	-4.165351	36048.504162
HLA A*3001	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.271589	0.106226	-4.165364	18689.138587
HLA B*2705	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.439032	0.273594	-4.165439	27480.990478
HLA B*5401	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.549996	0.384545	-4.165452	35481.029189
HLA A*0212	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.405294	0.239809	-4.165485	25426.921193
HLA A*2601	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.382577	0.217015	-4.165562	24131.071503
HLA A*6802	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.390720	0.225072	-4.165648	24587.814135
HLA B*0802	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.434272	0.268538	-4.165735	27181.431504
HLA B*3901	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.361826	0.196045	-4.165781	23005.196914
HLA A*1101	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.434239	0.268381	-4.165858	27179.372903
HLA A*2301	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.513076	0.347215	-4.165862	32589.402753
HLA B*1509	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.450691	0.284825	-4.165866	28228.677115
HLA A*3002	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.587017	0.421060	-4.165957	38638.214041
HLA A*0202	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.377849	0.211872	-4.165977	23869.836414
HLA B*7301	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.560919	0.394899	-4.166020	36384.713921
HLA A*0212	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.317656	0.151627	-4.166028	20780.482967
HLA A*0206	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.380669	0.214632	-4.166037	24025.300296
HLA B*5301	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.603506	0.437367	-4.166139	40133.379310
HLA B*4402	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.419231	0.252948	-4.166283	26256.142577
HLA B*0802	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.439657	0.273190	-4.166467	27520.564929
HLA B*5401	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.525298	0.358727	-4.166571	33519.568745
HLA A*0203	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.297598	0.131008	-4.166590	19842.577420
HLA B*3901	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.514089	0.347463	-4.166626	32665.478890
HLA B*4002	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.631761	0.464975	-4.166785	42831.238876
HLA B*1502	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.551364	0.384545	-4.166819	35592.919231
HLA A*0216	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.419959	0.252948	-4.167011	26300.212796
HLA A*0250	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.579059	0.412011	-4.167048	37936.681487
HLA B*4403	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.625593	0.458535	-4.167058	42227.292666
HLA A*2501	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.501512	0.334311	-4.167201	31733.080709
HLA A*0101	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.384221	0.217015	-4.167207	24222.627246
HLA A*2902	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.392320	0.225072	-4.167248	24678.566018
HLA B*7301	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.610270	0.442758	-4.167512	40763.352741
HLA A*2402	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.579529	0.412011	-4.167518	37977.750349
HLA A*0201	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.392623	0.225072	-4.167551	24695.794601
HLA B*3801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.531994	0.364340	-4.167654	34040.384323
HLA A*0301	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.365125	0.197447	-4.167678	23180.597811
HLA B*3501	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.425419	0.257713	-4.167706	26632.961761
HLA B*7301	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.606372	0.438531	-4.167841	40399.138261
HLA A*0212	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.402942	0.235091	-4.167851	25289.598967
HLA B*5101	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.515405	0.347463	-4.167942	32764.590252
HLA B*5801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.319580	0.151627	-4.167952	20872.759310
HLA B*4402	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.437625	0.269593	-4.168032	27392.081813
HLA B*0801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.385149	0.217015	-4.168135	24274.444073
HLA A*2501	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.489990	0.321711	-4.168279	30902.268514
HLA B*4402	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.453136	0.284825	-4.168312	28388.100895
HLA A*2602	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.532688	0.364340	-4.168347	34094.753334
HLA B*0803	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.498030	0.329580	-4.168450	31479.679315
HLA A*3301	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.565714	0.397240	-4.168474	36788.684922
HLA A*6802	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.424374	0.255887	-4.168487	26568.922666
HLA A*3301	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.280000	0.111406	-4.168595	19054.626520
HLA A*2403	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.396178	0.227561	-4.168617	24898.763219
HLA B*2705	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.441892	0.273190	-4.168702	27662.517704
HLA B*3801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.503084	0.334311	-4.168773	31848.137660

HLA B*4501	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.633755	0.464975	-4.168780	43028.415047
HLA B*4801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.317439	0.148579	-4.168860	20770.142890
HLA B*4601	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.396577	0.227561	-4.169017	24921.672676
HLA B*1517	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.468890	0.299836	-4.169053	29436.734921
HLA A*0250	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.466491	0.297408	-4.169083	29274.589427
HLA A*2301	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.528670	0.359537	-4.169132	33780.800240
HLA B*0702	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.454050	0.284825	-4.169226	28447.905051
HLA A*0203	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.415265	0.245974	-4.169291	26017.465740
HLA B*2705	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.516782	0.347463	-4.169318	32868.625212
HLA A*3002	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.510346	0.340987	-4.169359	32385.178856
HLA B*2705	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.457490	0.287962	-4.169528	28674.109264
HLA A*0216	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.439223	0.269593	-4.169630	27493.035315
HLA A*3301	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.550335	0.380458	-4.169877	35508.680532
HLA A*2403	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.384534	0.214632	-4.169902	24240.062068
HLA B*1509	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.551803	0.381754	-4.170049	35628.945001
HLA B*1502	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.612864	0.442758	-4.170106	41007.541067
HLA A*6801	1:277-285	9	PEGLLNYLA	1.068480	-0.565621	-4.672996	0.502859	-4.170138	47097.347400
HLA B*1501	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.397745	0.227561	-4.170184	24988.770111
HLA A*2601	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.382128	0.211872	-4.170256	24106.150015
HLA B*3801	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.571041	0.400734	-4.170306	37242.647457
HLA B*3901	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.460382	0.289933	-4.170449	28865.703865
HLA B*7301	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.551079	0.380458	-4.170621	35569.627852
HLA B*4601	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.402019	0.231300	-4.170718	25235.888211
HLA A*2602	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.613493	0.442758	-4.170736	41067.038983
HLA A*0203	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.440395	0.269593	-4.170802	27567.353985
HLA A*0250	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.535147	0.364340	-4.170807	34288.419224
HLA B*7301	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.571729	0.400734	-4.170995	37301.727496
HLA B*1801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.459872	0.288865	-4.171007	28831.836972
HLA A*6901	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.367199	0.196045	-4.171154	23291.594855
HLA B*4403	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.646377	0.475212	-4.171164	44297.251710
HLA B*3901	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.294332	0.123142	-4.171191	19693.925891
HLA A*0211	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.530820	0.359537	-4.171282	33948.431390
HLA A*0250	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.592374	0.421060	-4.171314	39117.750269
HLA A*0202	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.471216	0.299836	-4.171379	29594.814843
HLA A*0216	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.282789	0.111406	-4.171383	19177.380248
HLA A*3101	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.350440	0.178924	-4.171516	22409.922296
HLA A*2602	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.583580	0.412011	-4.171568	38333.612412
HLA A*2403	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.388587	0.217015	-4.171572	24467.330544
HLA A*2603	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.614339	0.442758	-4.171581	41147.097444
HLA B*1801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.448426	0.276822	-4.171603	28081.844016
HLA A*2403	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.396716	0.225072	-4.171644	24929.628531
HLA A*3201	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.518922	0.347215	-4.171707	33031.015073
HLA A*3201	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.609269	0.437367	-4.171902	40669.517167
HLA A*2603	1:431-439	9	ALKDALIEG	0.943116	-0.467904	-4.647194	0.475212	-4.171982	44380.726103
HLA B*5701	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.407119	0.235091	-4.172029	25534.027798
HLA B*1503	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.427926	0.255887	-4.172039	26787.141144
HLA B*5101	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.501653	0.329580	-4.172073	31743.382728
HLA A*0201	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.386712	0.214632	-4.172080	24361.930513
HLA B*4001	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.386733	0.214632	-4.172101	24363.116699
HLA B*5401	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.329927	0.157454	-4.172473	21376.027382
HLA A*0250	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.557094	0.384545	-4.172549	36065.669868
HLA A*2403	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.384491	0.211872	-4.172619	24237.701734
HLA A*0250	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.587755	0.415126	-4.172629	38703.904754
HLA A*3101	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.407770	0.235091	-4.172679	25572.320226
HLA A*6801	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.569993	0.397240	-4.172752	37152.896324
HLA B*1517	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.462699	0.289933	-4.172766	29020.089270
HLA B*0803	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.430718	0.257713	-4.173004	26959.855133
HLA A*0216	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.385081	0.211872	-4.173209	24270.636032
HLA A*0250	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.553605	0.380348	-4.173257	35777.090354
HLA A*0211	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.518569	0.345166	-4.173403	33004.221827
HLA A*2301	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.532138	0.358727	-4.173411	34051.619614
HLA B*4801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.434418	0.261006	-4.173412	27190.550042
HLA A*0250	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.581794	0.408334	-4.173460	38176.326724
HLA B*5301	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.585011	0.411532	-4.173478	38460.115469
HLA B*1801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.461475	0.287962	-4.173512	28938.409796

HLA A*2402	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.515886	0.342354	-4.173533	32800.947233
HLA B*5701	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.413350	0.239809	-4.173541	25903.005698
HLA B*3901	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.499073	0.325371	-4.173703	31555.384099
HLA B*3901	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.442167	0.268381	-4.173785	27680.032431
HLA A*0202	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.388429	0.214632	-4.173797	24458.463659
HLA A*2902	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.447547	0.273594	-4.173953	28025.083503
HLA A*1101	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.462898	0.288865	-4.174033	29033.436954
HLA B*4002	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.622144	0.448098	-4.174046	41893.263585
HLA A*6802	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.435118	0.261006	-4.174112	27234.420558
HLA A*2301	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.538538	0.364340	-4.174197	34557.138250
HLA B*0802	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.471624	0.297408	-4.174217	29622.686171
HLA A*8001	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.447427	0.273190	-4.174237	28017.352327
HLA A*2603	1:22-30	9	GLVRTALFN	1.049559	-0.584584	-4.639321	0.464975	-4.174346	43583.417258
HLA A*2402	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.556053	0.381582	-4.174471	35979.339063
HLA B*2705	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.331929	0.157454	-4.174475	21474.781729
HLA A*2403	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.370538	0.196045	-4.174493	23471.337881
HLA A*0202	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.538347	0.363771	-4.174576	34541.998594
HLA A*0211	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.508948	0.334311	-4.174638	32281.102316
HLA A*3301	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.496419	0.321711	-4.174707	31363.068949
HLA A*0101	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.370862	0.196045	-4.174817	23488.867296
HLA B*4403	1:323-331	9	KADALNAEH	0.661781	-0.194938	-4.641680	0.466843	-4.174837	43820.785893
HLA B*4001	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.402467	0.227561	-4.174907	25261.977649
HLA A*2301	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.540392	0.365377	-4.175015	34704.957278
HLA A*0202	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.462988	0.287962	-4.175025	29039.406139
HLA B*1801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.517425	0.342354	-4.175071	32917.382819
HLA A*2902	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.102652	-0.072551	-4.175203	12666.362556
HLA A*0216	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.448816	0.273594	-4.175222	28107.074007
HLA A*1101	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.475069	0.299836	-4.175232	29858.554747
HLA B*1801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.500619	0.325371	-4.175249	31667.912187
HLA A*3001	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.243186	0.067914	-4.175272	17505.977273
HLA A*0202	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.540683	0.365377	-4.175306	34728.246085
HLA B*2705	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.460941	0.285370	-4.175572	28902.893943
HLA A*0219	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.403156	0.227561	-4.175595	25302.052099
HLA A*2601	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.371689	0.196045	-4.175644	23533.639315
HLA A*3002	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.587275	0.411532	-4.175743	38661.214014
HLA B*1517	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.422156	0.246392	-4.175764	26433.582776
HLA A*3301	1:322-330	9	KKADALNAE	1.083044	-0.624509	-4.634352	0.458535	-4.175817	43087.581543
HLA B*4002	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.628866	0.452989	-4.175877	42546.718593
HLA B*2705	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.460749	0.284825	-4.175924	28890.075147
HLA B*1517	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.372013	0.196045	-4.175968	23551.215260
HLA A*2501	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.172413	-0.003611	-4.176024	14873.487870
HLA B*1509	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.556504	0.380458	-4.176046	36016.730172
HLA A*3201	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.628582	0.452486	-4.176096	42518.876770
HLA B*4002	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.628812	0.452486	-4.176326	42541.424943
HLA B*4001	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.198243	0.021903	-4.176340	15784.944589
HLA A*0211	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.518706	0.342354	-4.176352	33014.579304
HLA A*0219	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.445952	0.269593	-4.176359	27922.327394
HLA A*3101	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.422335	0.245974	-4.176361	26444.453219
HLA A*0250	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.571290	0.394899	-4.176391	37264.010313
HLA B*4002	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.615145	0.438531	-4.176614	41223.520551
HLA B*5401	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.557071	0.380348	-4.176723	36063.718808
HLA B*5801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.355698	0.178924	-4.176774	22682.895819
HLA B*1509	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.574085	0.397240	-4.176845	37504.681229
HLA B*1517	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.464938	0.287962	-4.176975	29170.092297
HLA A*2501	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.412086	0.235091	-4.176995	25827.724080
HLA B*1503	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.394096	0.217015	-4.177082	24779.704980
HLA A*2402	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.557705	0.380458	-4.177247	36116.434493
HLA B*2705	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.446920	0.269593	-4.177327	27984.632162
HLA B*4801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.412471	0.235091	-4.177381	25850.649168
HLA A*2402	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.574624	0.397240	-4.177383	37551.173244
HLA B*3801	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.557759	0.380348	-4.177411	36120.928649
HLA A*0206	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.524993	0.347463	-4.177530	33496.003203
HLA A*0212	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.402660	0.225072	-4.177588	25273.186624
HLA A*0203	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.435374	0.257713	-4.177661	27250.484831
HLA A*0201	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.394702	0.217015	-4.177688	24814.315436

HLA B*2705	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.430868	0.252948	-4.177920	26969.191138
HLA B*5801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.344287	0.166266	-4.178021	22094.646089
HLA B*7301	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.335484	0.157454	-4.178030	21651.277641
HLA A*2402	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.599098	0.421060	-4.178038	39728.127488
HLA A*0206	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.477992	0.299836	-4.178155	30060.177587
HLA A*0206	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.507889	0.329580	-4.178309	32202.436951
HLA B*5801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.350368	0.171999	-4.178368	22406.164320
HLA B*4002	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.525851	0.347463	-4.178387	33562.210075
HLA A*0250	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.589989	0.411532	-4.178457	38903.541887
HLA A*2603	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.565515	0.387024	-4.178491	36771.771881
HLA A*3101	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.272200	0.093574	-4.178627	18715.444687
HLA A*0203	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.409965	0.231300	-4.178664	25701.859974
HLA A*0212	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.406379	0.227561	-4.178819	25490.551931
HLA B*5401	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.504240	0.325371	-4.178869	31933.019661
HLA B*1517	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.413973	0.235091	-4.178882	25940.167412
HLA A*3002	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.612323	0.433440	-4.178884	40956.548160
HLA B*2705	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.439913	0.261006	-4.178907	27536.797984
HLA B*7301	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.526156	0.347179	-4.178977	33585.822196
HLA B*1502	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.591039	0.412011	-4.179028	38997.733069
HLA B*1509	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.543754	0.364340	-4.179413	34974.670138
HLA B*4501	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.631904	0.452486	-4.179418	42845.375656
HLA A*2501	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.464332	0.284825	-4.179507	29129.406500
HLA B*1509	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.527117	0.347463	-4.179654	33660.217961
HLA B*5301	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.595050	0.415126	-4.179924	39359.532666
HLA B*3801	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.574905	0.394899	-4.180007	37575.558881
HLA A*0201	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.359065	0.178924	-4.180141	22859.425423
HLA A*3002	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.346625	0.166266	-4.180359	22213.898698
HLA A*0216	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.466051	0.285370	-4.180682	29244.988785
HLA B*5401	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.525848	0.345166	-4.180682	33562.028508
HLA A*3201	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.102840	-0.077849	-4.180689	12671.845632
HLA B*3901	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.392665	0.211872	-4.180793	24698.199545
HLA A*6801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.457636	0.276822	-4.180813	28683.728550
HLA B*3501	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.470779	0.289933	-4.180846	29565.050352
HLA A*2601	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.378373	0.197447	-4.180926	23898.650488
HLA A*2603	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.614440	0.433440	-4.181001	41156.670410
HLA A*6901	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.398029	0.217015	-4.181015	25005.133030
HLA B*1503	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.528583	0.347463	-4.181120	33774.039152
HLA B*5101	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.450721	0.269593	-4.181128	28230.662467
HLA B*3501	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.421014	0.239809	-4.181205	26364.174722
HLA A*0211	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.332993	0.151627	-4.181366	21527.474082
HLA B*5401	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.523825	0.342354	-4.181471	33406.062966
HLA B*0801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.275252	0.093574	-4.181679	18847.429680
HLA B*5701	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.409422	0.227561	-4.181861	25669.760822
HLA A*3201	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.562521	0.380348	-4.182174	36519.204891
HLA A*8001	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.378244	0.196045	-4.182199	23891.540648
HLA A*2902	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.362437	0.180214	-4.182223	23037.578129
HLA A*8001	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.428678	0.246392	-4.182286	26833.554255
HLA A*3201	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.615761	0.433440	-4.182321	41281.991824
HLA A*2301	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.546096	0.363771	-4.182325	35163.821249
HLA A*2501	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.479733	0.297408	-4.182325	30180.922513
HLA B*0802	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.482178	0.299836	-4.182342	30351.371760
HLA A*2402	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.576642	0.394299	-4.182343	37726.083202
HLA B*0802	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.428775	0.246392	-4.182382	26839.506744
HLA A*6802	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.440097	0.257713	-4.182383	27548.420176
HLA A*1101	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.443529	0.261006	-4.182523	27767.021460
HLA B*5801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.349606	0.166895	-4.182711	22366.925103
HLA A*8001	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.443743	0.261006	-4.182737	27780.694528
HLA B*1503	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.486591	0.303652	-4.182939	30661.306538
HLA B*5801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.351394	0.168455	-4.182939	22459.197880
HLA B*4001	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.394876	0.211872	-4.183004	24824.251384
HLA B*1801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.504769	0.321711	-4.183057	31971.912999
HLA B*3801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.541806	0.358727	-4.183079	34818.167008
HLA B*3901	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.468063	0.284825	-4.183238	29380.732446
HLA A*8001	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.468124	0.284825	-4.183299	29384.865346
HLA A*0202	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.487037	0.303652	-4.183385	30692.838852

HLA A*2301	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.530641	0.347179	-4.183462	33934.476308
HLA A*0219	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.439385	0.255887	-4.183498	27503.299895
HLA A*0211	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.398149	0.214632	-4.183517	25012.033006
HLA A*0219	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.468899	0.285370	-4.183529	29437.371926
HLA A*0216	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.411167	0.227561	-4.183607	25773.149297
HLA B*4601	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.349881	0.166266	-4.183616	22381.086887
HLA B*4601	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.400656	0.217015	-4.183641	25156.828762
HLA B*0802	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.469026	0.285370	-4.183656	29445.972840
HLA A*2602	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.598793	0.415126	-4.183667	39700.197091
HLA A*0219	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.430224	0.246392	-4.183832	26929.244061
HLA B*5801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.354519	0.170588	-4.183931	22621.377991
HLA A*2501	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.509475	0.325371	-4.184104	32320.244757
HLA B*7301	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.525242	0.340987	-4.184255	33515.216936
HLA B*1501	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.307449	0.123142	-4.184308	20297.823608
HLA B*0801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.352973	0.168455	-4.184518	22540.995665
HLA B*7301	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.424395	0.239809	-4.184586	26570.216312
HLA B*2705	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.363076	0.178488	-4.184587	23071.502645
HLA B*1502	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.618033	0.433440	-4.184593	41498.518772
HLA A*0202	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.531795	0.347179	-4.184616	34024.734772
HLA B*3901	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.430605	0.245974	-4.184631	26952.855250
HLA B*5401	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.549240	0.364577	-4.184662	35419.275595
HLA B*0802	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.458289	0.273594	-4.184695	28726.899876
HLA A*3201	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.529990	0.345166	-4.184824	33883.662245
HLA B*1801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.431249	0.246392	-4.184856	26992.837352
HLA A*0203	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.424691	0.239809	-4.184882	26588.333968
HLA A*0216	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.419987	0.235091	-4.184897	26301.920226
HLA B*3801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.550358	0.365377	-4.184981	35510.601564
HLA A*2501	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.424884	0.239809	-4.185075	26600.131460
HLA A*1101	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.475012	0.289933	-4.185079	29854.678243
HLA A*3201	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.566732	0.381582	-4.185150	36874.962767
HLA A*2301	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.527568	0.342354	-4.185214	33695.198951
HLA B*1502	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.596765	0.411532	-4.185233	39515.279419
HLA A*3002	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.549811	0.364577	-4.185233	35465.868502
HLA A*6901	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.351573	0.166266	-4.185307	22468.433913
HLA A*8001	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.402340	0.217015	-4.185326	25254.598844
HLA B*4801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.431321	0.245974	-4.185347	26997.364608
HLA A*2603	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.633448	0.448098	-4.185349	42997.931807
HLA B*4501	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.544090	0.358727	-4.185363	35001.737506
HLA A*6802	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.431432	0.245974	-4.185458	27004.229960
HLA A*3002	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.532763	0.347179	-4.185584	34100.656208
HLA A*2902	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.397519	0.211872	-4.185647	24975.795579
HLA A*0206	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.520005	0.334311	-4.185694	33113.495876
HLA A*2602	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.544458	0.358727	-4.185731	35031.478951
HLA B*0801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.443532	0.257713	-4.185818	27767.171677
HLA B*7301	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.623465	0.437367	-4.186098	42020.827913
HLA A*2601	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.354580	0.168455	-4.186125	22624.560072
HLA A*3301	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.638826	0.452486	-4.186340	43533.695754
HLA A*0202	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.568226	0.381754	-4.186472	37002.056584
HLA A*2501	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.475344	0.288865	-4.186479	29877.459911
HLA B*0801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.365517	0.178924	-4.186593	23201.549820
HLA A*2602	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.598158	0.411532	-4.186626	39642.250532
HLA B*5701	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.398537	0.211872	-4.186664	25034.369508
HLA A*0201	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.382727	0.196045	-4.186682	24139.427921
HLA A*3002	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.472412	0.285370	-4.187042	29676.420423
HLA B*1502	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.567514	0.380348	-4.187166	36941.452630
HLA B*0702	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.455599	0.268381	-4.187217	28549.506162
HLA A*0201	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.280802	0.093574	-4.187228	19089.810408
HLA B*4002	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.534443	0.347215	-4.187228	34232.815394
HLA B*0802	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.298698	0.111406	-4.187292	19892.879066
HLA A*3101	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.204253	0.016864	-4.187389	16004.902925
HLA A*2402	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.569229	0.381754	-4.187476	37087.630974
HLA A*0206	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.547337	0.359537	-4.187799	35264.407532
HLA A*2902	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.383850	0.196045	-4.187805	24201.931500
HLA A*1101	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.461134	0.273190	-4.187944	28915.718426
HLA A*0219	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.449236	0.261006	-4.188230	28134.305241

HLA B*5301	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.596692	0.408334	-4.188358	39508.653003
HLA A*3201	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.492187	0.303652	-4.188535	31058.975799
HLA B*3501	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-3.964216	-0.224369	-4.188585	9209.065451
HLA A*8001	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.458195	0.269593	-4.188602	28720.684175
HLA B*1502	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.510335	0.321711	-4.188623	32384.302867
HLA B*3801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.569154	0.380458	-4.188696	37081.211051
HLA B*4403	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.597073	0.408334	-4.188738	39543.293645
HLA A*6802	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.420159	0.231300	-4.188859	26312.309482
HLA B*1509	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.552708	0.363771	-4.188936	35703.230563
HLA B*0702	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.424031	0.235091	-4.188940	26547.945652
HLA A*0202	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.312106	0.123142	-4.188964	20516.635998
HLA A*3201	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.597341	0.408334	-4.189006	39567.688598
HLA A*3201	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.604373	0.415126	-4.189247	40213.575551
HLA B*0803	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.457753	0.268381	-4.189372	28691.488389
HLA B*5401	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.553772	0.364340	-4.189431	35790.835050
HLA B*0802	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.474434	0.284825	-4.189610	29814.973086
HLA B*3801	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.568827	0.379131	-4.189696	37053.337404
HLA B*5301	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.574302	0.384545	-4.189757	37523.352323
HLA B*4801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.436262	0.246392	-4.189870	27306.267402
HLA A*2402	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.537213	0.347179	-4.190034	34451.858983
HLA A*6801	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.598020	0.407915	-4.190105	39629.599400
HLA B*0802	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.458496	0.268381	-4.190114	28740.579154
HLA B*1503	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.429926	0.239809	-4.190117	26910.748518
HLA A*8001	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.283828	0.093574	-4.190254	19223.291513
HLA B*1502	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.591032	0.400734	-4.190298	38997.100154
HLA A*3002	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.446215	0.255887	-4.190328	27939.250871
HLA A*0301	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.358833	0.168455	-4.190377	22847.185672
HLA B*1509	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.520050	0.329580	-4.190470	33116.899718
HLA A*0206	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.369528	0.178924	-4.190603	23416.801085
HLA A*3301	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.443595	0.252948	-4.190647	27771.227841
HLA A*6802	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.313824	0.123142	-4.190682	20597.932324
HLA A*0202	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.407810	0.217015	-4.190795	25574.672173
HLA B*3901	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.494541	0.303652	-4.190889	31227.794611
HLA A*0301	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.361565	0.170588	-4.190977	22991.386493
HLA B*1509	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.538387	0.347215	-4.191173	34545.175503
HLA A*0206	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.494931	0.303652	-4.191279	31255.851066
HLA A*8001	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.437254	0.245974	-4.191280	27368.678093
HLA A*0101	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.357587	0.166266	-4.191322	22781.771104
HLA A*2902	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.388897	0.197447	-4.191450	24484.809036
HLA A*0201	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.388972	0.197447	-4.191525	24489.048126
HLA A*2501	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.419125	0.227561	-4.191565	26249.751428
HLA A*8001	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.465229	0.273594	-4.191636	29189.666925
HLA B*4402	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.406271	0.214632	-4.191639	25484.209271
HLA B*1501	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.275339	0.083388	-4.191951	18851.202670
HLA B*0802	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.481943	0.289933	-4.192010	30334.956445
HLA B*1509	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.298237	0.106226	-4.192012	19871.797064
HLA B*5701	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.406727	0.214632	-4.192095	25510.969460
HLA B*4001	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.370693	0.178488	-4.192205	23479.719882
HLA A*2501	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.469404	0.276822	-4.192582	29471.631224
HLA A*0250	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.571720	0.379131	-4.192589	37300.920312
HLA A*2301	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.526920	0.334311	-4.192609	33644.925200
HLA A*6901	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.371609	0.178924	-4.192685	23529.311024
HLA A*1101	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.462323	0.269593	-4.192730	28994.980864
HLA A*6801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.533773	0.340987	-4.192786	34180.075277
HLA A*0212	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.438896	0.245974	-4.192922	27472.369022
HLA B*1502	1:56-64	9	ESYLALLDA	0.685714	-0.294177	-4.584668	0.391537	-4.193131	38429.749978
HLA B*1517	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.462920	0.269593	-4.193327	29034.850597
HLA A*2601	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.342330	0.148579	-4.193751	21995.301956
HLA A*0211	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.541237	0.347463	-4.193774	34772.613128
HLA A*3101	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.317028	0.123142	-4.193887	20750.488466
HLA B*4403	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.632522	0.438531	-4.193991	42906.379480
HLA A*8001	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.406034	0.211872	-4.194162	25470.288533
HLA A*2603	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.632783	0.438531	-4.194252	42932.152400
HLA A*3301	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.637101	0.442758	-4.194343	43361.172363
HLA A*2403	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.374605	0.180214	-4.194391	23692.168020

HLA B*5401	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.558212	0.363771	-4.194441	36158.662517
HLA A*2501	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.484403	0.289933	-4.194470	30507.265840
HLA A*0250	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.288233	0.093574	-4.194659	19419.276089
HLA B*7301	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.528975	0.334311	-4.194665	33804.566146
HLA B*0803	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.542149	0.347463	-4.194686	34845.678786
HLA B*1501	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.392318	0.197447	-4.194871	24678.432510
HLA A*2402	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.589825	0.394899	-4.194926	38888.812207
HLA B*5801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.352484	0.157454	-4.195031	22515.645519
HLA A*2602	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.628673	0.433440	-4.195234	42527.848590
HLA B*1503	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.520670	0.325371	-4.195299	33164.231421
HLA B*5101	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.407366	0.211872	-4.195494	25548.536226
HLA A*0301	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.367495	0.171999	-4.195496	23307.476891
HLA B*4501	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.582544	0.387024	-4.195520	38242.266578
HLA A*6901	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.353044	0.157454	-4.195590	22544.654291
HLA A*0212	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.407491	0.211872	-4.195618	25555.862658
HLA A*0212	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.426930	0.231300	-4.195630	26725.767404
HLA A*3101	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.412746	0.217015	-4.195732	25867.016698
HLA B*3901	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.493150	0.297408	-4.195743	31127.942759
HLA A*6901	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.319004	0.123142	-4.195863	20845.112404
HLA A*2301	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.541031	0.345166	-4.195864	34756.062861
HLA B*4403	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.543108	0.347215	-4.195893	34922.676324
HLA B*5401	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.543117	0.347215	-4.195902	34923.432044
HLA A*0250	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.517898	0.321711	-4.196186	32953.196245
HLA A*2402	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.530561	0.334311	-4.196250	33928.235103
HLA A*0250	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.590694	0.394299	-4.196395	38966.732306
HLA B*5301	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.583540	0.387024	-4.196516	38330.087104
HLA B*7301	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.578138	0.381582	-4.196557	37856.315302
HLA A*3101	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.394009	0.197447	-4.196562	24774.745424
HLA A*3002	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.413806	0.217015	-4.196791	25930.205652
HLA A*1101	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.470438	0.273594	-4.196844	29541.867618
HLA B*0802	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.473715	0.276822	-4.196893	29765.657433
HLA B*5401	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.556591	0.359537	-4.197054	36023.940215
HLA B*1502	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.618167	0.421060	-4.197107	41511.317382
HLA A*0301	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.334203	0.136944	-4.197259	21587.535254
HLA B*1517	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.470459	0.273190	-4.197269	29543.306017
HLA B*3801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.526920	0.329580	-4.197340	33644.925200
HLA B*3901	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.474195	0.276822	-4.197372	29798.525463
HLA A*3101	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.367989	0.170588	-4.197400	23333.971019
HLA A*0250	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.280898	0.083388	-4.197510	19094.045102
HLA A*0101	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.376435	0.178924	-4.197511	23792.224696
HLA A*3201	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.618817	0.421060	-4.197758	41573.570354
HLA A*0301	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.362200	0.164416	-4.197783	23024.993862
HLA B*1502	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.613023	0.415126	-4.197897	41022.629387
HLA A*0211	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.527483	0.329580	-4.197904	33688.637247
HLA B*0702	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.471542	0.273594	-4.197949	29617.077761
HLA B*0803	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.487904	0.289933	-4.197971	30754.170600
HLA A*2902	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.444392	0.246392	-4.197999	27822.205683
HLA B*4601	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.349721	0.151627	-4.198094	22372.855015
HLA A*3201	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.349949	0.151627	-4.198322	22384.598459
HLA A*0211	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.523870	0.325371	-4.198499	33409.496881
HLA A*3002	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.580293	0.381754	-4.198539	38044.582095
HLA A*2602	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.606471	0.407915	-4.198556	40408.318608
HLA A*3002	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.413202	0.214632	-4.198570	25894.178861
HLA A*1101	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.483478	0.284825	-4.198653	30442.308968
HLA A*0212	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.394794	0.196045	-4.198749	24819.551453
HLA B*4403	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.646901	0.448098	-4.198803	44350.724397
HLA B*3801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.580558	0.381754	-4.198805	38067.846523
HLA B*2705	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.423935	0.225072	-4.198863	26542.057826
HLA A*0101	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.363417	0.164416	-4.199000	23089.607814
HLA A*2603	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.651494	0.452486	-4.199008	44822.281717
HLA B*5401	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.220699	0.021584	-4.199116	16622.618565
HLA B*4001	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.430480	0.231300	-4.199180	26945.128324
HLA B*3901	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.499071	0.299836	-4.199235	31555.213388
HLA A*6802	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.396970	0.197447	-4.199523	24944.198372
HLA B*7301	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.563355	0.363771	-4.199584	36589.407804

HLA A*2301	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.547186	0.347463	-4.199723	35252.199948
HLA A*1101	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.455646	0.255887	-4.199758	28552.595322
HLA B*3801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.468394	0.268538	-4.199856	29403.152453
HLA A*1101	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.503526	0.303652	-4.199874	31880.545577
HLA A*2602	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.452977	0.252948	-4.200029	28377.659615
HLA A*6801	1:202-210	9	CDDALMKIT	1.071519	-0.597921	-4.673628	0.473598	-4.200030	47165.936189
HLA B*4801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.425154	0.225072	-4.200082	26616.685541
HLA A*6901	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.370676	0.170588	-4.200088	23478.830740
HLA A*3201	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.612154	0.412011	-4.200143	40940.598199
HLA A*3002	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.468699	0.268381	-4.200318	29423.838540
HLA B*1503	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.529948	0.329580	-4.200368	33880.362882
HLA B*1509	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.545556	0.345166	-4.200390	35120.095012
HLA A*0212	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.294020	0.093574	-4.200446	19679.760908
HLA A*0219	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.379381	0.178924	-4.200457	23954.179903
HLA B*5301	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.580833	0.380348	-4.200486	38091.949461
HLA B*0802	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.488487	0.287962	-4.200524	30795.459702
HLA A*0206	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.473748	0.273190	-4.200558	29767.911923
HLA A*1101	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.412474	0.211872	-4.200601	25850.789018
HLA A*0216	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.469249	0.268538	-4.200712	29461.110177
HLA A*2602	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.581221	0.380458	-4.200763	38125.966724
HLA B*5101	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.469228	0.268381	-4.200847	29459.675780
HLA B*4801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.428690	0.227561	-4.201129	26834.280098
HLA A*0219	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.426301	0.225072	-4.201229	26687.047118
HLA B*3801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.565056	0.363771	-4.201285	36733.000749
HLA B*1801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.471025	0.269593	-4.201433	29581.849206
HLA A*2402	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.580568	0.379131	-4.201437	38068.670303
HLA A*2501	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.474916	0.273190	-4.201726	29848.057047
HLA B*0702	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.462736	0.261006	-4.201730	29022.601307
HLA A*0206	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.544094	0.342354	-4.201740	35002.116219
HLA A*2602	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.542753	0.340987	-4.201766	34894.159874
HLA B*4501	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.596666	0.394899	-4.201768	39506.301961
HLA B*7301	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.586392	0.384545	-4.201847	38582.652459
HLA A*1101	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.429503	0.227561	-4.201942	26884.556123
HLA A*6802	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.380887	0.178924	-4.201963	24037.390939
HLA B*1517	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.459708	0.257713	-4.201994	28820.920646
HLA B*5801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.338991	0.136944	-4.202047	21826.862382
HLA A*0301	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.369091	0.166895	-4.202196	23393.250028
HLA B*4601	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.398367	0.196045	-4.202322	25024.620219
HLA B*3901	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.400033	0.197447	-4.202586	25120.789253
HLA B*5701	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.419886	0.217015	-4.202872	26295.802447
HLA A*0201	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.130432	-0.072551	-4.202983	13503.060875
HLA B*3801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.548199	0.345166	-4.203033	35334.492072
HLA A*6901	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.375180	0.171999	-4.203181	23723.590980
HLA B*1502	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.600451	0.397240	-4.203211	39852.117234
HLA B*4403	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.655697	0.452486	-4.203211	45258.190858
HLA B*0702	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.417845	0.214632	-4.203213	26172.470917
HLA B*5801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.351810	0.148579	-4.203231	22480.713993
HLA B*5301	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.598161	0.394899	-4.203262	39642.464993
HLA A*3201	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.550544	0.347179	-4.203365	35525.781373
HLA B*5801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.367848	0.164416	-4.203431	23326.398197
HLA A*3301	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.598370	0.394899	-4.203471	39661.556648
HLA A*2403	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.198154	-0.005447	-4.203601	15781.699920
HLA B*2705	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.431169	0.227561	-4.203608	26987.872848
HLA A*0219	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.443569	0.239809	-4.203761	27769.575258
HLA B*5101	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.493862	0.289933	-4.203929	31179.009414
HLA A*6802	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.368459	0.164416	-4.204042	23359.231522
HLA B*5101	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.507710	0.303652	-4.204058	32189.199589
HLA A*2301	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.545065	0.340987	-4.204078	35080.408326
HLA B*4002	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.584656	0.380458	-4.204198	38428.710489
HLA A*0216	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.481159	0.276822	-4.204336	30280.193612
HLA B*4001	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.310671	0.106226	-4.204445	20448.931401
HLA A*2601	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.327004	0.122535	-4.204470	21232.651803
HLA A*3201	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.501886	0.297408	-4.204478	31760.388371
HLA A*2301	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.502029	0.297408	-4.204621	31770.871132
HLA B*4501	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.586223	0.381582	-4.204641	38567.626979

HLA A*0202	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.481560	0.276822	-4.204738	30308.218509
HLA B*4801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.444549	0.239809	-4.204740	27832.292019
HLA A*0101	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.373223	0.168455	-4.204768	23616.922624
HLA A*2402	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.564354	0.359537	-4.204816	36673.631062
HLA B*5101	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.478617	0.273594	-4.205023	30103.466239
HLA B*0803	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.401199	0.196045	-4.205153	25188.286510
HLA B*5401	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.552336	0.347179	-4.205157	35672.725820
HLA B*4501	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.584343	0.379131	-4.205212	38401.070391
HLA B*7301	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.527274	0.321711	-4.205563	33672.420742
HLA A*0301	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.357287	0.151627	-4.205659	22766.000967
HLA B*1503	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.370080	0.164416	-4.205663	23446.590357
HLA B*5701	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.384296	0.178488	-4.205808	24226.820945
HLA B*4001	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.370345	0.164416	-4.205929	23460.928049
HLA B*5101	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.493940	0.287962	-4.205977	31184.576185
HLA B*3501	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.467064	0.261006	-4.206058	29313.257780
HLA B*5401	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.547116	0.340987	-4.206129	35246.479097
HLA B*5701	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.386383	0.180214	-4.206169	24343.486150
HLA B*7301	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.452634	0.246392	-4.206241	28355.254546
HLA A*0250	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.553426	0.347179	-4.206248	35762.383570
HLA A*2402	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.570857	0.364340	-4.206517	37226.935442
HLA A*6802	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.423580	0.217015	-4.206565	26520.384651
HLA B*1502	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.566132	0.359537	-4.206595	36824.128026
HLA A*0211	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.506540	0.299836	-4.206704	32102.594583
HLA B*3901	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.344264	0.137558	-4.206706	22093.450825
HLA B*4501	1:41-49	9	FVFRIEDTD	1.164911	-0.716813	-4.654840	0.448098	-4.206741	45168.911778
HLA A*2403	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.385232	0.178488	-4.206743	24279.040780
HLA A*0202	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.052415	-0.154364	-4.206780	11282.756789
HLA A*0206	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.300721	0.093574	-4.207147	19985.754532
HLA A*0219	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.421956	0.214632	-4.207324	26421.430336
HLA A*6901	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.371936	0.164416	-4.207519	23547.011123
HLA B*4002	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.644995	0.437367	-4.207628	44156.565377
HLA A*2902	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.422306	0.214632	-4.207675	26442.736536
HLA B*0801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.289852	0.082100	-4.207752	19491.794833
HLA B*3901	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.422464	0.214632	-4.207832	26452.322776
HLA B*4002	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.628986	0.421060	-4.207926	42558.459037
HLA B*4403	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.587064	0.379131	-4.207933	38642.394836
HLA A*3201	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.374245	0.166266	-4.207980	23672.565817
HLA A*2301	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.443132	0.235091	-4.208041	27741.646472
HLA A*0101	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.388394	0.180214	-4.208180	24456.478976
HLA B*5301	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.590031	0.381754	-4.208278	38907.330421
HLA A*2602	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.616621	0.408334	-4.208286	41363.811946
HLA A*2402	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.555600	0.347215	-4.208385	35941.792331
HLA B*2705	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.388725	0.180214	-4.208512	24475.141357
HLA A*2902	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.425535	0.217015	-4.208520	26640.022684
HLA A*3201	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.605923	0.397240	-4.208683	40357.415842
HLA B*0802	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.478375	0.269593	-4.208782	30086.696701
HLA B*3801	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.573453	0.364577	-4.208876	37450.141854
HLA B*1501	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.345824	0.136944	-4.208879	22172.956891
HLA B*1502	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.588060	0.379131	-4.208929	38731.134227
HLA B*0702	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.345929	0.136944	-4.208985	22178.355443
HLA B*4403	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.646358	0.437367	-4.208991	44295.334606
HLA B*3901	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.494412	0.285370	-4.209042	31218.504354
HLA B*0801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.406527	0.197447	-4.209080	25499.241178
HLA B*4403	1:197-205	9	TLVNPCDDA	0.673773	-0.220784	-4.662224	0.452989	-4.209235	45943.498096
HLA A*3201	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.465138	0.255887	-4.209250	29183.508973
HLA B*1509	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.436854	0.227561	-4.209294	27343.519206
HLA B*0702	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.426315	0.217015	-4.209300	26687.913376
HLA A*0301	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.366924	0.157454	-4.209470	23276.856941
HLA B*0702	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.465417	0.255887	-4.209530	29202.302688
HLA B*1509	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.455928	0.246392	-4.209535	28571.137305
HLA A*1101	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.497504	0.287962	-4.209542	31441.554866
HLA A*2603	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.604558	0.394899	-4.209660	40230.765752
HLA B*3801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.556906	0.347215	-4.209691	36050.064343
HLA A*2501	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.434881	0.225072	-4.209809	27219.543768
HLA A*6901	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.390069	0.180214	-4.209855	24550.995924

HLA A*3301	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.535267	0.325371	-4.209897	34297.880853
HLA A*2902	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.361589	0.151627	-4.209961	22992.630335
HLA B*4501	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.590311	0.380348	-4.209963	38932.386122
HLA A*0201	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.367575	0.157454	-4.210121	23311.764374
HLA A*3002	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.574100	0.363771	-4.210328	37505.898626
HLA B*2705	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.456830	0.246392	-4.210437	28630.552605
HLA A*3201	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.605343	0.394899	-4.210444	40303.524557
HLA A*3002	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.507910	0.297408	-4.210502	32204.004893
HLA B*4403	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.592256	0.381754	-4.210503	39107.170565
HLA A*0206	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.456985	0.246392	-4.210593	28640.777046
HLA B*5301	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.591051	0.380458	-4.210593	38998.787951
HLA B*3501	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.466568	0.255887	-4.210681	29279.816179
HLA B*0802	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.463631	0.252948	-4.210684	29082.483449
HLA B*1517	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.456705	0.245974	-4.210731	28622.344712
HLA A*0219	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.456740	0.245974	-4.210767	28624.667462
HLA B*5101	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.496212	0.285370	-4.210842	31348.141479
HLA A*3101	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.359516	0.148579	-4.210937	22883.181815
HLA A*1101	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.389458	0.178488	-4.210970	24516.487475
HLA B*5401	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.169828	-0.041216	-4.211044	14785.240392
HLA B*4002	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.592656	0.381582	-4.211074	39143.153237
HLA A*2902	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.457051	0.245974	-4.211077	28645.115791
HLA B*4801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.408592	0.197447	-4.211146	25620.786292
HLA B*5701	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.407312	0.196045	-4.211267	25545.357484
HLA A*0101	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.383366	0.171999	-4.211367	24174.974991
HLA A*0203	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.138989	-0.072551	-4.211540	13771.747452
HLA B*1801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.509195	0.297408	-4.211787	32299.444429
HLA B*3901	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.472856	0.261006	-4.211850	29706.779162
HLA A*0219	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.443175	0.231300	-4.211874	27744.348030
HLA A*6801	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.598905	0.387024	-4.211881	39710.507565
HLA A*0101	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.363607	0.151627	-4.211979	23099.727921
HLA B*1503	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.500039	0.287962	-4.212077	31625.624433
HLA A*2602	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.554444	0.342354	-4.212090	35846.254505
HLA B*0803	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.512029	0.299836	-4.212192	32510.865484
HLA A*2902	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.380652	0.168455	-4.212197	24024.390494
HLA A*0216	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.473213	0.261006	-4.212207	29731.217187
HLA A*6802	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.305878	0.093574	-4.212304	20224.494181
HLA B*3801	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.571851	0.359537	-4.212314	37312.222479
HLA A*3301	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.633438	0.421060	-4.212378	42997.001361
HLA A*3201	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.554794	0.342354	-4.212440	35875.160869
HLA A*3301	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.553473	0.340987	-4.212487	35766.253190
HLA A*3201	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.613303	0.400734	-4.212569	41049.047307
HLA A*0250	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.594549	0.381754	-4.212796	39314.204546
HLA B*3801	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.553793	0.340987	-4.212806	35792.577712
HLA B*7301	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.610049	0.397240	-4.212809	40742.628640
HLA A*2602	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.577520	0.364577	-4.212943	37802.491603
HLA A*3301	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.646384	0.433440	-4.212944	44297.970646
HLA B*3801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.555360	0.342354	-4.213006	35921.964808
HLA A*2601	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.391624	0.178488	-4.213136	24639.079184
HLA A*0219	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.430288	0.217015	-4.213273	26933.177822
HLA B*4403	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.656099	0.442758	-4.213341	45300.078177
HLA B*7301	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.558539	0.345166	-4.213373	36185.863138
HLA A*0101	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.383996	0.170588	-4.213407	24210.050507
HLA B*4402	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.430452	0.217015	-4.213437	26943.379139
HLA B*0803	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.510854	0.297408	-4.213446	32423.044224
HLA B*3901	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.501529	0.287962	-4.213566	31734.282439
HLA B*1502	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.621914	0.408334	-4.213579	41871.058956
HLA B*0801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.281619	0.067914	-4.213705	19125.783528
HLA B*2705	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.378185	0.164416	-4.213769	23888.309602
HLA A*0206	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.441711	0.227561	-4.214150	27650.996965
HLA B*4002	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.629367	0.415126	-4.214240	42595.773707
HLA A*0250	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.573012	0.358727	-4.214285	37412.072207
HLA A*2301	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.544064	0.329580	-4.214484	34999.654657
HLA A*1101	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.472200	0.257713	-4.214487	29661.974787
HLA A*6801	1:134-142	9	NFDRHLTDA	0.717180	-0.278649	-4.653275	0.438531	-4.214744	45006.461642
HLA A*3301	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.503709	0.288865	-4.214844	31894.001093

HLA A*0206	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.540279	0.325371	-4.214908	34695.946449
HLA A*6802	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.366551	0.151627	-4.214923	23256.843441
HLA A*0101	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.372385	0.157454	-4.214931	23571.354561
HLA B*1517	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.395273	0.180214	-4.215060	24846.957862
HLA A*0211	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.499929	0.284825	-4.215104	31617.584172
HLA B*5701	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.383681	0.168455	-4.215225	24192.506392
HLA A*0203	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.383782	0.168455	-4.215327	24198.134834
HLA A*1101	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.450582	0.235091	-4.215492	28221.653145
HLA A*3301	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.623418	0.407915	-4.215503	42016.281599
HLA A*2402	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.574236	0.358727	-4.215509	37517.668832
HLA B*1503	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.326969	0.111406	-4.215563	21230.928879
HLA A*2603	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.519234	0.303652	-4.215583	33054.789945
HLA A*6801	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.597228	0.381582	-4.215646	39557.415205
HLA A*0206	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.489276	0.273594	-4.215683	30851.488217
HLA B*3501	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.411797	0.196045	-4.215752	25810.543606
HLA A*2501	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.489412	0.273594	-4.215819	30861.170117
HLA B*1501	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.384313	0.168455	-4.215857	24227.738413
HLA A*8001	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.430567	0.214632	-4.215935	26950.522360
HLA A*2402	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.561234	0.345166	-4.216068	36411.099678
HLA B*4001	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.384545	0.168455	-4.216090	24240.717757
HLA A*3101	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.367747	0.151627	-4.216119	23320.972519
HLA B*5801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.309766	0.093574	-4.216192	20406.384541
HLA B*5801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.354021	0.137558	-4.216463	22595.448483
HLA B*7301	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.580812	0.364340	-4.216472	38090.094848
HLA B*1503	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.365064	0.148579	-4.216484	23177.337525
HLA A*2601	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.396772	0.180214	-4.216559	24932.865538
HLA B*5301	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.595985	0.379131	-4.216854	39444.370388
HLA A*2402	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.581818	0.364577	-4.217240	38178.392077
HLA A*0250	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.582642	0.365377	-4.217266	38250.956795
HLA B*0803	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.502137	0.284825	-4.217313	31778.778453
HLA B*4801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.429204	0.211872	-4.217332	26866.091274
HLA A*2601	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.389414	0.171999	-4.217414	24513.967607
HLA A*2602	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.614661	0.397240	-4.217421	41177.605117
HLA A*8001	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.457321	0.239809	-4.217512	28662.942529
HLA A*6802	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.354474	0.136944	-4.217530	22619.052906
HLA A*0250	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.564791	0.347215	-4.217576	36710.552086
HLA A*2602	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.638694	0.421060	-4.217634	43520.509054
HLA B*2705	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.507593	0.289933	-4.217660	32180.493767
HLA A*2301	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.539778	0.321711	-4.218067	34655.989114
HLA A*0216	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.473995	0.255887	-4.218108	29784.826042
HLA A*1101	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.414217	0.196045	-4.218172	25954.766196
HLA B*1501	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.369882	0.151627	-4.218255	23435.937927
HLA A*3101	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.390285	0.171999	-4.218286	24563.218236
HLA A*0211	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.522049	0.303652	-4.218397	33269.715317
HLA A*8001	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.415930	0.197447	-4.218483	26057.328952
HLA A*0301	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.341919	0.123142	-4.218777	21974.488184
HLA B*1509	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.464804	0.245974	-4.218830	29161.098686
HLA A*0219	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.376313	0.157454	-4.218859	23785.532546
HLA A*0203	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.390866	0.171999	-4.218866	24596.062594
HLA A*2601	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.389519	0.170588	-4.218931	24519.936136
HLA A*2902	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.294574	0.075603	-4.218972	19704.902771
HLA B*1517	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.480202	0.261006	-4.219196	30213.595274
HLA A*0301	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.367794	0.148579	-4.219215	23323.495933
HLA A*2501	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.487648	0.268381	-4.219267	30736.040891
HLA B*4601	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.416823	0.197447	-4.219376	26110.951610
HLA A*0206	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.377001	0.157454	-4.219547	23823.264832
HLA B*0802	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.477301	0.257713	-4.219587	30012.404653
HLA A*2601	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.356551	0.136944	-4.219607	22727.484024
HLA A*0250	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.564782	0.345166	-4.219615	36709.757695
HLA B*4801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.434317	0.214632	-4.219685	27184.225570
HLA A*2501	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.489335	0.269593	-4.219742	30855.661077
HLA B*4001	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.368383	0.148579	-4.219804	23355.188005
HLA B*4501	1:339-347	9	DFTVRLRDH	0.761903	-0.324536	-4.657213	0.437367	-4.219846	45416.389663
HLA B*0802	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.455002	0.235091	-4.219911	28510.302888
HLA A*3201	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.466315	0.246392	-4.219922	29262.713915

HLA A*2501	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.466338	0.246392	-4.219946	29264.297039
HLA A*0202	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.562338	0.342354	-4.219984	36503.798083
HLA B*0801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.390600	0.170588	-4.220012	24581.031186
HLA B*5401	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.493724	0.273594	-4.220130	31169.059178
HLA B*2705	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.434763	0.214632	-4.220131	27212.182028
HLA B*5401	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.567641	0.347463	-4.220178	36952.246061
HLA A*2403	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.371917	0.151627	-4.220290	23545.992051
HLA B*5701	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.417892	0.197447	-4.220445	26175.302874
HLA B*4001	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.400701	0.180214	-4.220487	25159.414712
HLA A*2501	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.481497	0.261006	-4.220491	30303.791801
HLA B*5101	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.473459	0.252948	-4.220511	29748.110456
HLA B*5101	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.460417	0.239809	-4.220609	28868.046364
HLA A*3101	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.336207	0.115588	-4.220619	21687.384065
HLA B*1503	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.497466	0.276822	-4.220644	31438.833459
HLA A*2601	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.399744	0.178924	-4.220820	25104.079029
HLA A*0216	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.467280	0.246392	-4.220888	29327.850907
HLA A*0201	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.332302	0.111406	-4.220896	21493.261690
HLA A*0212	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.332347	0.111406	-4.220941	21495.471050
HLA A*0211	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.438046	0.217015	-4.221031	27418.620335
HLA B*7301	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.568599	0.347463	-4.221136	37033.898423
HLA A*2602	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.621996	0.400734	-4.221262	41878.987829
HLA B*7301	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.417323	0.196045	-4.221278	26141.056768
HLA A*0206	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.509430	0.287962	-4.221468	32316.922798
HLA B*1801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.433551	0.211872	-4.221679	27136.325073
HLA B*4601	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.401969	0.180214	-4.221756	25233.021383
HLA A*6801	1:255-263	9	TKKLSKRDP	0.410515	0.041971	-4.674260	0.452486	-4.221775	47234.624866
HLA B*4403	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.490197	0.268381	-4.221816	30916.983667
HLA A*6801	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.586178	0.364340	-4.221838	38563.662897
HLA B*1503	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.495093	0.273190	-4.221903	31267.520501
HLA A*3002	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.547315	0.325371	-4.221945	35262.690585
HLA B*1801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.345168	0.123142	-4.222026	22139.515181
HLA B*0801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.373721	0.151627	-4.222094	23644.024329
HLA B*1801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.453418	0.231300	-4.222118	28406.536056
HLA A*0201	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.394124	0.171999	-4.222125	24781.313698
HLA A*1101	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.468535	0.246392	-4.222143	29412.698070
HLA A*2603	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.622894	0.400734	-4.222159	41965.623498
HLA B*4002	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.634216	0.412011	-4.222204	43074.063920
HLA A*3002	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.400785	0.178488	-4.222297	25164.315137
HLA A*1101	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.453618	0.231300	-4.222318	28419.601538
HLA B*3901	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.495582	0.273190	-4.222392	31302.724299
HLA A*3301	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.604063	0.381582	-4.222481	40184.869072
HLA A*2501	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.359681	0.136944	-4.222737	22891.849139
HLA B*4402	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.447890	0.225072	-4.222818	28047.227686
HLA B*1503	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.374490	0.151627	-4.222862	23685.888424
HLA B*3501	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.454245	0.231300	-4.222945	28460.681620
HLA A*0201	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.393633	0.170588	-4.223045	24753.310123
HLA A*2603	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.586848	0.363771	-4.223076	38623.166923
HLA B*0702	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.462889	0.239809	-4.223080	29032.808690
HLA B*4002	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.354171	0.131008	-4.223163	22603.273126
HLA A*2602	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.087286	-0.136008	-4.223295	12226.053250
HLA A*0216	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.454652	0.231300	-4.223351	28487.330749
HLA B*4601	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.402303	0.178924	-4.223379	25252.412945
HLA A*2501	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.479307	0.255887	-4.223420	30151.384122
HLA A*3002	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.588998	0.365377	-4.223621	38814.827448
HLA B*4402	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.435503	0.211872	-4.223631	27258.594253
HLA A*6801	1:214-222	9	RGEDLLPST	0.801061	-0.358303	-4.666505	0.442758	-4.223747	46398.594010
HLA B*4801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.440818	0.217015	-4.223803	27594.211599
HLA B*3501	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.388394	0.164416	-4.223978	24456.478976
HLA A*3001	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.271014	0.046803	-4.224211	18664.383985
HLA A*3301	1:410-418	9	LDAALAALT	0.811732	-0.410998	-4.624999	0.400734	-4.224265	42169.535623
HLA B*1501	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.391223	0.166895	-4.224328	24616.296332
HLA A*2402	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.459421	0.235091	-4.224330	28801.904927
HLA B*0802	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.470379	0.245974	-4.224405	29537.872432
HLA A*2602	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.569596	0.345166	-4.224430	37118.944021
HLA A*2602	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.618730	0.394299	-4.224432	41565.249576

HLA B*5101	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.509296	0.284825	-4.224472	32306.958969
HLA A*2402	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.588288	0.363771	-4.224517	38751.464081
HLA A*3002	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.477484	0.252948	-4.224536	30025.071701
HLA B*3901	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.482305	0.257713	-4.224592	30360.239723
HLA B*4403	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.554239	0.329580	-4.224660	35829.387064
HLA B*1502	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.583498	0.358727	-4.224770	38326.354779
HLA B*1502	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.567260	0.342354	-4.224906	36919.875224
HLA B*4501	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.570073	0.345166	-4.224906	37159.730716
HLA B*4501	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.640092	0.415126	-4.224966	43660.822230
HLA A*2603	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.589308	0.364340	-4.224967	38842.555224
HLA B*1801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.498277	0.273190	-4.225087	31497.566060
HLA A*2603	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.584632	0.359537	-4.225095	38426.631595
HLA B*1509	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.566109	0.340987	-4.225122	36822.135936
HLA B*0702	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.456475	0.231300	-4.225175	28607.174050
HLA A*0202	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.584745	0.359537	-4.225208	38436.611314
HLA A*2601	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.391542	0.166266	-4.225277	24634.414311
HLA B*1517	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.404251	0.178924	-4.225326	25365.919255
HLA B*3901	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.481290	0.255887	-4.225403	30289.368501
HLA A*3002	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.529215	0.303652	-4.225563	33823.224947
HLA A*2902	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.465426	0.239809	-4.225618	29202.934620
HLA B*3801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.573200	0.347463	-4.225737	37428.267325
HLA B*5801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.348885	0.123142	-4.225743	22329.808140
HLA A*8001	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.377431	0.151627	-4.225804	23846.861774
HLA A*0203	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.423251	0.197447	-4.225804	26500.306128
HLA A*3001	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.309197	0.083388	-4.225809	20379.686122
HLA B*1801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.460970	0.235091	-4.225879	28904.770341
HLA B*1517	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.242834	0.016864	-4.225970	17491.777226
HLA B*5401	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.555609	0.329580	-4.226029	35942.570104
HLA A*0212	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.392945	0.166895	-4.226050	24714.104792
HLA B*1502	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.590520	0.364340	-4.226180	38951.135806
HLA A*0206	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.516152	0.289933	-4.226219	32821.005155
HLA A*6801	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.634615	0.408334	-4.226281	43113.696547
HLA A*0219	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.378054	0.151627	-4.226426	23881.073644
HLA B*5101	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.461597	0.235091	-4.226506	28946.551728
HLA B*0802	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.454090	0.227561	-4.226530	28450.521471
HLA A*0201	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.394989	0.168455	-4.226534	24830.698451
HLA A*0202	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.499919	0.273190	-4.226729	31616.899989
HLA A*2402	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.548446	0.321711	-4.226734	35354.569121
HLA A*2902	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.393006	0.166266	-4.226740	24717.581252
HLA B*0803	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.495328	0.268538	-4.226791	31284.440460
HLA A*0201	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.391237	0.164416	-4.226820	24617.095374
HLA B*0702	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.393220	0.166266	-4.226954	24729.752710
HLA B*3901	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.500570	0.273594	-4.226976	31664.314673
HLA B*1509	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.530754	0.303652	-4.227102	33943.289377
HLA A*0201	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.394162	0.166895	-4.227267	24783.458817
HLA A*2402	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.592672	0.365377	-4.227295	39144.635586
HLA A*2601	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.350476	0.123142	-4.227334	22411.740897
HLA B*7301	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.569713	0.342354	-4.227359	37128.985848
HLA B*1801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.495808	0.268381	-4.227427	31318.985571
HLA B*1517	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.309684	0.082100	-4.227584	20402.521037
HLA B*3801	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.462856	0.235091	-4.227765	29030.609873
HLA B*3801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.483682	0.255887	-4.227795	30456.640328
HLA A*0301	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.365503	0.137558	-4.227945	23200.796725
HLA B*5701	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.406870	0.178924	-4.227946	25519.389552
HLA B*7301	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.608334	0.380348	-4.227986	40582.044374
HLA A*0202	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.573179	0.345166	-4.228012	37426.445024
HLA A*6901	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.394944	0.166895	-4.228049	24828.146287
HLA A*2301	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.527892	0.299836	-4.228056	33720.363989
HLA B*4501	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.640083	0.412011	-4.228071	43659.877440
HLA A*0216	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.385542	0.157454	-4.228088	24296.384765
HLA A*0206	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.453176	0.225072	-4.228105	28390.711816
HLA A*3201	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.591883	0.363771	-4.228111	39073.546121
HLA B*1501	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.400113	0.171999	-4.228114	25125.410301
HLA B*4601	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.406605	0.178488	-4.228116	25503.793871
HLA B*0803	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.484009	0.255887	-4.228121	30479.551561

HLA A*2602	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.609795	0.381582	-4.228214	40718.830978
HLA A*0202	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.557794	0.329580	-4.228214	36123.859921
HLA A*6901	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.376872	0.148579	-4.228293	23816.177419
HLA A*3301	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.636659	0.408334	-4.228325	43317.093904
HLA A*3301	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.639859	0.411532	-4.228327	43637.444671
HLA A*8001	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.459675	0.231300	-4.228375	28818.737877
HLA B*2705	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.445658	0.217015	-4.228643	27903.451690
HLA B*5101	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.505473	0.276822	-4.228651	32023.844481
HLA B*1503	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.518598	0.289933	-4.228665	33006.364486
HLA B*1502	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.532335	0.303652	-4.228683	34067.097231
HLA A*2601	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.395675	0.166895	-4.228780	24869.954196
HLA B*5301	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.593386	0.364577	-4.228809	39209.066067
HLA A*3301	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.623279	0.394299	-4.228980	42002.872837
HLA A*2902	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.460328	0.231300	-4.229028	28862.112402
HLA A*3101	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.366071	0.136944	-4.229127	23231.190942
HLA B*5801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.351688	0.122535	-4.229153	22474.390738
HLA A*2301	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.502360	0.273190	-4.229170	31795.115019
HLA A*8001	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.408120	0.178924	-4.229196	25592.941706
HLA B*4403	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.644391	0.415126	-4.229265	44095.215330
HLA A*2501	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.380913	0.151627	-4.229286	24038.821418
HLA B*0702	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.401307	0.171999	-4.229307	25194.555519
HLA A*0201	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.380970	0.151627	-4.229342	24041.942757
HLA B*1517	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.514188	0.284825	-4.229363	32672.901831
HLA A*3002	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.503100	0.273594	-4.229507	31849.343747
HLA B*4501	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.559098	0.329580	-4.229518	36232.484384
HLA A*0211	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.503284	0.273594	-4.229690	31862.786093
HLA B*4001	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.396079	0.166266	-4.229814	24893.106481
HLA A*3101	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.387339	0.157454	-4.229885	24397.145296
HLA A*3002	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.564208	0.334311	-4.229897	36661.332307
HLA A*0216	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.455030	0.225072	-4.229958	28512.153799
HLA B*5101	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.503258	0.273190	-4.230068	31860.890034
HLA A*2602	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.611823	0.381754	-4.230069	40909.380849
HLA A*6901	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.361128	0.131008	-4.230120	22968.263290
HLA B*3901	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.457833	0.227561	-4.230272	28696.766279
HLA A*2402	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.515456	0.284825	-4.230632	32768.490046
HLA B*4403	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.651741	0.421060	-4.230681	44847.749725
HLA A*2602	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.578021	0.347215	-4.230806	37846.076763
HLA B*4801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.354012	0.123142	-4.230870	22594.959533
HLA B*1509	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.516265	0.285370	-4.230895	32829.529046
HLA B*4002	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.578310	0.347179	-4.231131	37871.268542
HLA B*4403	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.625480	0.394299	-4.231182	42216.328731
HLA B*3501	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.445970	0.214632	-4.231339	27923.535874
HLA A*2301	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.519455	0.287962	-4.231493	33071.603558
HLA A*2501	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.446215	0.214632	-4.231583	27939.250871
HLA B*1509	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.557378	0.325371	-4.232008	36089.286061
HLA B*0801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.249525	0.017415	-4.232110	17763.366272
HLA B*1517	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.471979	0.239809	-4.232171	29646.894630
HLA B*0702	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.459731	0.227561	-4.232171	28822.479868
HLA B*4403	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.616785	0.384545	-4.232240	41379.479067
HLA B*4501	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.653357	0.421060	-4.232297	45014.984247
HLA A*3201	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.412575	0.180214	-4.232361	25856.803263
HLA A*0212	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.396906	0.164416	-4.232490	24940.555114
HLA A*0301	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.363536	0.131008	-4.232528	23095.979216
HLA A*0250	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.521466	0.288865	-4.232601	33225.108850
HLA A*0211	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.460164	0.227561	-4.232603	28851.184613
HLA B*4601	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.401093	0.168455	-4.232638	25182.155294
HLA A*0211	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.490568	0.257713	-4.232855	30943.421642
HLA A*2602	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.596758	0.363771	-4.232987	39514.638105
HLA B*7301	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.536656	0.303652	-4.233004	34407.715053
HLA A*2402	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.574142	0.340987	-4.233155	37509.551053
HLA A*0206	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.468380	0.235091	-4.233289	29402.198062
HLA A*6802	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.413522	0.180214	-4.233308	25913.237382
HLA B*5301	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.558774	0.325371	-4.233403	36205.444585
HLA A*2601	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.390908	0.157454	-4.233454	24598.457826
HLA B*1517	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.461167	0.227561	-4.233606	28917.908541

HLA A*0206	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.518539	0.284825	-4.233714	33001.900769
HLA A*2301	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.502109	0.268381	-4.233728	31776.715484
HLA A*2603	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.628093	0.394299	-4.233794	42471.059018
HLA A*3301	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.615671	0.381754	-4.233918	41273.506119
HLA A*0250	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.593499	0.359537	-4.233962	39219.248990
HLA B*0802	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.494978	0.261006	-4.233972	31259.233063
HLA B*3501	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.479986	0.245974	-4.234012	30198.561413
HLA B*5301	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.592747	0.358727	-4.234020	39151.412753
HLA A*2403	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.400395	0.166266	-4.234130	25141.726679
HLA A*8001	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.400466	0.166266	-4.234200	25145.807429
HLA A*0101	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.401100	0.166895	-4.234205	25182.563995
HLA B*0802	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.430304	0.196045	-4.234259	26934.197780
HLA A*1101	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.459360	0.225072	-4.234289	28797.854019
HLA B*4002	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.614654	0.380348	-4.234306	41176.936824
HLA B*0702	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.412826	0.178488	-4.234338	25871.775017
HLA B*0803	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.511213	0.276822	-4.234391	32449.892311
HLA B*0803	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.469569	0.235091	-4.234478	29482.794015
HLA B*3501	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.365557	0.131008	-4.234549	23203.683721
HLA B*5101	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.462123	0.227561	-4.234562	28981.650860
HLA A*0301	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.316721	0.082100	-4.234621	20735.787898
HLA B*4403	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.594181	0.359537	-4.234643	39280.827101
HLA B*4801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.414992	0.180214	-4.234779	26001.143676
HLA B*1502	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.616595	0.381754	-4.234841	41361.350509
HLA B*5301	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.252335	0.017415	-4.234920	17878.671916
HLA B*0803	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.508168	0.273190	-4.234978	32223.174807
HLA B*4601	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.399397	0.164416	-4.234980	25083.987152
HLA B*0702	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.252401	0.017415	-4.234986	17881.380327
HLA A*3002	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.372039	0.136944	-4.235095	23552.616805
HLA B*3501	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.318628	0.083388	-4.235240	20827.077051
HLA A*1101	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.481222	0.245974	-4.235248	30284.616872
HLA B*5401	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.470431	0.235091	-4.235340	29541.388167
HLA A*0211	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.508582	0.273190	-4.235392	32253.870408
HLA B*0702	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.406116	0.170588	-4.235528	25475.111690
HLA B*0802	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.491438	0.255887	-4.235550	31005.421851
HLA B*1517	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.491461	0.255887	-4.235574	31007.099255
HLA B*1503	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.493388	0.257713	-4.235674	31144.955677
HLA A*0212	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.452692	0.217015	-4.235678	28359.089775
HLA B*3901	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.460901	0.225072	-4.235830	28900.235921
HLA B*2705	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.471044	0.235091	-4.235953	29583.129510
HLA B*4403	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.616456	0.380458	-4.235998	41348.150757
HLA B*2705	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.402340	0.166266	-4.236075	25254.598844
HLA A*2602	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.615253	0.379131	-4.236122	41233.780502
HLA B*1801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.304226	0.067914	-4.236311	20147.723432
HLA B*1502	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.583554	0.347179	-4.236375	38331.331294
HLA B*5701	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.388096	0.151627	-4.236468	24439.681778
HLA A*0216	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.482474	0.245974	-4.236500	30372.067705
HLA B*4001	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.403421	0.166895	-4.236526	25317.524415
HLA B*0803	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.524525	0.287962	-4.236563	33459.961884
HLA A*2501	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.494351	0.257713	-4.236638	31214.113557
HLA B*1509	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.505067	0.268381	-4.236686	31993.887039
HLA B*4402	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.408764	0.171999	-4.236765	25630.906500
HLA A*6901	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.352412	0.115588	-4.236824	22511.869814
HLA B*7301	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.602237	0.365377	-4.236860	40016.307145
HLA A*0211	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.526826	0.289933	-4.236893	33637.645375
HLA B*0801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.343195	0.106226	-4.236969	22039.134683
HLA B*4601	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.409011	0.171999	-4.237011	25645.469974
HLA B*3801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.562747	0.325371	-4.237376	36538.176042
HLA B*5701	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.403673	0.166266	-4.237407	25332.183912
HLA B*5301	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.584724	0.347179	-4.237545	38434.739919
HLA B*4001	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.408221	0.170588	-4.237633	25598.895962
HLA B*0802	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.449840	0.211872	-4.237968	28173.448739
HLA A*0250	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.580584	0.342354	-4.238230	38070.111962
HLA A*2403	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.435750	0.197447	-4.238303	27274.082578
HLA B*3501	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.455401	0.217015	-4.238387	28536.535337
HLA A*3201	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.620281	0.381754	-4.238528	41713.924681

HLA B*5301	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.602319	0.363771	-4.238548	40023.884795
HLA A*2601	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.402970	0.164416	-4.238554	25291.240787
HLA B*1801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.494473	0.255887	-4.238586	31222.895767
HLA A*3201	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.526586	0.287962	-4.238624	33619.088951
HLA B*5401	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.014316	-0.224369	-4.238685	10335.130810
HLA A*0211	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.473777	0.235091	-4.238686	29769.844479
HLA A*0216	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.375756	0.136944	-4.238812	23755.055617
HLA B*1501	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.409401	0.170588	-4.238812	25668.511018
HLA B*4801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.396375	0.157454	-4.238921	24910.080553
HLA B*3901	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.417483	0.178488	-4.238995	26150.675112
HLA A*2601	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.390633	0.151627	-4.239006	24582.892986
HLA A*2403	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.396544	0.157454	-4.239090	24919.785219
HLA A*0101	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.387682	0.148579	-4.239103	24416.422842
HLA A*3002	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.507644	0.268538	-4.239107	32184.324039
HLA B*5401	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.543375	0.303652	-4.239723	34944.220737
HLA A*0206	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.508347	0.268538	-4.239809	32236.426140
HLA A*3002	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.485883	0.245974	-4.239910	30611.419012
HLA A*0212	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.371005	0.131008	-4.239997	23496.619978
HLA A*2902	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.406908	0.166895	-4.240013	25521.598561
HLA B*4402	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.418961	0.178924	-4.240037	26239.812733
HLA A*0219	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.323426	0.083388	-4.240038	21058.429158
HLA A*0212	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.437543	0.197447	-4.240096	27386.895719
HLA B*0803	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.467684	0.227561	-4.240124	29355.153200
HLA B*0803	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.486781	0.246392	-4.240389	30674.745298
HLA A*3301	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.604189	0.363771	-4.240418	40196.610154
HLA B*5101	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.501470	0.261006	-4.240464	31729.990755
HLA A*0201	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.389205	0.148579	-4.240625	24502.167459
HLA A*2601	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.378270	0.137558	-4.240712	23892.962447
HLA B*4402	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.409173	0.168455	-4.240717	25655.044763
HLA B*5701	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.407798	0.166895	-4.240903	25573.980401
HLA B*5801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.372089	0.131008	-4.241081	23555.292715
HLA A*3001	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.097257	-0.143836	-4.241093	12510.005405
HLA A*6802	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.378662	0.137558	-4.241104	23914.558333
HLA B*4402	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.408118	0.166895	-4.241223	25592.803251
HLA B*4002	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.636215	0.394899	-4.241316	43272.826151
HLA A*2902	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.420349	0.178924	-4.241425	26323.842089
HLA A*8001	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.421651	0.180214	-4.241437	26402.855057
HLA B*4001	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.420504	0.178924	-4.241580	26333.242766
HLA B*5301	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.575944	0.334311	-4.241633	37665.515976
HLA B*1801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.515313	0.273594	-4.241720	32757.678122
HLA A*2402	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.497643	0.255887	-4.241755	31451.592092
HLA A*2301	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.545497	0.303652	-4.241845	35115.345437
HLA B*4002	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.639131	0.397240	-4.241891	43564.323144
HLA A*3001	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.301543	0.059535	-4.242007	20023.632632
HLA B*4403	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.587217	0.345166	-4.242051	38655.985545
HLA A*3301	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.606440	0.364340	-4.242100	40405.476849
HLA A*0250	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.583124	0.340987	-4.242137	38293.401682
HLA B*5701	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.412777	0.170588	-4.242189	25868.835952
HLA A*0101	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.364873	0.122535	-4.242339	23167.183417
HLA B*1502	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.587527	0.345166	-4.242361	38683.599851
HLA A*0211	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.454271	0.211872	-4.242399	28462.375331
HLA A*3301	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.358095	0.115588	-4.242507	22808.407985
HLA A*0301	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.365073	0.122535	-4.242538	23177.839077
HLA A*0203	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.407018	0.164416	-4.242602	25528.088630
HLA B*1501	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.400163	0.157454	-4.242709	25128.264903
HLA B*5801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.354153	0.111406	-4.242747	22602.294897
HLA A*8001	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.400205	0.157454	-4.242751	25130.711962
HLA A*2603	1:39-47	9	GTFVFRIED	1.219702	-0.840571	-4.621968	0.379131	-4.242837	41876.269189
HLA A*0203	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.379804	0.136944	-4.242860	23977.517367
HLA A*2603	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.624677	0.381754	-4.242923	42138.293048
HLA A*0250	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.568313	0.325371	-4.242942	37009.463875
HLA B*3501	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.421928	0.178924	-4.243004	26419.715147
HLA A*1101	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.482855	0.239809	-4.243046	30398.697514
HLA B*5301	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.496061	0.252948	-4.243114	31337.289599
HLA A*2603	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.664397	0.421060	-4.243338	46173.982343

HLA A*0203	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.401145	0.157454	-4.243691	25185.152591
HLA A*2603	1:433-441	9	KDALIEGLA	0.698799	-0.290465	-4.652037	0.408334	-4.243702	44878.330437
HLA B*0802	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.460753	0.217015	-4.243739	28890.387733
HLA A*0216	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.440125	0.196045	-4.244080	27550.208641
HLA B*5801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.359726	0.115588	-4.244138	22894.202265
HLA B*0802	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.458839	0.214632	-4.244207	28763.288690
HLA B*4403	1:98-106	9	LARLLAAGE	1.024125	-0.612114	-4.656357	0.412011	-4.244346	45327.043724
HLA B*1517	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.410618	0.166266	-4.244352	25740.543347
HLA B*2705	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.337934	0.093574	-4.244360	21773.790601
HLA B*0801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.381999	0.137558	-4.244441	24098.978444
HLA B*0802	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.484326	0.239809	-4.244517	30501.819976
HLA A*2301	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.529401	0.284825	-4.244576	33837.683448
HLA B*5301	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.608973	0.364340	-4.244633	40641.804398
HLA A*0211	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.491076	0.246392	-4.244684	30979.601280
HLA B*4002	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.626486	0.381754	-4.244733	42314.191046
HLA A*2902	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.367345	0.122535	-4.244810	23299.408472
HLA B*0801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.360588	0.115588	-4.245000	22939.702239
HLA A*0211	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.476302	0.231300	-4.245002	29943.479313
HLA B*4801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.423582	0.178488	-4.245094	26520.528124
HLA B*3501	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.442625	0.197447	-4.245178	27709.248291
HLA A*2402	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.592698	0.347463	-4.245235	39146.965104
HLA A*2301	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.534259	0.288865	-4.245394	34218.373174
HLA A*3201	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.604159	0.358727	-4.245432	40193.783284
HLA B*4403	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.642674	0.397240	-4.245434	43921.179465
HLA B*0803	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.423979	0.178488	-4.245491	26544.786168
HLA A*3101	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.414074	0.168455	-4.245618	25946.202452
HLA B*0702	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.425887	0.180214	-4.245673	26661.649393
HLA B*0702	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.443146	0.197447	-4.245699	27742.546962
HLA A*0101	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.361307	0.115588	-4.245719	22977.708670
HLA B*3801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.519077	0.273190	-4.245887	33042.810992
HLA A*3002	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.262779	0.016864	-4.245914	18313.810487
HLA B*5401	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.531369	0.285370	-4.246000	33991.434400
HLA B*4002	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.640329	0.394299	-4.246030	43684.684970
HLA B*3901	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.477352	0.231300	-4.246052	30015.976869
HLA A*0212	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.418122	0.171999	-4.246123	26189.183891
HLA B*1502	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.587139	0.340987	-4.246152	38649.085050
HLA B*5801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.352397	0.106226	-4.246172	22511.139106
HLA A*6802	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.442218	0.196045	-4.246173	27683.327038
HLA B*1509	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.543587	0.297408	-4.246179	34961.238872
HLA A*0301	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.361918	0.115588	-4.246330	23010.051193
HLA B*4402	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.426564	0.180214	-4.246350	26703.221902
HLA A*2603	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.626775	0.380348	-4.246427	42342.356971
HLA A*2301	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.531799	0.285370	-4.246430	34025.102914
HLA A*3101	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.368971	0.122535	-4.246436	23386.796619
HLA A*0202	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.593936	0.347463	-4.246473	39258.732805
HLA B*5701	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.418507	0.171999	-4.246508	26212.429817
HLA A*2603	1:195-203	9	LYTLVNPCD	1.165828	-0.750702	-4.661771	0.415126	-4.246645	45895.553128
HLA B*4601	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.417624	0.170588	-4.247036	26159.164825
HLA B*5301	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.606699	0.359537	-4.247161	40429.528811
HLA A*0101	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.378310	0.131008	-4.247302	23895.159939
HLA A*6901	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.353577	0.106226	-4.247351	22572.357144
HLA A*3301	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.425946	0.178488	-4.247457	26665.255551
HLA A*2603	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.577039	0.329580	-4.247459	37760.590848
HLA B*0702	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.411943	0.164416	-4.247526	25819.202253
HLA B*2705	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.459635	0.211872	-4.247763	28816.087593
HLA A*2501	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.459846	0.211872	-4.247974	28830.121275
HLA A*0219	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.445719	0.197447	-4.248272	27907.376785
HLA A*6801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.551935	0.303652	-4.248283	35639.740561
HLA B*0801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.420429	0.171999	-4.248430	26328.684443
HLA B*1801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.509613	0.261006	-4.248607	32330.562491
HLA B*4601	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.379642	0.131008	-4.248634	23968.568653
HLA A*6801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.476321	0.227561	-4.248760	29944.775268
HLA A*2602	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.614398	0.365377	-4.249021	41152.662851
HLA B*0802	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.480395	0.231300	-4.249095	30227.001328
HLA A*0219	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.445169	0.196045	-4.249124	27872.070797

HLA A*3002	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.608750	0.359537	-4.249212	40620.922337
HLA B*4403	1:40-48	9	TFVFRIEDT	0.603016	-0.222668	-4.629752	0.380348	-4.249404	42633.582376
HLA A*0203	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.332862	0.083388	-4.249474	21520.953240
HLA B*1503	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.477188	0.227561	-4.249627	30004.612203
HLA A*0250	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.597113	0.347463	-4.249650	39546.930534
HLA A*2902	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.407110	0.157454	-4.249656	25533.475259
HLA A*0201	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.387619	0.137558	-4.250061	24412.856669
HLA A*0201	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.333545	0.083388	-4.250157	21554.859880
HLA B*4002	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.615577	0.365377	-4.250201	41264.575681
HLA B*5701	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.387280	0.136944	-4.250336	24393.845873
HLA A*2603	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.630847	0.380458	-4.250389	42741.197586
HLA A*0101	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.388168	0.137558	-4.250610	24443.780817
HLA A*0101	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.387579	0.136944	-4.250634	24410.611568
HLA A*3002	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.523915	0.273190	-4.250725	33412.931150
HLA A*6801	1:404-412	9	PDGAAVLDA	1.090786	-0.657346	-4.684234	0.433440	-4.250794	48331.918491
HLA B*5301	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.580561	0.329580	-4.250981	38068.052466
HLA B*5101	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.506923	0.255887	-4.251036	32130.915519
HLA B*0803	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.497088	0.245974	-4.251114	31411.462403
HLA B*4601	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.408583	0.157454	-4.251129	25620.231876
HLA A*2603	1:105-113	9	GEAYHAFST	0.777510	-0.369595	-4.659116	0.407915	-4.251201	45615.841427
HLA A*3001	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.272874	0.021584	-4.251291	18744.525572
HLA B*1801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.466007	0.214632	-4.251375	29241.982909
HLA A*6802	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.268265	0.016864	-4.251400	18546.619547
HLA B*1503	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.512592	0.261006	-4.251586	32553.104142
HLA B*5301	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.594199	0.342354	-4.251846	39282.527177
HLA B*4402	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.400543	0.148579	-4.251964	25150.297019
HLA B*4002	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.636633	0.384545	-4.252089	43314.516233
HLA B*5301	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.599436	0.347215	-4.252222	39759.088712
HLA B*5401	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.529401	0.276822	-4.252578	33837.683448
HLA A*2403	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.423187	0.170588	-4.252599	26496.435590
HLA B*4402	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.404385	0.151627	-4.252757	25373.742389
HLA B*0702	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.383885	0.131008	-4.252877	24203.895526
HLA A*2403	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.424898	0.171999	-4.252898	26600.994896
HLA A*3001	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.180373	-0.072551	-4.252924	15148.613276
HLA A*0211	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.529840	0.276822	-4.253018	33871.932637
HLA A*2501	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.449128	0.196045	-4.253083	28127.304753
HLA A*0250	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.587503	0.334311	-4.253193	38681.507167
HLA A*2902	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.423824	0.170588	-4.253236	26535.309973
HLA A*2603	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.600517	0.347179	-4.253338	39858.154366
HLA A*0206	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.538745	0.285370	-4.253375	34573.593792
HLA B*4801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.425403	0.171999	-4.253404	26631.953210
HLA B*1502	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.470548	0.217015	-4.253534	29549.380030
HLA B*3801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.543528	0.289933	-4.253595	34956.510781
HLA A*0201	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.390544	0.136944	-4.253599	24577.839858
HLA A*3002	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.601126	0.347463	-4.253663	39914.041213
HLA B*3801	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.575427	0.321711	-4.253716	37620.714064
HLA B*4001	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.391284	0.137558	-4.253726	24619.759033
HLA B*4501	1:458-466	9	TTVSPPLFE	1.060848	-0.676303	-4.638353	0.384545	-4.253809	43486.383476
HLA B*5701	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.418235	0.164416	-4.253818	26195.985442
HLA B*4801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.422476	0.168455	-4.254020	26453.038306
HLA A*6801	1:344-352	9	LRDHLDTHG	0.953859	-0.532799	-4.675144	0.421060	-4.254084	47330.803468
HLA B*1503	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.539630	0.285370	-4.254261	34644.179568
HLA B*0702	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.406050	0.151627	-4.254423	25471.253092
HLA A*2902	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.426488	0.171999	-4.254489	26698.599535
HLA A*2403	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.433492	0.178924	-4.254568	27132.655208
HLA B*2705	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.494515	0.239809	-4.254707	31225.936339
HLA A*6901	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.391683	0.136944	-4.254739	24642.411776
HLA A*3301	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.552191	0.297408	-4.254783	35660.762726
HLA A*3101	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.392543	0.137558	-4.254985	24691.252567
HLA B*7301	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.452448	0.197447	-4.255001	28343.138631
HLA A*3001	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.306749	0.051538	-4.255212	20265.126897
HLA A*3001	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.249786	-0.005447	-4.255233	17774.036336
HLA A*0219	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.423784	0.168455	-4.255329	26532.869683
HLA B*1509	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.545495	0.289933	-4.255562	35115.155468
HLA A*0203	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.426230	0.170588	-4.255642	26682.716251

HLA B*2705	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.404281	0.148579	-4.255702	25367.703266
HLA A*2301	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.545645	0.289933	-4.255712	35127.315595
HLA A*0201	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.386728	0.131008	-4.255720	24362.853097
HLA A*3201	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.577779	0.321711	-4.256068	37824.994100
HLA B*5101	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.513840	0.257713	-4.256127	32646.752298
HLA B*3501	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.436380	0.180214	-4.256166	27313.654595
HLA B*4501	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.638003	0.381754	-4.256250	43451.344380
HLA A*3301	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.598633	0.342354	-4.256279	39685.595167
HLA B*7301	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.546326	0.289933	-4.256393	35182.468964
HLA B*0803	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.526034	0.269593	-4.256441	33576.375355
HLA B*4501	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.653686	0.397240	-4.256446	45049.090812
HLA B*4001	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.393542	0.136944	-4.256597	24748.088080
HLA A*3101	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.387666	0.131008	-4.256658	24415.498229
HLA A*0250	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.560346	0.303652	-4.256694	36336.717312
HLA B*3501	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.435271	0.178488	-4.256782	27243.999030
HLA B*1502	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.591267	0.334311	-4.256956	39018.202861
HLA B*3501	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.228260	-0.028903	-4.257163	16914.535742
HLA B*0702	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.414936	0.157454	-4.257482	25997.767976
HLA B*7301	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.513379	0.255887	-4.257492	32612.154043
HLA A*0211	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.527140	0.269593	-4.257548	33662.038991
HLA A*2603	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.546456	0.288865	-4.257590	35192.938851
HLA A*0206	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.369135	0.111406	-4.257729	23395.654695
HLA A*3101	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.424670	0.166895	-4.257775	26587.039440
HLA B*0702	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.436772	0.178924	-4.257848	27338.342307
HLA A*2501	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.426392	0.168455	-4.257937	26692.678297
HLA B*4801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.436946	0.178924	-4.258022	27349.288906
HLA A*0212	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.426517	0.168455	-4.258061	26700.332829
HLA B*5101	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.504050	0.245974	-4.258076	31919.029645
HLA A*3101	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.304940	0.046803	-4.258138	20180.885767
HLA B*0803	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.511169	0.252948	-4.258221	32446.557026
HLA A*0301	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.364455	0.106226	-4.258229	23144.885077
HLA B*4601	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.425133	0.166895	-4.258238	26615.389633
HLA A*0216	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.498136	0.239809	-4.258327	31487.343818
HLA A*2501	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.489821	0.231300	-4.258521	30890.234053
HLA B*4601	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.396107	0.137558	-4.258549	24894.722561
HLA B*1502	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.483658	0.225072	-4.258587	30454.992702
HLA B*4601	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.395600	0.136944	-4.258655	24865.649170
HLA A*3301	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.624050	0.365377	-4.258673	42077.470733
HLA A*2602	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.562347	0.303652	-4.258696	36504.588018
HLA B*4501	1:287-295	9	LGWSIADDH	0.644080	-0.249781	-4.653056	0.394299	-4.258758	44983.823700
HLA A*2602	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.605952	0.347179	-4.258773	40360.035877
HLA B*1509	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.470652	0.211872	-4.258779	29556.414657
HLA B*1517	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.475795	0.217015	-4.258780	29908.509713
HLA A*8001	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.334443	0.075603	-4.258840	21599.450731
HLA A*2402	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.544496	0.285370	-4.259126	35034.511345
HLA B*1501	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-3.955541	-0.303590	-4.259131	9026.954657
HLA A*1101	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.476293	0.217015	-4.259278	29942.831356
HLA B*3801	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.563182	0.303652	-4.259530	36574.762832
HLA B*7301	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.547515	0.287962	-4.259553	35278.909530
HLA A*3201	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.624975	0.365377	-4.259599	42167.254360
HLA A*0206	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.536541	0.276822	-4.259718	34398.595308
HLA B*3801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.559582	0.299836	-4.259746	36272.885719
HLA B*2705	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.225699	-0.034117	-4.259816	16815.087959
HLA B*4402	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.438422	0.178488	-4.259933	27442.363681
HLA A*0101	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.383267	0.123142	-4.260126	24169.482690
HLA B*4801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.427313	0.166895	-4.260418	26749.344898
HLA B*7301	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.590102	0.329580	-4.260522	38913.645464
HLA B*5401	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.488104	0.227561	-4.260543	30768.315868
HLA B*0801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.041330	-0.219267	-4.260597	10998.421422
HLA A*1101	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.440844	0.180214	-4.260630	27595.853745
HLA B*5301	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.608151	0.347463	-4.260688	40564.923526
HLA B*0803	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.500901	0.239809	-4.261093	31688.477249
HLA A*3002	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.560989	0.299836	-4.261153	36390.619518
HLA A*0211	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.546571	0.285370	-4.261201	35202.269192
HLA A*6802	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.418679	0.157454	-4.261225	26222.783724

HLA A*0206	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.530864	0.269593	-4.261272	33951.921057
HLA A*2403	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.392437	0.131008	-4.261429	24685.242337
HLA A*0201	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.384625	0.123142	-4.261484	24245.176913
HLA B*1503	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.546333	0.284825	-4.261509	35183.039969
HLA A*0206	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.392543	0.131008	-4.261535	24691.252567
HLA A*2403	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.399143	0.137558	-4.261585	25069.335660
HLA A*2402	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.549566	0.287962	-4.261604	35445.920007
HLA A*2902	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.399185	0.137558	-4.261627	25071.776981
HLA A*6802	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.433699	0.171999	-4.261700	27145.575333
HLA B*4001	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.433941	0.171999	-4.261942	27160.705567
HLA A*3002	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.583761	0.321711	-4.262049	38349.584044
HLA A*2603	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.643813	0.381582	-4.262232	44036.571006
HLA B*1517	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.426665	0.164416	-4.262248	26709.434468
HLA B*4601	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.385485	0.123142	-4.262344	24293.230392
HLA A*6801	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.530907	0.268538	-4.262369	33955.227389
HLA A*2402	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.592068	0.329580	-4.262489	39090.248991
HLA B*5301	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.603494	0.340987	-4.262507	40132.293739
HLA A*0212	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.400278	0.137558	-4.262720	25134.926901
HLA B*5801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.346115	0.083388	-4.262727	22187.836082
HLA B*1509	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.518739	0.255887	-4.262851	33017.079872
HLA B*4403	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.284819	0.021903	-4.262916	19267.227906
HLA A*6802	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.433607	0.170588	-4.263019	27139.848610
HLA B*1502	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.610531	0.347463	-4.263068	40787.838392
HLA B*4801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.433673	0.170588	-4.263085	27143.959981
HLA A*0206	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.524436	0.261006	-4.263430	33453.084033
HLA A*6802	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.394460	0.131008	-4.263452	24800.492290
HLA A*2603	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.610991	0.347463	-4.263528	40831.110235
HLA B*3801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.521271	0.257713	-4.263558	33210.193434
HLA B*4403	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.459607	0.196045	-4.263562	28814.216952
HLA B*1517	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.442317	0.178488	-4.263829	27689.617829
HLA A*0101	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.347278	0.083388	-4.263890	22247.332407
HLA B*5701	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.421545	0.157454	-4.264091	26396.428196
HLA A*0203	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.415920	0.151627	-4.264293	26056.765089
HLA B*5401	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.552271	0.287962	-4.264308	35667.322636
HLA A*0219	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.401950	0.137558	-4.264393	25231.929344
HLA A*2603	1:291-299	9	IADDHDLFG	1.022984	-0.625744	-4.661869	0.397240	-4.264629	45905.982487
HLA A*0250	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.594286	0.329580	-4.264707	39290.390986
HLA A*3301	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.612013	0.347215	-4.264799	40927.311310
HLA A*0212	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.413423	0.148579	-4.264844	25907.350166
HLA A*6802	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.376654	0.111406	-4.265248	23804.198045
HLA A*6802	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-3.961669	-0.303590	-4.265258	9155.218588
HLA A*2602	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.624846	0.359537	-4.265309	42154.709617
HLA B*3501	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.417051	0.151627	-4.265423	26124.657169
HLA A*2601	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.381108	0.115588	-4.265520	24049.617772
HLA A*0301	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.341150	0.075603	-4.265548	21935.648937
HLA A*2402	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.563304	0.297408	-4.265896	36585.053281
HLA B*2705	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.463476	0.197447	-4.266030	29072.101324
HLA A*6801	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.611358	0.345166	-4.266192	40865.583897
HLA A*3001	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.288167	0.021903	-4.266264	19416.334740
HLA A*8001	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.434723	0.168455	-4.266268	27209.679490
HLA B*4403	1:405-413	9	DGAAVLDAA	0.935191	-0.540292	-4.661411	0.394899	-4.266512	45857.580498
HLA A*0203	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.415129	0.148579	-4.266550	26009.303428
HLA A*2501	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.512538	0.245974	-4.266564	32549.053894
HLA B*4501	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.543603	0.276822	-4.266781	34962.562852
HLA A*6801	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.625727	0.358727	-4.267000	42240.316037
HLA A*0206	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.523010	0.255887	-4.267123	33343.410876
HLA A*1101	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.431545	0.164416	-4.267128	27011.243185
HLA B*4002	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.625859	0.358727	-4.267132	42253.114840
HLA A*2501	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.447528	0.180214	-4.267314	28023.870628
HLA B*0702	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.435821	0.168455	-4.267365	27278.509430
HLA A*6801	1:76-84	9	PEVGGPYGP	0.614487	-0.202955	-4.679164	0.411532	-4.267632	47770.946455
HLA A*6802	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.434535	0.166895	-4.267641	27197.905930
HLA A*6901	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.379069	0.111406	-4.267663	23936.950704
HLA A*0101	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.373949	0.106226	-4.267724	23656.435005
HLA A*2603	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.626465	0.358727	-4.267738	42312.130860

HLA A*6802	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.390309	0.122535	-4.267774	24564.547115
HLA B*4002	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.628053	0.359537	-4.268516	42467.153214
HLA A*0202	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.526248	0.257713	-4.268534	33592.909071
HLA A*2301	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.545419	0.276822	-4.268597	35109.076983
HLA A*2403	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.384209	0.115588	-4.268622	24221.972047
HLA B*7301	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.554192	0.285370	-4.268823	35825.510613
HLA A*3301	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.627628	0.358727	-4.268901	42425.590157
HLA B*0802	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.449213	0.180214	-4.268999	28132.783248
HLA A*0216	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.437510	0.168455	-4.269055	27384.821557
HLA A*0212	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.439951	0.170588	-4.269363	27539.181624
HLA B*4002	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.603778	0.334311	-4.269467	40158.572802
HLA B*3501	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.418232	0.148579	-4.269653	26195.843725
HLA B*4801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.435940	0.166266	-4.269675	27286.036728
HLA B*0702	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.407307	0.137558	-4.269749	25545.081091
HLA A*2501	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.467236	0.197447	-4.269789	29324.836514
HLA B*5701	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.418402	0.148579	-4.269822	26206.049308
HLA B*1509	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.543021	0.273190	-4.269831	34915.686695
HLA A*2601	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.381261	0.111406	-4.269855	24058.076134
HLA B*0803	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.501317	0.231300	-4.270017	31718.835094
HLA A*0250	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.522987	0.252948	-4.270039	33341.607083
HLA B*4002	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.560038	0.289933	-4.270105	36310.974768
HLA B*1517	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.467553	0.197447	-4.270106	29346.261292
HLA B*3501	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.376517	0.106226	-4.270292	23796.730088
HLA B*5801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.345896	0.075603	-4.270294	22176.675753
HLA A*2301	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.510196	0.239809	-4.270387	32373.967982
HLA A*2501	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.487415	0.217015	-4.270401	30719.583720
HLA A*2601	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.401556	0.131008	-4.270548	25209.007436
HLA B*1517	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.382358	0.111406	-4.270952	24118.933740
HLA B*0702	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.377257	0.106226	-4.271032	23837.317028
HLA B*1801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.510884	0.239809	-4.271076	32425.324571
HLA B*4001	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.422840	0.151627	-4.271212	26475.229350
HLA A*0202	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.408181	0.136944	-4.271237	25596.541788
HLA B*4601	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.419825	0.148579	-4.271246	26292.104015
HLA A*2602	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.556662	0.285370	-4.271292	36029.787255
HLA B*4002	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.635893	0.364577	-4.271316	43240.766170
HLA A*0206	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.502635	0.231300	-4.271335	31815.246331
HLA B*0801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.408527	0.136944	-4.271582	25616.905629
HLA A*3001	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.289095	0.017415	-4.271680	19457.869989
HLA A*0211	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.199150	-0.072551	-4.271701	15817.941422
HLA A*0250	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.545412	0.273594	-4.271819	35108.507179
HLA A*6801	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.614243	0.342354	-4.271889	41137.971805
HLA A*6801	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.637280	0.365377	-4.271903	43379.004042
HLA B*0801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.395050	0.123142	-4.271908	24834.191311
HLA B*5401	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.438215	0.166266	-4.271949	27429.302297
HLA A*6901	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.365526	0.093574	-4.271953	23202.051897
HLA A*3101	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.378216	0.106226	-4.271990	23889.989692
HLA A*2301	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.525061	0.252948	-4.272113	33501.258695
HLA A*2602	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.619769	0.347463	-4.272306	41664.758119
HLA A*0202	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.557193	0.284825	-4.272368	36073.865472
HLA B*5301	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.561516	0.288865	-4.272651	36434.744953
HLA B*7301	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.546289	0.273594	-4.272695	35179.423764
HLA A*2601	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.378928	0.106226	-4.272702	23929.182190
HLA A*2301	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.528606	0.255887	-4.272719	33775.866340
HLA A*8001	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.379036	0.106226	-4.272810	23935.137826
HLA B*2705	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.384386	0.111406	-4.272980	24231.801904
HLA A*8001	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.410004	0.136944	-4.273060	25704.223835
HLA B*1509	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.530806	0.257713	-4.273092	33947.329465
HLA A*2301	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.546831	0.273594	-4.273238	35223.414422
HLA A*0250	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.541653	0.268381	-4.273272	34805.925603
HLA B*3501	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.232064	-0.041216	-4.273280	17063.334256
HLA A*2402	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.562296	0.288865	-4.273431	36500.243589
HLA B*3801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.570984	0.297408	-4.273576	37237.812285
HLA A*2301	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.501195	0.227561	-4.273634	31709.913389
HLA B*5401	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.563604	0.289933	-4.273671	36610.395953
HLA A*2501	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.422375	0.148579	-4.273795	26446.885378

HLA A*8001	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.445860	0.171999	-4.273861	27916.436805
HLA A*2602	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.595583	0.321711	-4.273872	39407.897627
HLA A*1101	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.444474	0.170588	-4.273885	27827.474208
HLA B*4403	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.444587	0.170588	-4.273998	27834.701237
HLA B*5801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.356131	0.082100	-4.274031	22705.486059
HLA A*0206	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.295768	0.021584	-4.274184	19759.130732
HLA A*2402	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.547379	0.273190	-4.274189	35267.841677
HLA B*5101	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.505530	0.231300	-4.274229	32028.002641
HLA B*7301	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.505560	0.231300	-4.274260	32030.255204
HLA B*4501	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.615277	0.340987	-4.274290	41236.011264
HLA A*0203	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.411938	0.137558	-4.274380	25818.922897
HLA A*2603	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.489112	0.214632	-4.274480	30839.807209
HLA B*4001	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.397750	0.123142	-4.274608	24989.040486
HLA B*4501	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.640010	0.365377	-4.274633	43652.556006
HLA B*1502	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.562662	0.287962	-4.274700	36531.060706
HLA A*0203	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.441603	0.166895	-4.274708	27644.116735
HLA A*0212	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.380998	0.106226	-4.274772	24043.503579
HLA A*8001	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.445374	0.170588	-4.274785	27885.192163
HLA A*2603	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.596504	0.321711	-4.274793	39491.557708
HLA A*2301	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.543397	0.268538	-4.274859	34945.922178
HLA A*3201	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.604507	0.329580	-4.274927	40225.977869
HLA B*4403	1:8-16	9	RVRFCPSPT	0.486320	-0.099296	-4.661980	0.387024	-4.274956	45917.656246
HLA A*0206	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.492138	0.217015	-4.275123	31055.447461
HLA A*0203	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.398311	0.123142	-4.275169	25021.371300
HLA A*2403	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.223773	-0.051442	-4.275215	16740.659603
HLA A*0211	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.536261	0.261006	-4.275255	34376.457417
HLA B*3901	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.406274	0.131008	-4.275266	25484.347138
HLA A*2301	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.545004	0.269593	-4.275411	35075.474364
HLA B*0702	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.442444	0.166895	-4.275549	27697.708090
HLA B*5701	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.413118	0.137558	-4.275560	25889.136306
HLA A*3201	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.609957	0.334311	-4.275647	40734.033436
HLA B*4001	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.391361	0.115588	-4.275773	24624.154701
HLA A*2403	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.424616	0.148579	-4.276037	26583.731489
HLA A*8001	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.440623	0.164416	-4.276207	27581.824005
HLA B*4403	1:309-317	9	VADVNSSPA	0.699843	-0.318261	-4.658035	0.381582	-4.276453	45502.465300
HLA A*6802	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.425105	0.148579	-4.276526	26613.661854
HLA B*2705	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.455476	0.178924	-4.276552	28541.475909
HLA B*1501	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.414163	0.137558	-4.276605	25951.536911
HLA A*2403	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.445160	0.168455	-4.276704	27871.467664
HLA A*2501	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.434174	0.157454	-4.276720	27175.256167
HLA B*4002	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.641079	0.364340	-4.276738	43760.139107
HLA A*2602	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.523151	0.246392	-4.276759	33354.235682
HLA A*0211	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.414389	0.137558	-4.276831	25965.018326
HLA B*0702	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.425497	0.148579	-4.276918	26637.716871
HLA B*3801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.523332	0.246392	-4.276940	33368.132665
HLA A*6802	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.248503	-0.028903	-4.277406	17721.612859
HLA A*2603	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.642784	0.365377	-4.277408	43932.348494
HLA B*1509	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.554277	0.276822	-4.277455	35832.488526
HLA B*3801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.551460	0.273594	-4.277866	35600.814810
HLA B*4801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.408938	0.131008	-4.277930	25641.169421
HLA A*2301	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.538979	0.261006	-4.277973	34592.302783
HLA B*0801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.426620	0.148579	-4.278041	26706.689202
HLA A*6901	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.329610	0.051538	-4.278072	21360.421419
HLA B*0803	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.495265	0.217015	-4.278250	31279.871169
HLA A*3201	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.625746	0.347463	-4.278283	42242.144200
HLA B*4002	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.642061	0.363771	-4.278289	43859.207353
HLA A*2602	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.575714	0.297408	-4.278306	37645.552175
HLA A*2902	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.389752	0.111406	-4.278346	24533.072017
HLA A*0216	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.415956	0.137558	-4.278398	26058.879638
HLA A*0211	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.534523	0.255887	-4.278635	34239.112628
HLA A*0211	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.547264	0.268538	-4.278726	35258.493956
HLA A*0101	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.390158	0.111406	-4.278753	24556.043533
HLA A*3201	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.567671	0.288865	-4.278806	36954.844951
HLA A*1101	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.476422	0.197447	-4.278975	29951.741989
HLA A*2602	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.514253	0.235091	-4.279163	32677.851396

HLA B*4801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.430823	0.151627	-4.279196	26966.419174
HLA A*2402	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.519065	0.239809	-4.279257	33041.917214
HLA A*0212	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.402439	0.123142	-4.279297	25260.337728
HLA B*4402	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.445590	0.166266	-4.279324	27899.074351
HLA A*0250	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.491240	0.211872	-4.279368	30991.335237
HLA B*5101	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.448148	0.168455	-4.279693	28063.923216
HLA B*3501	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.373425	0.093574	-4.279852	23627.912965
HLA A*6801	1:285-293	9	ALLGWSIAD	1.068959	-0.688501	-4.660323	0.380458	-4.279865	45742.861142
HLA A*3001	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.297864	0.017995	-4.279868	19854.711243
HLA A*1101	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.391274	0.111406	-4.279869	24619.226278
HLA A*3301	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.416879	0.136944	-4.279935	26114.342006
HLA A*0216	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.403078	0.123142	-4.279936	25297.535420
HLA B*4001	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.391392	0.111406	-4.279986	24625.886543
HLA A*0201	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.386239	0.106226	-4.280014	24335.454046
HLA A*6901	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.363426	0.083388	-4.280038	23090.107469
HLA B*0803	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.541324	0.261006	-4.280318	34779.574116
HLA B*2705	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.448849	0.168455	-4.280393	28109.202874
HLA B*0802	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.477891	0.197447	-4.280444	30053.185644
HLA B*4002	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.625624	0.345166	-4.280458	42230.262555
HLA B*1503	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.374067	0.093574	-4.280493	23662.834805
HLA A*0201	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.396309	0.115588	-4.280721	24906.307537
HLA B*5701	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.403339	0.122535	-4.280804	25312.731093
HLA B*4403	1:143-151	9	QRAAYLAEG	0.794744	-0.436017	-4.639559	0.358727	-4.280832	43607.237692
HLA A*2402	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.404495	0.123142	-4.281353	25380.194859
HLA B*1517	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.282651	0.001267	-4.281384	19171.260122
HLA B*3801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.549825	0.268381	-4.281444	35467.019719
HLA A*2902	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.397237	0.115588	-4.281650	24959.586886
HLA B*4601	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.393147	0.111406	-4.281741	24725.605716
HLA A*2501	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.460345	0.178488	-4.281856	28863.205409
HLA B*1502	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.607411	0.325371	-4.282040	40495.855096
HLA A*6901	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.303798	0.021584	-4.282215	20127.895750
HLA A*2403	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.388443	0.106226	-4.282218	24459.257577
HLA B*4501	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.647009	0.364577	-4.282432	44361.762665
HLA A*2601	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.376153	0.093574	-4.282579	23776.784113
HLA A*0201	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.405134	0.122535	-4.282599	25417.569049
HLA A*3002	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.447044	0.164416	-4.282628	27992.657182
HLA B*0702	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.394056	0.111406	-4.282650	24777.426142
HLA B*7301	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.431270	0.148579	-4.282691	26994.151639
HLA B*4402	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.447227	0.164416	-4.282811	28004.471773
HLA B*3901	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.499999	0.217015	-4.282985	31622.716017
HLA A*3001	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.306364	0.023199	-4.283165	20247.155207
HLA B*1801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.420145	0.136944	-4.283200	26311.455415
HLA B*5101	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.497861	0.214632	-4.283229	31467.419989
HLA B*4501	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.556890	0.273594	-4.283296	36048.699181
HLA B*1801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.421012	0.137558	-4.283454	26364.032095
HLA A*2603	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.568877	0.285370	-4.283507	37057.547186
HLA A*2603	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.648090	0.364577	-4.283512	44472.296563
HLA A*2402	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.530040	0.246392	-4.283647	33887.511908
HLA A*3201	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.609043	0.325371	-4.283673	40648.400963
HLA B*4402	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.406842	0.123142	-4.283700	25517.732921
HLA B*4402	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.420732	0.136944	-4.283788	26347.065005
HLA B*3901	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.452244	0.168455	-4.283788	28329.801778
HLA B*5401	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.568834	0.284825	-4.284010	37053.938772
HLA A*2601	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.278605	-0.005447	-4.284052	18993.493248
HLA B*3801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.572070	0.287962	-4.284107	37330.999716
HLA B*4501	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.647946	0.363771	-4.284175	44457.622983
HLA A*0301	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.367780	0.083388	-4.284392	23322.738880
HLA B*4501	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.618740	0.334311	-4.284429	41566.149039
HLA B*3801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.569330	0.284825	-4.284506	37096.259497
HLA A*6801	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.609967	0.325371	-4.284596	40734.914912
HLA B*3801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.554232	0.269593	-4.284640	35828.805569
HLA A*2402	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.584501	0.299836	-4.284664	38414.991864
HLA B*0801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.360287	0.075603	-4.284684	22923.822778
HLA B*1801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.530761	0.245974	-4.284787	33943.840269
HLA B*7301	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.512388	0.227561	-4.284827	32537.786291

HLA B*4501	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.649377	0.364340	-4.285037	44604.335616
HLA B*1502	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.570676	0.285370	-4.285307	37211.431364
HLA A*2501	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.451715	0.166266	-4.285449	28295.339013
HLA A*0206	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.423061	0.137558	-4.285503	26488.696211
HLA A*3002	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.464449	0.178924	-4.285525	29137.286909
HLA B*1801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.408212	0.122535	-4.285677	25598.342019
HLA B*3801	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.574640	0.288865	-4.285775	37552.595305
HLA A*0219	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.457800	0.171999	-4.285801	28694.592913
HLA B*1503	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.555459	0.269593	-4.285866	35930.127757
HLA A*0219	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.397322	0.111406	-4.285916	24964.448389
HLA B*1509	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.559711	0.273594	-4.286118	36283.680101
HLA B*5401	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.542090	0.255887	-4.286203	34840.966323
HLA A*2603	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.628643	0.342354	-4.286289	42524.857773
HLA A*2602	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.620643	0.334311	-4.286332	41748.691989
HLA B*0802	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.454800	0.168455	-4.286344	28497.041541
HLA B*4403	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.627527	0.340987	-4.286540	42415.722042
HLA A*3002	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.616151	0.329580	-4.286571	41319.081422
HLA B*5701	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.417617	0.131008	-4.286609	26158.740274
HLA B*1801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.465098	0.178488	-4.286609	29180.825144
HLA A*0250	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.586448	0.299836	-4.286612	38587.662253
HLA A*3101	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.368740	0.082100	-4.286641	23374.400948
HLA A*3002	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.533054	0.246392	-4.286662	34123.539498
HLA B*5101	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.484349	0.197447	-4.286902	30503.470135
HLA B*3501	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.214403	-0.072551	-4.286954	16383.354161
HLA A*0219	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.457753	0.170588	-4.287165	28691.488389
HLA B*1502	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.555579	0.268381	-4.287197	35940.042403
HLA B*1503	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.466199	0.178924	-4.287275	29254.957849
HLA B*4001	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.370669	0.083388	-4.287281	23478.449689
HLA B*1509	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.338874	0.051538	-4.287336	21820.959136
HLA A*2403	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.398859	0.111406	-4.287453	25052.930729
HLA A*0219	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.381033	0.093574	-4.287459	24045.454748
HLA B*0802	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.465962	0.178488	-4.287474	29238.977342
HLA B*0803	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.502149	0.214632	-4.287517	31779.638063
HLA B*7301	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.564488	0.276822	-4.287665	36684.941621
HLA A*0202	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.561363	0.273594	-4.287769	36421.935190
HLA A*0250	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.515372	0.227561	-4.287811	32762.108807
HLA B*3501	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.403440	0.115588	-4.287852	25318.620158
HLA A*3301	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.635275	0.347179	-4.288097	43179.286918
HLA A*3002	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.576118	0.287962	-4.288155	37680.597699
HLA B*1509	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.484241	0.196045	-4.288196	30495.880142
HLA A*3301	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.635673	0.347463	-4.288209	43218.782552
HLA A*3301	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.633579	0.345166	-4.288413	43010.960167
HLA B*1501	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.404096	0.115588	-4.288508	25356.863902
HLA A*3002	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.484662	0.196045	-4.288616	30525.425745
HLA A*2301	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.535044	0.246392	-4.288652	34280.258347
HLA A*0216	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.486412	0.197447	-4.288965	30648.702685
HLA B*5401	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.562199	0.273190	-4.289009	36492.148534
HLA B*1509	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.514110	0.225072	-4.289039	32667.069378
HLA A*2603	1:430-438	9	AALKDALIE	1.002563	-0.657397	-4.634230	0.345166	-4.289064	43075.462098
HLA A*0250	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.574511	0.285370	-4.289141	37541.423421
HLA B*7301	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.614717	0.325371	-4.289347	41182.951855
HLA A*6801	1:128-136	9	PKLGYDNFD	1.288408	-0.906654	-4.671131	0.381754	-4.289377	46895.476879
HLA B*4402	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.426977	0.137558	-4.289419	26728.659229
HLA B*5701	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.400924	0.111406	-4.289518	25172.348452
HLA B*1502	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.501726	0.211872	-4.289854	31748.706748
HLA A*6801	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.653688	0.363771	-4.289917	45049.334523
HLA A*1101	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.456374	0.166266	-4.290108	28600.520074
HLA B*4501	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.536308	0.245974	-4.290334	34380.177074
HLA B*4501	1:133-141	9	DNFDRHLTD	1.325406	-0.965869	-4.649896	0.359537	-4.290359	44657.695805
HLA B*4501	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.558819	0.268381	-4.290437	36209.166258
HLA A*0206	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.136146	-0.154364	-4.290511	13681.892478
HLA B*4403	1:247-255	9	LPTVLGEGT	0.828162	-0.462785	-4.656021	0.365377	-4.290645	45291.991642
HLA B*5701	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.384240	0.093574	-4.290666	24223.675603
HLA A*0206	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.530484	0.239809	-4.290675	33922.178560
HLA B*4002	1:370-378	9	QTRIVVLGD	1.092268	-0.751281	-4.631709	0.340987	-4.290722	42826.141509

HLA B*5101	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.507846	0.217015	-4.290832	32199.301294
HLA B*4002	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.633208	0.342354	-4.290854	42974.211720
HLA A*0216	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.462990	0.171999	-4.290991	29039.563239
HLA A*0202	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.581038	0.289933	-4.291105	38109.882052
HLA A*8001	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.414276	0.123142	-4.291134	25958.276743
HLA B*1509	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.579240	0.287962	-4.291278	37952.487738
HLA B*3501	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.458174	0.166895	-4.291279	28719.285827
HLA B*0801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.413886	0.122535	-4.291351	25934.975595
HLA B*5301	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.503359	0.211872	-4.291487	31868.302543
HLA B*1502	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.621122	0.329580	-4.291542	41794.792005
HLA B*1509	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.506181	0.214632	-4.291549	32076.033841
HLA B*0802	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.458230	0.166266	-4.291964	28723.014905
HLA A*2602	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.591829	0.299836	-4.291992	39068.684602
HLA B*1517	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.423016	0.131008	-4.292008	26485.973633
HLA A*1101	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.464087	0.171999	-4.292088	29113.022076
HLA B*5401	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.553147	0.261006	-4.292141	35739.367986
HLA A*6901	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.309665	0.017415	-4.292250	20401.638053
HLA A*0219	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.440860	0.148579	-4.292281	27596.898799
HLA A*3301	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.440863	0.148579	-4.292283	27597.048095
HLA A*3002	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.582278	0.289933	-4.292345	38218.895557
HLA A*0202	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.577873	0.285370	-4.292503	37833.180147
HLA B*3501	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.450080	0.157454	-4.292626	28188.999383
HLA A*2402	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.596488	0.303652	-4.292836	39490.062222
HLA A*0211	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.488910	0.196045	-4.292864	30825.462312
HLA B*4403	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.627205	0.334311	-4.292894	42384.297073
HLA B*4601	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.415512	0.122535	-4.292977	26032.248857
HLA A*0219	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.457412	0.164416	-4.292996	28668.990638
HLA A*2603	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.640247	0.347215	-4.293032	43676.414228
HLA B*5701	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.416228	0.123142	-4.293087	26075.237946
HLA A*6901	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.361349	0.067914	-4.293435	22979.946302
HLA A*0219	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.430562	0.136944	-4.293618	26950.230762
HLA B*1509	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.546606	0.252948	-4.293658	35205.125914
HLA B*1502	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.528853	0.235091	-4.293762	33795.057778
HLA A*8001	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.461249	0.166895	-4.294354	28923.384553
HLA B*1517	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.290876	-0.003611	-4.294487	19537.824621
HLA B*5801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.354322	0.059535	-4.294786	22611.100478
HLA B*4403	1:266-274	9	NLFAHRDRG	0.872841	-0.508264	-4.659433	0.364577	-4.294856	45649.168443
HLA A*2902	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.459273	0.164416	-4.294857	28792.090248
HLA B*1501	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.401091	0.106226	-4.294865	25182.019062
HLA B*4801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.431913	0.136944	-4.294969	27034.195000
HLA B*4501	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.568317	0.273190	-4.295127	37009.864311
HLA A*0101	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.346839	0.051538	-4.295301	22224.837290
HLA B*1501	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.370930	0.075603	-4.295328	23492.552678
HLA A*3101	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.363285	0.067914	-4.295370	23082.613790
HLA B*1509	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.565214	0.269593	-4.295621	36746.317500
HLA B*0802	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.402075	0.106226	-4.295849	25239.164984
HLA B*4601	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.402181	0.106226	-4.295955	25245.310081
HLA A*3301	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.630398	0.334311	-4.296087	42697.056393
HLA A*2402	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.573063	0.276822	-4.296241	37416.525166
HLA A*0216	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.460662	0.164416	-4.296245	28884.292918
HLA A*2402	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.586307	0.289933	-4.296374	38575.138987
HLA B*1502	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.444984	0.148579	-4.296404	27860.161342
HLA B*5801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.348037	0.051538	-4.296499	22286.241251
HLA A*8001	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.445110	0.148579	-4.296531	27868.301431
HLA B*4601	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.380027	0.083388	-4.296639	23989.843526
HLA B*1503	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.468709	0.171999	-4.296709	29424.475266
HLA B*4601	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.412340	0.115588	-4.296752	25842.818802
HLA A*0211	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.542840	0.245974	-4.296866	34901.145194
HLA B*5301	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.600548	0.303652	-4.296896	39860.957632
HLA B*3801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.477287	0.180214	-4.297073	30011.430486
HLA B*1517	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.390649	0.093574	-4.297076	24583.823939
HLA A*0216	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.291633	-0.005447	-4.297080	19571.888866
HLA A*0250	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.570385	0.273190	-4.297195	37186.477330
HLA B*5801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.365143	0.067914	-4.297229	23181.601069
HLA B*3801	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.582666	0.285370	-4.297296	38253.026186

HLA A*0202	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.553398	0.255887	-4.297511	35760.061999
HLA A*6901	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.373129	0.075603	-4.297527	23611.812580
HLA A*2403	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.380955	0.083388	-4.297567	24041.162384
HLA B*3901	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.463850	0.166266	-4.297584	29097.119101
HLA A*2301	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.543674	0.245974	-4.297700	34968.237620
HLA B*5301	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.597620	0.299836	-4.297784	39593.169559
HLA B*0801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.464698	0.166895	-4.297803	29154.000426
HLA B*0802	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.455258	0.157454	-4.297804	28527.119742
HLA A*2902	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.446685	0.148579	-4.298106	27969.496881
HLA B*3801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.544083	0.245974	-4.298109	35001.169444
HLA A*2501	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.477052	0.178924	-4.298128	29995.199026
HLA B*1502	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.571574	0.273190	-4.298384	37288.411192
HLA B*1501	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.420970	0.122535	-4.298435	26361.464943
HLA A*2301	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.513199	0.214632	-4.298567	32598.571906
HLA B*5701	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.414161	0.115588	-4.298573	25951.396517
HLA A*0216	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.320409	0.021584	-4.298826	20912.657913
HLA A*0301	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.366746	0.067914	-4.298831	23267.288592
HLA B*3901	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.463298	0.164416	-4.298882	29060.150741
HLA B*4001	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.421606	0.122535	-4.299072	26400.141303
HLA B*5101	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.495256	0.196045	-4.299210	31279.194293
HLA A*0211	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.524373	0.225072	-4.299301	33448.197998
HLA B*0803	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.511420	0.211872	-4.299548	32465.344417
HLA B*4403	1:208-216	9	KITHVLRGE	0.940432	-0.576092	-4.664052	0.364340	-4.299712	46137.276909
HLA A*2403	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.317226	0.017415	-4.299811	20759.920267
HLA A*2402	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.561011	0.261006	-4.300005	36392.391384
HLA B*3801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.539821	0.239809	-4.300012	34659.364010
HLA A*2602	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.629641	0.329580	-4.300062	42622.743536
HLA A*3002	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.585278	0.284825	-4.300454	38483.842190
HLA B*1517	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.471049	0.170588	-4.300460	29583.449594
HLA B*4601	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.394115	0.093574	-4.300541	24780.777447
HLA B*5301	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.568931	0.268381	-4.300550	37062.158449
HLA B*4801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.438182	0.137558	-4.300624	27427.224923
HLA B*3901	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.480942	0.180214	-4.300729	30265.126613
HLA B*3501	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.376444	0.075603	-4.300842	23792.739555
HLA A*2301	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.526175	0.225072	-4.301103	33587.275792
HLA A*0202	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.541251	0.239809	-4.301443	34773.741842
HLA A*3001	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.281053	-0.020620	-4.301673	19100.863899
HLA B*5401	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.424301	0.122535	-4.301767	26564.467257
HLA B*0702	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.424980	0.123142	-4.301838	26606.032169
HLA B*4403	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.579050	0.276822	-4.302227	37935.860563
HLA A*6802	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.298716	-0.003611	-4.302327	19893.740031
HLA B*7301	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.555308	0.252948	-4.302360	35917.689718
HLA A*0216	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.469277	0.166895	-4.302382	29463.022815
HLA B*3501	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.323966	0.021584	-4.302383	21084.647933
HLA B*4501	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.624120	0.321711	-4.302409	42084.300320
HLA B*3501	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.473079	0.170588	-4.302490	29722.050572
HLA A*3301	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.579454	0.276822	-4.302632	37971.176344
HLA A*0250	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.592719	0.289933	-4.302786	39148.871177
HLA A*0101	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.384896	0.082100	-4.302796	24260.265434
HLA A*0219	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.426000	0.123142	-4.302858	26668.573647
HLA A*2602	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.579767	0.276822	-4.302944	37998.507016
HLA A*3001	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.299367	-0.003611	-4.302978	19923.573930
HLA B*4501	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.645442	0.342354	-4.303088	44201.976315
HLA A*6901	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.385210	0.082100	-4.303110	24277.858687
HLA B*1501	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.385342	0.082100	-4.303242	24285.214870
HLA B*1503	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.225558	-0.077849	-4.303408	16809.630779
HLA A*0211	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.543359	0.239809	-4.303550	34942.897452
HLA A*2602	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.591547	0.287962	-4.303584	39043.329962
HLA A*0202	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.564789	0.261006	-4.303783	36710.353487
HLA A*2402	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.529069	0.225072	-4.303998	33811.882095
HLA B*5301	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.592054	0.287962	-4.304092	39088.980168
HLA B*5101	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.482601	0.178488	-4.304113	30380.941715
HLA B*4801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.410350	0.106226	-4.304124	25724.673344
HLA B*1502	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.604074	0.299836	-4.304238	40185.956065
HLA A*6802	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.387767	0.083388	-4.304379	24421.178550

HLA B*3801	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.581235	0.276822	-4.304413	38127.204287
HLA B*1501	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.372349	0.067914	-4.304435	23569.441862
HLA B*0803	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.484702	0.180214	-4.304488	30528.233240
HLA A*1101	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.483489	0.178924	-4.304565	30443.132426
HLA A*0212	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.441511	0.136944	-4.304567	27638.284837
HLA A*2601	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.387978	0.083388	-4.304590	24433.071874
HLA B*5701	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.411149	0.106226	-4.304923	25772.033882
HLA B*5401	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.562646	0.257713	-4.304932	36529.677329
HLA B*3901	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.462443	0.157454	-4.304989	29002.981809
HLA B*1502	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.602453	0.297408	-4.305045	40036.228611
HLA B*1801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.484018	0.178924	-4.305094	30480.211132
HLA A*0212	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.427717	0.122535	-4.305183	26774.246772
HLA A*0219	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.436206	0.131008	-4.305198	27302.722259
HLA B*1503	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.502713	0.197447	-4.305266	31820.926698
HLA A*0101	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.380960	0.075603	-4.305358	24041.422506
HLA B*0802	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.457105	0.151627	-4.305477	28648.680251
HLA A*0216	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.436530	0.131008	-4.305522	27323.113118
HLA A*2601	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.169523	-0.136008	-4.305531	14774.845801
HLA B*1509	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.457276	0.151627	-4.305649	28659.996477
HLA B*5301	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.579273	0.273594	-4.305680	37955.362310
HLA A*0202	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.575458	0.269593	-4.305865	37623.359968
HLA B*4002	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.574356	0.268381	-4.305975	37528.021548
HLA B*5301	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.591408	0.285370	-4.306038	39030.869966
HLA A*0216	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.476763	0.170588	-4.306174	29975.246369
HLA A*0203	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.421790	0.115588	-4.306202	26411.283757
HLA B*5401	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.537621	0.231300	-4.306321	34484.304500
HLA A*6801	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.552801	0.246392	-4.306409	35710.957420
HLA B*0802	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.477139	0.170588	-4.306550	30001.203643
HLA B*7301	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.564312	0.257713	-4.306598	36670.060031
HLA B*0802	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.437735	0.131008	-4.306728	27399.047540
HLA A*0219	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.473821	0.166895	-4.306926	29772.904616
HLA A*2602	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.632343	0.325371	-4.306973	42888.742081
HLA A*8001	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.418531	0.111406	-4.307125	26213.847918
HLA B*4801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.430071	0.122535	-4.307537	26919.776251
HLA B*1801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.473979	0.166266	-4.307713	29783.698135
HLA B*5301	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.535340	0.227561	-4.307779	34303.633315
HLA A*3002	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.539151	0.231300	-4.307851	34605.966739
HLA A*0211	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.438873	0.131008	-4.307865	27470.882837
HLA B*5101	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.465342	0.157454	-4.307888	29197.247727
HLA A*2601	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.390097	0.082100	-4.307997	24552.589793
HLA A*2603	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.547931	0.239809	-4.308122	35312.707042
HLA A*6802	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.376054	0.067914	-4.308140	23771.382277
HLA A*0206	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.459863	0.151627	-4.308235	28831.213070
HLA A*2403	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.430830	0.122535	-4.308296	26966.856834
HLA B*4403	1:450-458	9	PIRVAATGT	0.779142	-0.415371	-4.672233	0.363771	-4.308461	47014.612939
HLA A*3301	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.566327	0.257713	-4.308614	36840.666538
HLA A*0206	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.554871	0.245974	-4.308897	35881.566102
HLA B*4801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.424538	0.115588	-4.308951	26578.986016
HLA A*3002	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.597966	0.288865	-4.309100	39624.668697
HLA A*3301	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.638689	0.329580	-4.309109	43520.038174
HLA B*4501	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.548991	0.239809	-4.309182	35398.970296
HLA B*5301	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.599119	0.289933	-4.309186	39730.061858
HLA A*0301	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.368762	0.059535	-4.309226	23375.539052
HLA A*2301	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.540579	0.231300	-4.309279	34719.980526
HLA A*0250	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.594127	0.284825	-4.309302	39275.939791
HLA A*3201	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.594768	0.285370	-4.309398	39333.989273
HLA A*1101	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.403097	0.093574	-4.309523	25298.630298
HLA A*2501	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.447084	0.137558	-4.309526	27995.231732
HLA B*4002	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.631239	0.321711	-4.309528	42779.829633
HLA B*5101	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.461204	0.151627	-4.309577	28920.411732
HLA B*0803	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.458209	0.148579	-4.309630	28721.616444
HLA B*1501	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.304475	-0.005447	-4.309922	20159.280422
HLA B*4402	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.425513	0.115588	-4.309926	26638.725639
HLA A*3101	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.385593	0.075603	-4.309991	24299.276634
HLA A*6801	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.607415	0.297408	-4.310007	40496.293254

HLA A*0202	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.441253	0.131008	-4.310245	27621.842524
HLA B*0803	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.507722	0.197447	-4.310275	32190.070301
HLA A*2602	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.476622	0.166266	-4.310356	29965.518182
HLA A*0301	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.357228	0.046803	-4.310425	22762.922136
HLA A*2601	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.307062	-0.003611	-4.310673	20279.713211
HLA B*1801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.527690	0.217015	-4.310676	33704.679223
HLA A*0206	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.479166	0.168455	-4.310711	30141.598771
HLA A*8001	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.441748	0.131008	-4.310740	27653.390490
HLA A*6801	1:245-253	9	AHLPTVLGE	0.997208	-0.650029	-4.657932	0.347179	-4.310753	45491.635404
HLA A*0216	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.417018	0.106226	-4.310792	26122.678603
HLA A*2501	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.475290	0.164416	-4.310873	29873.742566
HLA A*8001	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.448503	0.137558	-4.310945	28086.857812
HLA B*7301	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.595907	0.284825	-4.311083	39437.329158
HLA B*5301	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.587999	0.276822	-4.311177	38725.686800
HLA A*2602	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.600085	0.288865	-4.311220	39818.498519
HLA B*3901	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.481892	0.170588	-4.311303	30331.346267
HLA A*2603	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.507381	0.196045	-4.311336	32164.829219
HLA A*8001	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.433901	0.122535	-4.311367	27158.207763
HLA A*0101	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.379294	0.067914	-4.311380	23949.385573
HLA A*6802	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.157071	-0.154364	-4.311435	14357.230951
HLA B*4403	1:258-266	9	LSKRDPQSN	0.849492	-0.507138	-4.653975	0.342354	-4.311621	45079.077190
HLA B*3801	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.564587	0.252948	-4.311639	36693.277950
HLA A*3201	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.523515	0.211872	-4.311643	33382.216033
HLA B*3501	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.379595	0.067914	-4.311681	23965.975447
HLA B*5401	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.480355	0.168455	-4.311900	30224.221536
HLA A*1101	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.469555	0.157454	-4.312101	29481.837039
HLA A*2601	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.380037	0.067914	-4.312122	23990.362661
HLA A*0202	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.558748	0.246392	-4.312356	36203.290107
HLA B*5801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.359246	0.046803	-4.312444	22868.949762
HLA B*1509	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.573554	0.261006	-4.312548	37458.854716
HLA A*2402	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.581099	0.268538	-4.312561	38115.242855
HLA A*2403	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.449551	0.136944	-4.312607	28154.707901
HLA B*2705	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.479624	0.166895	-4.312730	30173.412777
HLA B*4501	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.540448	0.227561	-4.312887	34709.463569
HLA B*4402	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.435475	0.122535	-4.312941	27256.824718
HLA B*3501	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.485045	0.171999	-4.313045	30552.355301
HLA B*0803	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.479373	0.166266	-4.313107	30155.951706
HLA A*0250	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.307828	-0.005447	-4.313275	20315.510555
HLA B*3801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.527935	0.214632	-4.313303	33723.647771
HLA A*6801	1:88-96	9	SQRAEIYRD	1.080908	-0.733693	-4.660831	0.347215	-4.313616	45796.344567
HLA A*0201	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.389284	0.075603	-4.313682	24506.674710
HLA B*1502	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.560245	0.246392	-4.313852	36328.265458
HLA B*1503	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.482557	0.168455	-4.314101	30377.819082
HLA A*2402	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.587748	0.273594	-4.314154	38703.276608
HLA A*2902	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.397548	0.083388	-4.314160	24977.417027
HLA A*3301	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.539238	0.225072	-4.314166	34612.894367
HLA B*0802	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.493183	0.178924	-4.314259	31130.300430
HLA B*1517	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.451886	0.137558	-4.314328	28306.515669
HLA B*4001	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.408031	0.093574	-4.314457	25587.680957
HLA A*0203	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.437113	0.122535	-4.314578	27359.795843
HLA B*1502	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.599418	0.284825	-4.314593	39757.368011
HLA A*0219	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.437214	0.122535	-4.314679	27366.161163
HLA A*3201	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.587903	0.273190	-4.314713	38717.098184
HLA B*3801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.546033	0.231300	-4.314732	35158.685350
HLA A*3201	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.604713	0.289933	-4.314780	40245.132820
HLA B*1517	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.242310	-0.072551	-4.314861	17470.687777
HLA A*2902	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.446212	0.131008	-4.315204	27939.099723
HLA A*0250	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.550391	0.235091	-4.315300	35513.291184
HLA B*5101	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.481570	0.166266	-4.315304	30308.874372
HLA B*5101	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.494229	0.178924	-4.315305	31205.333818
HLA B*4002	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.640729	0.325371	-4.315358	43724.879432
HLA A*0202	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.190936	-0.124662	-4.315598	15521.588424
HLA A*6801	1:73-81	9	DEGPEVGGP	0.594745	-0.247282	-4.663112	0.347463	-4.315649	46037.545834
HLA A*0201	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.398064	0.082100	-4.315965	25007.162237
HLA A*6802	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.367507	0.051538	-4.315969	23308.107353

HLA B*1502	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.589569	0.273594	-4.315975	38865.887093
HLA B*4001	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.391702	0.075603	-4.316099	24643.478301
HLA A*1101	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.483043	0.166895	-4.316148	30411.856648
HLA A*0202	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.584698	0.268538	-4.316161	38432.452782
HLA A*0301	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.367916	0.051538	-4.316378	23330.058087
HLA B*2705	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.487049	0.170588	-4.316460	30693.669088
HLA B*0802	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.465062	0.148579	-4.316483	29178.457265
HLA B*4501	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.569546	0.252948	-4.316598	37114.727264
HLA A*2902	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.423133	0.106226	-4.316908	26493.138911
HLA B*5301	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.590349	0.273190	-4.317159	38935.756186
HLA B*5401	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.563424	0.245974	-4.317450	36595.148649
HLA A*0250	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.594322	0.276822	-4.317499	39293.579465
HLA A*2601	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.393175	0.075603	-4.317573	24727.210922
HLA B*4601	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.393203	0.075603	-4.317601	24728.816232
HLA A*6801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.440846	0.123142	-4.317704	27596.003036
HLA B*1801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.424078	0.106226	-4.317852	26550.818236
HLA A*2402	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.570876	0.252948	-4.317928	37228.546625
HLA B*0802	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.482427	0.164416	-4.318011	30368.781692
HLA B*4403	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.643687	0.325371	-4.318316	44023.708305
HLA A*3201	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.618345	0.299836	-4.318509	41528.388334
HLA B*5401	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.497382	0.178488	-4.318893	31432.711153
HLA A*3301	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.603966	0.284825	-4.319142	40175.956837
HLA B*4501	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.644685	0.325371	-4.319315	44125.044193
HLA B*4601	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.401450	0.082100	-4.319350	25202.871176
HLA A*3001	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.232719	-0.086740	-4.319459	17089.108401
HLA B*1517	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.486572	0.166895	-4.319677	30659.979573
HLA A*0216	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.468281	0.148579	-4.319702	29395.518190
HLA B*0801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.403165	0.083388	-4.319777	25302.599630
HLA B*0803	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.477270	0.157454	-4.319816	30010.293998
HLA A*3301	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.588243	0.268381	-4.319862	38747.481105
HLA B*1517	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.477498	0.157454	-4.320044	30026.046310
HLA B*1517	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.492185	0.171999	-4.320185	31058.807773
HLA A*0219	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.426449	0.106226	-4.320223	26696.144228
HLA A*0250	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.577983	0.257713	-4.320270	37842.801015
HLA A*2602	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.588751	0.268381	-4.320370	38792.785398
HLA A*2603	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.654776	0.334311	-4.320465	45162.314572
HLA B*1801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.264494	-0.055990	-4.320484	18386.278739
HLA A*6802	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.426799	0.106226	-4.320573	26717.671957
HLA A*3101	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.322009	0.001267	-4.320743	20989.845054
HLA B*2705	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.472449	0.151627	-4.320822	29678.989273
HLA A*2402	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.590574	0.269593	-4.320982	38955.982698
HLA A*2902	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.388930	0.067914	-4.321015	24486.663547
HLA B*1801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.492086	0.170588	-4.321498	31051.751537
HLA A*1101	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.444732	0.123142	-4.321591	27844.038927
HLA A*2602	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.590330	0.268538	-4.321792	38934.071118
HLA B*4801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.433290	0.111406	-4.321884	27120.034664
HLA B*3501	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.444516	0.122535	-4.321982	27830.184124
HLA B*4002	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.621966	0.299836	-4.322129	41876.042644
HLA B*1503	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.479674	0.157454	-4.322220	30176.840903
HLA B*4402	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.433638	0.111406	-4.322232	27141.757383
HLA A*3002	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.494320	0.171999	-4.322321	31211.918391
HLA B*1509	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.445519	0.123142	-4.322378	27894.546791
HLA A*3201	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.553753	0.231300	-4.322453	35789.286088
HLA A*3301	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.622306	0.299836	-4.322470	41908.904520
HLA A*6901	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.382036	0.059535	-4.322501	24101.064499
HLA A*0250	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.592108	0.269593	-4.322516	39093.844212
HLA B*4002	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.578437	0.255887	-4.322549	37882.333644
HLA A*0203	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.429024	0.106226	-4.322798	26854.902226
HLA A*1101	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.491266	0.168455	-4.322811	30993.179548
HLA A*3002	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.562641	0.239809	-4.322832	36529.282088
HLA B*5401	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.487277	0.164416	-4.322860	30709.780101
HLA A*0101	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.382403	0.059535	-4.322867	24121.413002
HLA B*1502	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.612861	0.289933	-4.322928	41007.319221
HLA B*1509	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.453959	0.131008	-4.322951	28441.903584
HLA A*2602	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.596554	0.273594	-4.322960	39496.044507

HLA B*0802	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.460758	0.137558	-4.323200	28890.700323
HLA B*5301	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.608423	0.284825	-4.323599	40590.387917
HLA B*1801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.504097	0.180214	-4.323883	31922.483400
HLA A*3201	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.608848	0.284825	-4.324024	40630.153082
HLA A*3002	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.549146	0.225072	-4.324074	35411.611850
HLA B*4402	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.301529	-0.022687	-4.324216	20022.982689
HLA A*0250	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.592776	0.268538	-4.324238	39153.954493
HLA A*6801	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.592621	0.268381	-4.324239	39139.976964
HLA A*2301	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.541385	0.217015	-4.324371	34784.466455
HLA A*6901	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.295502	-0.028903	-4.324405	19747.055322
HLA B*5801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.346033	0.021584	-4.324449	22183.635299
HLA B*4002	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.628220	0.303652	-4.324568	42483.468071
HLA B*3801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.585708	0.261006	-4.324702	38521.960434
HLA A*8001	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.406901	0.082100	-4.324801	25521.184357
HLA A*2402	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.536700	0.211872	-4.324828	34411.251932
HLA B*5701	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.400555	0.075603	-4.324952	25150.977329
HLA B*0802	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.496959	0.171999	-4.324960	31402.117505
HLA B*3901	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.504097	0.178924	-4.325172	31922.483400
HLA A*3201	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.598811	0.273594	-4.325218	39701.915317
HLA A*0216	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.447836	0.122535	-4.325301	28043.738058
HLA A*3001	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.278990	-0.046382	-4.325372	19010.352167
HLA A*0212	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.320064	-0.005447	-4.325511	20896.033655
HLA A*0202	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.556981	0.231300	-4.325681	36056.305742
HLA B*0802	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.462812	0.136944	-4.325867	29027.626031
HLA A*3002	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.493012	0.166895	-4.326117	31118.008820
HLA B*1502	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.492403	0.166266	-4.326138	31074.438003
HLA A*0250	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.540878	0.214632	-4.326246	34743.843291
HLA A*6802	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.348058	0.021584	-4.326474	22287.326373
HLA A*2301	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.483936	0.157454	-4.326482	30474.440369
HLA B*1502	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.603348	0.276822	-4.326526	40118.835098
HLA A*3301	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.599960	0.273190	-4.326770	39807.083231
HLA B*4801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.420464	0.093574	-4.326891	26330.821058
HLA B*1503	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.505532	0.178488	-4.327044	32028.175910
HLA A*2501	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.499149	0.171999	-4.327149	31560.847328
HLA B*4402	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.420746	0.093574	-4.327173	26347.920227
HLA A*2301	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.539095	0.211872	-4.327222	34601.473884
HLA A*2602	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.539182	0.211872	-4.327309	34608.400613
HLA B*1502	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.573566	0.245974	-4.327592	37459.867970
HLA B*5101	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.507828	0.180214	-4.327614	32197.907767
HLA B*5701	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.409748	0.082100	-4.327648	25689.071090
HLA B*2705	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.450829	0.123142	-4.327687	28237.688680
HLA B*1801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.479455	0.151627	-4.327828	30161.662159
HLA B*1509	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.559201	0.231300	-4.327901	36241.110015
HLA A*0301	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.344919	0.016864	-4.328055	22126.822954
HLA A*6901	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.344921	0.016864	-4.328057	22126.942658
HLA B*4402	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.434359	0.106226	-4.328134	27186.872844
HLA B*5301	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.585957	0.257713	-4.328244	38544.057119
HLA B*1509	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.496802	0.168455	-4.328346	31390.737475
HLA A*0212	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.444114	0.115588	-4.328526	27804.450575
HLA A*2601	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.380244	0.051538	-4.328706	24001.786478
HLA A*2603	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.586439	0.257713	-4.328726	38586.827242
HLA B*5101	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.493202	0.164416	-4.328786	31131.647751
HLA B*1801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.444490	0.115588	-4.328902	27828.528033
HLA B*1502	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.585051	0.255887	-4.329163	38463.652736
HLA A*1101	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.466789	0.137558	-4.329231	29294.709618
HLA A*2601	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.388777	0.059535	-4.329242	24478.054502
HLA B*5401	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.543916	0.214632	-4.329284	34987.728002
HLA B*5801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.346359	0.016864	-4.329495	22200.323103
HLA A*3301	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.617812	0.287962	-4.329849	41477.420913
HLA B*3801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.555123	0.225072	-4.330051	35902.342451
HLA B*4801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.389712	0.059535	-4.330177	24530.815860
HLA B*4001	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.377011	0.046803	-4.330208	23823.780362
HLA B*5701	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.413738	0.083388	-4.330350	25926.137865
HLA B*0802	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.497337	0.166895	-4.330442	31429.480417
HLA A*3201	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.547611	0.217015	-4.330597	35286.735453

HLA B*4002	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.619626	0.288865	-4.330760	41651.010883
HLA A*2301	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.526814	0.196045	-4.330769	33636.735508
HLA A*3001	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.308126	-0.022687	-4.330813	20329.473243
HLA A*3301	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.599521	0.268538	-4.330983	39766.832788
HLA A*8001	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.446621	0.115588	-4.331033	27965.411758
HLA B*0702	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.453674	0.122535	-4.331140	28423.291703
HLA A*2602	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.616038	0.284825	-4.331213	41308.353296
HLA B*2705	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.462257	0.131008	-4.331249	28990.589127
HLA A*2402	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.545920	0.214632	-4.331288	35149.556715
HLA B*5801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.354820	0.023199	-4.331621	22637.047946
HLA A*3001	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.290503	-0.041216	-4.331719	19521.025950
HLA B*5101	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.502417	0.170588	-4.331828	31799.243480
HLA B*4403	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.605080	0.273190	-4.331890	40279.111742
HLA A*2501	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.443478	0.111406	-4.332072	27763.716894
HLA A*2501	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.438847	0.106226	-4.332621	27469.248127
HLA B*1503	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.503371	0.170588	-4.332782	31869.164575
HLA B*5301	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.572676	0.239809	-4.332867	37383.140891
HLA B*5401	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.448595	0.115588	-4.333007	28092.784362
HLA A*3001	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.304153	-0.028903	-4.333056	20144.344810
HLA A*1101	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.470217	0.136944	-4.333273	29526.848523
HLA A*6901	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.356476	0.023199	-4.333278	22723.549863
HLA B*4002	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.573106	0.239809	-4.333297	37420.168890
HLA A*2501	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.500265	0.166895	-4.333370	31642.053446
HLA A*1101	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.464475	0.131008	-4.333467	29139.020885
HLA B*4002	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.568569	0.235091	-4.333478	37031.293974
HLA B*1509	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.531214	0.197447	-4.333768	33979.299834
HLA A*2501	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.504487	0.170588	-4.333898	31951.163994
HLA B*4403	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.607570	0.273594	-4.333977	40510.755146
HLA B*2705	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.471716	0.137558	-4.334158	29628.936793
HLA B*4403	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.634110	0.299836	-4.334274	43063.579030
HLA B*4501	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.634213	0.299836	-4.334377	43073.830895
HLA B*1501	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.381282	0.046803	-4.334479	24059.247526
HLA B*3801	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.546481	0.211872	-4.334609	35195.033202
HLA A*0201	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.402550	0.067914	-4.334635	25266.761359
HLA B*3901	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.386197	0.051538	-4.334660	24333.084424
HLA A*0301	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.356251	0.021584	-4.334667	22711.751466
HLA A*0101	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.381515	0.046803	-4.334712	24072.136606
HLA A*2603	1:464-472	9	LFESLELLG	0.981509	-0.656138	-4.660178	0.325371	-4.334807	45727.520958
HLA A*0202	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.560153	0.225072	-4.335081	36320.601523
HLA B*5101	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.507189	0.171999	-4.335189	32150.563714
HLA B*4001	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.417330	0.082100	-4.335230	26141.481032
HLA B*1517	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.458385	0.123142	-4.335243	28733.272366
HLA A*0202	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.531308	0.196045	-4.335263	33986.653599
HLA B*5101	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.472252	0.136944	-4.335307	29665.505293
HLA A*0203	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.410951	0.075603	-4.335349	25760.324939
HLA B*4801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.410963	0.075603	-4.335361	25761.021751
HLA A*2403	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.428974	0.093574	-4.335401	26851.851477
HLA B*4002	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.593163	0.257713	-4.335450	39188.920157
HLA B*4002	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.609112	0.273594	-4.335518	40654.778660
HLA A*2602	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.625459	0.289933	-4.335526	42214.273310
HLA A*0201	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.387168	0.051538	-4.335630	24387.512231
HLA A*3002	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.484382	0.148579	-4.335803	30505.780508
HLA B*5401	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.466886	0.131008	-4.335878	29301.208065
HLA A*3001	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.301893	-0.034117	-4.336010	20039.779658
HLA A*2601	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.357696	0.021584	-4.336112	22787.441164
HLA B*5801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.354200	0.017995	-4.336204	22604.740548
HLA B*3801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.553347	0.217015	-4.336332	35755.806177
HLA B*0802	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.452039	0.115588	-4.336451	28316.471201
HLA A*6801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.533923	0.197447	-4.336476	34191.911593
HLA A*0250	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.597597	0.261006	-4.336591	39591.027670
HLA B*1801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.501024	0.164416	-4.336607	31697.392922
HLA B*1517	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.200644	-0.136008	-4.336653	15872.459784
HLA A*2601	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.383512	0.046803	-4.336709	24183.084955
HLA A*2603	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.624679	0.287962	-4.336717	42138.521012
HLA B*1517	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.412377	0.075603	-4.336775	25845.055808

HLA B*5801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.358680	0.021903	-4.336777	22839.153036
HLA A*3201	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.605547	0.268538	-4.337010	40322.498293
HLA A*0201	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.396664	0.059535	-4.337129	24926.661644
HLA A*6801	1:387-395	9	NDDQYVIDP	0.524632	-0.195052	-4.666784	0.329580	-4.337205	46428.473966
HLA A*2301	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.515886	0.178488	-4.337398	32800.947233
HLA B*2705	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.421019	0.083388	-4.337631	26364.459978
HLA B*7301	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.607239	0.269593	-4.337646	40479.865553
HLA A*6801	1:228-236	9	LHQALIRIG	0.881868	-0.547557	-4.672221	0.334311	-4.337910	47013.341237
HLA A*2301	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.489546	0.151627	-4.337919	30870.688049
HLA B*4403	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.577781	0.239809	-4.337973	37825.198730
HLA B*1509	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.355445	0.017415	-4.338030	22669.646799
HLA A*0216	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.389592	0.051538	-4.338055	24524.048635
HLA B*0801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.385044	0.046803	-4.338241	24268.535300
HLA B*4001	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.406175	0.067914	-4.338260	25478.557362
HLA B*4002	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.611543	0.273190	-4.338353	40883.052814
HLA A*3002	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.608031	0.269593	-4.338438	40553.733032
HLA A*2403	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.360376	0.021903	-4.338473	22928.535845
HLA A*0203	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.360177	0.021584	-4.338593	22917.994798
HLA B*4501	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.553236	0.214632	-4.338604	35746.715890
HLA A*3201	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.534661	0.196045	-4.338616	34250.042931
HLA A*0203	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.420728	0.082100	-4.338628	26346.779937
HLA B*1502	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.518967	0.180214	-4.338753	33034.410436
HLA A*0250	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.585473	0.246392	-4.339081	38501.126116
HLA B*4403	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.570392	0.231300	-4.339092	37187.080859
HLA B*1509	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.230429	-0.108675	-4.339103	16999.206781
HLA B*4403	1:244-252	9	FAHLPTVLG	0.888690	-0.566979	-4.660859	0.321711	-4.339148	45799.317701
HLA B*7301	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.600299	0.261006	-4.339293	39838.105988
HLA B*4601	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.361025	0.021584	-4.339441	22962.796688
HLA A*2301	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.506371	0.166895	-4.339476	32090.092672
HLA B*2705	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.462180	0.122535	-4.339645	28985.414005
HLA A*2902	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.262041	-0.077849	-4.339890	18282.727130
HLA B*3901	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.507017	0.166895	-4.340122	32137.869259
HLA A*3002	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.601262	0.261006	-4.340256	39926.567150
HLA A*2603	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.477284	0.136944	-4.340340	30011.268128
HLA B*3901	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.492197	0.151627	-4.340569	31059.647908
HLA B*4002	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.565822	0.225072	-4.340751	36797.841106
HLA A*3201	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.610392	0.269593	-4.340799	40774.821666
HLA A*2501	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.463357	0.122535	-4.340822	29064.081311
HLA B*3901	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.512912	0.171999	-4.340913	32577.063736
HLA A*8001	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.424416	0.083388	-4.341028	26571.510020
HLA B*1509	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.489668	0.148579	-4.341089	30879.373634
HLA B*5301	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.576292	0.235091	-4.341201	37695.685460
HLA B*0702	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.423350	0.082100	-4.341250	26506.328088
HLA B*0802	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.464684	0.123142	-4.341542	29153.054122
HLA A*0212	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.393147	0.051538	-4.341609	24725.605716
HLA B*7301	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.566687	0.225072	-4.341615	36871.172662
HLA B*4002	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.639025	0.297408	-4.341617	43553.718917
HLA B*1502	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.611454	0.269593	-4.341861	40874.649112
HLA A*2501	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.409833	0.067914	-4.341918	25694.074678
HLA B*1509	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.559032	0.217015	-4.342018	36226.996416
HLA A*6901	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.388911	0.046803	-4.342108	24485.603809
HLA A*0250	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.598036	0.255887	-4.342149	39631.100171
HLA B*4501	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.645801	0.303652	-4.342149	44238.578013
HLA B*4402	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.410141	0.067914	-4.342226	25712.290406
HLA B*1509	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.514312	0.171999	-4.342313	32682.271284
HLA A*0250	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.573674	0.231300	-4.342374	37469.191202
HLA A*0206	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.509352	0.166895	-4.342458	32311.153891
HLA A*6802	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.418265	0.075603	-4.342663	26197.827832
HLA B*4402	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.418296	0.075603	-4.342693	26199.670352
HLA B*5401	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.559838	0.217015	-4.342824	36294.281347
HLA B*1509	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.509113	0.166266	-4.342847	32293.329234
HLA B*7301	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.364906	0.021903	-4.343003	23168.938130
HLA A*2902	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.394552	0.051538	-4.343014	24805.725391
HLA A*2602	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.616266	0.273190	-4.343076	41330.035924
HLA A*2501	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.474094	0.131008	-4.343086	29791.594381

HLA B*1502	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.600973	0.257713	-4.343260	39900.008196
HLA B*1503	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.188906	-0.154364	-4.343271	15449.207572
HLA B*1501	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.402836	0.059535	-4.343301	25283.443090
HLA B*0803	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.522244	0.178924	-4.343320	33284.657465
HLA A*1101	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.458937	0.115588	-4.343349	28769.824893
HLA B*5801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.360863	0.017415	-4.343448	22954.226681
HLA B*7301	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.612131	0.268538	-4.343593	40938.383418
HLA B*4001	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.395186	0.051538	-4.343649	24841.984846
HLA B*0803	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.474752	0.131008	-4.343744	29836.755959
HLA A*0202	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.508309	0.164416	-4.343893	32233.635933
HLA A*3101	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.234583	-0.109399	-4.343981	17162.578878
HLA A*0301	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.362477	0.017995	-4.344482	23039.696949
HLA A*2603	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.629338	0.284825	-4.344514	42593.008535
HLA B*0803	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.508974	0.164416	-4.344558	32283.023382
HLA B*5301	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.605761	0.261006	-4.344755	40342.353942
HLA A*2301	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.523774	0.178924	-4.344849	33402.087294
HLA A*0212	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.366466	0.021584	-4.344883	23252.314472
HLA B*5701	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.413061	0.067914	-4.345147	25885.775147
HLA A*2402	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.572878	0.227561	-4.345317	37400.537461
HLA A*0211	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.509787	0.164416	-4.345371	32343.508034
HLA A*2403	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.362340	0.016864	-4.345476	23032.468835
HLA A*0301	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.368762	0.023199	-4.345563	23375.539052
HLA B*1517	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.468103	0.122535	-4.345568	29383.434661
HLA A*0206	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.543042	0.197447	-4.345595	34917.386746
HLA A*0212	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.413526	0.067914	-4.345612	25913.517759
HLA B*4403	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.603517	0.257713	-4.345804	40134.464910
HLA A*2402	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.591796	0.245974	-4.345822	39065.725712
HLA A*1101	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.497473	0.151627	-4.345846	31439.343705
HLA A*2403	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.367484	0.021584	-4.345900	23306.846445
HLA B*5301	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.601798	0.255887	-4.345910	39975.845147
HLA B*7301	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.619127	0.273190	-4.345937	41603.268867
HLA B*4601	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.413886	0.067914	-4.345971	25934.975595
HLA B*5701	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.362989	0.016864	-4.346125	23066.884979
HLA B*5101	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.468664	0.122535	-4.346130	29421.450941
HLA A*0301	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.368033	0.021903	-4.346130	23336.369592
HLA A*0202	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.592111	0.245974	-4.346137	39094.055706
HLA B*3801	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.573698	0.227561	-4.346137	37471.218299
HLA B*3501	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.457572	0.111406	-4.346166	28679.539110
HLA B*0803	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.516805	0.170588	-4.346217	32870.403416
HLA A*3101	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.397923	0.051538	-4.346386	24999.046396
HLA B*1503	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.469592	0.123142	-4.346450	29484.389045
HLA B*1509	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.414527	0.067914	-4.346613	25973.307253
HLA A*2301	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.544139	0.197447	-4.346692	35005.714198
HLA A*3201	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.469879	0.123142	-4.346737	29503.855356
HLA A*0101	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.368325	0.021584	-4.346741	23352.029494
HLA A*2902	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.428918	0.082100	-4.346818	26848.365330
HLA B*5401	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.543046	0.196045	-4.347001	34917.764547
HLA A*3201	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.608031	0.261006	-4.347025	40553.733032
HLA B*4801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.430429	0.083388	-4.347041	26941.921571
HLA A*2603	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.647060	0.299836	-4.347224	44367.042808
HLA A*3002	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.469912	0.122535	-4.347377	29506.090017
HLA B*5101	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.514284	0.166895	-4.347389	32680.149663
HLA A*0201	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.394256	0.046803	-4.347453	24788.822428
HLA B*3901	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.463084	0.115588	-4.347496	29045.847952
HLA B*1509	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.527993	0.180214	-4.347780	33728.209109
HLA A*2402	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.499581	0.151627	-4.347953	31592.279255
HLA B*4601	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.399528	0.051538	-4.347991	25091.587592
HLA A*2403	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.399556	0.051538	-4.348019	25093.216557
HLA A*2403	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.416054	0.067914	-4.348140	26064.801288
HLA B*0702	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.123431	-0.224761	-4.348191	13287.117032
HLA A*0301	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.275948	-0.072551	-4.348498	18877.634759
HLA A*3101	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.343108	-0.005447	-4.348555	22034.723641
HLA A*0250	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.594545	0.245974	-4.348571	39313.779177
HLA B*5401	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.546159	0.197447	-4.348713	35168.957898
HLA A*0219	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.464400	0.115588	-4.348812	29133.976877

HLA B*4501	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.637796	0.288865	-4.348931	43430.663411
HLA A*0201	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.343559	-0.005447	-4.349006	22057.622971
HLA A*2501	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.472155	0.123142	-4.349014	29658.926052
HLA A*0211	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.521217	0.171999	-4.349218	33206.061431
HLA A*2602	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.480289	0.131008	-4.349281	30219.643611
HLA A*3101	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.409079	0.059535	-4.349543	25649.493725
HLA B*4501	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.647032	0.297408	-4.349624	44364.162652
HLA B*4002	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.626669	0.276822	-4.349847	42332.050190
HLA A*3201	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.584961	0.235091	-4.349870	38455.746353
HLA A*0301	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.367617	0.017415	-4.350202	23314.034538
HLA B*5401	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.473652	0.123142	-4.350510	29761.309970
HLA A*3101	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.434047	0.083388	-4.350659	27167.318510
HLA A*1101	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.457001	0.106226	-4.350776	28641.861671
HLA A*2602	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.596840	0.245974	-4.350866	39522.120756
HLA B*1517	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.499546	0.148579	-4.350967	31589.715698
HLA A*0211	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.508439	0.157454	-4.350985	32243.228282
HLA B*0803	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.502725	0.151627	-4.351097	31821.787448
HLA B*0803	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.433323	0.082100	-4.351223	27122.088771
HLA A*2402	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.582844	0.231300	-4.351544	38268.757211
HLA B*4403	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.639568	0.287962	-4.351606	43608.181344
HLA A*0202	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.518539	0.166895	-4.351644	33001.900769
HLA A*2301	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.532154	0.180214	-4.351941	34052.909147
HLA B*1501	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.403668	0.051538	-4.352130	25331.909825
HLA B*4403	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.598151	0.245974	-4.352177	39641.607157
HLA B*0803	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.524201	0.171999	-4.352202	33434.991180
HLA B*5101	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.445841	0.093574	-4.352268	27915.228632
HLA A*0301	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.347010	-0.005447	-4.352457	22233.616099
HLA B*3501	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.404025	0.051538	-4.352488	25352.748901
HLA B*4501	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.613578	0.261006	-4.352572	41075.037815
HLA A*2301	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.517254	0.164416	-4.352837	32904.385590
HLA A*0101	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.370496	0.017415	-4.353081	23469.052401
HLA B*4402	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.435210	0.082100	-4.353110	27240.167237
HLA A*2603	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.621656	0.268538	-4.353118	41846.149412
HLA B*2705	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.468709	0.115588	-4.353121	29424.475266
HLA A*3001	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.297199	-0.055990	-4.353189	19824.336965
HLA A*2402	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.549599	0.196045	-4.353554	35448.604728
HLA A*2301	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.524154	0.170588	-4.353566	33431.373783
HLA B*0801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.405160	0.051538	-4.353622	25419.081662
HLA A*6801	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.593466	0.239809	-4.353658	39216.278698
HLA B*5401	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.532617	0.178924	-4.353693	34089.220318
HLA B*2705	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.490639	0.136944	-4.353694	30948.444064
HLA B*1502	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.465159	0.111406	-4.353753	29184.929924
HLA A*2602	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.611673	0.257713	-4.353959	40895.219127
HLA B*1801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.520881	0.166895	-4.353987	33180.382686
HLA B*0702	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.469630	0.115588	-4.354042	29486.941272
HLA A*2402	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.511556	0.157454	-4.354102	32475.532782
HLA A*2301	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.477298	0.123142	-4.354157	30012.242290
HLA A*2402	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.518574	0.164416	-4.354158	33004.578927
HLA A*2603	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.651691	0.297408	-4.354283	44842.654966
HLA A*0101	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.376454	0.021903	-4.354551	23793.254425
HLA B*5801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.351140	-0.003611	-4.354751	22446.079521
HLA A*0250	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.594789	0.239809	-4.354980	39335.904452
HLA A*3301	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.582558	0.227561	-4.354997	38243.507917
HLA A*3201	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.533663	0.178488	-4.355174	34171.385592
HLA A*3301	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.645117	0.289933	-4.355184	44168.988995
HLA B*4402	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.438656	0.083388	-4.355268	27457.213712
HLA A*2402	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.521676	0.166266	-4.355410	33241.109931
HLA B*3901	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.504019	0.148579	-4.355440	31916.784904
HLA B*1502	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.616773	0.261006	-4.355767	41378.359790
HLA B*5801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.357158	0.001267	-4.355891	22759.228090
HLA A*3301	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.629808	0.273594	-4.356215	42639.118167
HLA B*3801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.552320	0.196045	-4.356275	35671.374947
HLA B*5101	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.487326	0.131008	-4.356318	30713.269166
HLA A*0206	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.479469	0.123142	-4.356328	30162.641202
HLA A*0301	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.357634	0.001267	-4.356368	22784.236174

HLA B*4801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.438539	0.082100	-4.356439	27449.787692
HLA A*1101	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.505356	0.148579	-4.356777	32015.183380
HLA A*2402	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.573886	0.217015	-4.356871	37487.439020
HLA B*0702	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.424863	0.067914	-4.356948	26598.836358
HLA A*2402	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.535697	0.178488	-4.357209	34331.852902
HLA B*1501	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.374126	0.016864	-4.357261	23666.035354
HLA B*1502	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.571922	0.214632	-4.357290	37318.278621
HLA B*4403	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.618434	0.261006	-4.357428	41536.926443
HLA B*0801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.379487	0.021903	-4.357584	23960.012139
HLA B*5701	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.417328	0.059535	-4.357792	26141.339610
HLA A*2602	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.553910	0.196045	-4.357865	35802.260716
HLA B*1501	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.379459	0.021584	-4.357875	23958.456737
HLA B*3901	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.379593	0.021584	-4.358009	23965.845794
HLA B*0702	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.451731	0.093574	-4.358158	28296.410555
HLA A*0202	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.515734	0.157454	-4.358280	32789.415044
HLA B*0803	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.525294	0.166895	-4.358399	33519.206073
HLA B*0803	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.526976	0.168455	-4.358521	33649.293851
HLA A*0250	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.583657	0.225072	-4.358586	38340.456583
HLA A*0211	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.556044	0.197447	-4.358597	35978.560495
HLA B*4501	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.616372	0.257713	-4.358658	41340.098740
HLA B*7301	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.570557	0.211872	-4.358684	37201.165985
HLA B*7301	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.489697	0.131008	-4.358689	30881.378347
HLA A*0201	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.380312	0.021584	-4.358728	24005.552337
HLA A*3201	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.583986	0.225072	-4.358915	38369.506049
HLA A*6802	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.441086	0.082100	-4.358986	27611.234953
HLA B*4002	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.644391	0.285370	-4.359022	44095.215330
HLA B*3901	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.495977	0.136944	-4.359032	31331.187068
HLA B*1503	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.324967	-0.034117	-4.359085	21133.295918
HLA A*2602	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.586723	0.227561	-4.359163	38612.094317
HLA A*0212	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.441274	0.082100	-4.359174	27623.187437
HLA B*4801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.410770	0.051538	-4.359233	25749.596415
HLA B*4403	1:165-173	9	LAWNDLVRG	0.863670	-0.566262	-4.656684	0.297408	-4.359276	45361.141328
HLA A*2402	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.539853	0.180214	-4.359640	34661.989155
HLA A*2301	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.525926	0.166266	-4.359660	33568.020749
HLA A*0101	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.376564	0.016864	-4.359700	23799.304981
HLA A*6901	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.381752	0.021903	-4.359849	24085.293187
HLA B*4403	1:331-339	9	HIRMLDVGD	1.128015	-0.824363	-4.663683	0.303652	-4.360031	46098.106730
HLA A*0101	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.378077	0.017995	-4.360082	23882.365619
HLA B*4601	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.419922	0.059535	-4.360386	26297.936394
HLA B*4002	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.606379	0.245974	-4.360405	40399.793930
HLA A*2602	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.585690	0.225072	-4.360618	38520.293273
HLA B*1501	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.378056	0.017415	-4.360641	23881.202839
HLA B*0801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.420232	0.059535	-4.360696	26316.722599
HLA A*0203	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.428617	0.067914	-4.360703	26829.780190
HLA B*4002	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.648924	0.287962	-4.360961	44557.788150
HLA A*6901	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.378975	0.017995	-4.360980	23931.771415
HLA B*1501	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.362371	0.001267	-4.361105	23034.088732
HLA B*5301	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.592465	0.231300	-4.361165	39126.004425
HLA B*1502	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.589068	0.227561	-4.361507	38821.127477
HLA B*1517	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.467814	0.106226	-4.361588	29363.888947
HLA B*5401	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.513311	0.151627	-4.361684	32607.038029
HLA B*0702	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.445244	0.083388	-4.361856	27876.896328
HLA A*2603	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.618009	0.255887	-4.362122	41496.273809
HLA B*0803	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.499182	0.136944	-4.362237	31563.237788
HLA A*2603	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.652258	0.289933	-4.362324	44901.158199
HLA B*4002	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.631171	0.268538	-4.362633	42773.118569
HLA A*6801	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.650740	0.287962	-4.362777	44744.512035
HLA B*4601	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.409650	0.046803	-4.362847	25683.234801
HLA B*1509	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.541750	0.178488	-4.363261	34813.646604
HLA B*3501	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.209088	-0.154364	-4.363453	16184.089985
HLA A*6901	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.358064	-0.005447	-4.363512	22806.803958
HLA B*5301	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.609542	0.245974	-4.363568	40695.047216
HLA A*2403	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.423124	0.059535	-4.363589	26492.565618
HLA B*1503	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.530801	0.166895	-4.363906	33946.962164
HLA A*2501	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.446184	0.082100	-4.364084	27937.286013

HLA A*0206	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.536169	0.171999	-4.364170	34369.205242
HLA A*2402	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.532763	0.168455	-4.364307	34100.656208
HLA A*0212	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.440017	0.075603	-4.364414	27543.353489
HLA A*3301	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.610893	0.246392	-4.364500	40821.833834
HLA A*6801	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.579158	0.214632	-4.364526	37945.302262
HLA B*7301	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.579177	0.214632	-4.364545	37946.944537
HLA B*0702	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.416113	0.051538	-4.364576	26068.326719
HLA B*4501	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.650134	0.285370	-4.364764	44682.103384
HLA B*5401	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.416489	0.051538	-4.364952	26090.900768
HLA B*0803	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.471296	0.106226	-4.365070	29600.258902
HLA B*5401	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.042200	-0.322910	-4.365109	11020.458559
HLA A*0202	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.562810	0.197447	-4.365363	36543.513454
HLA B*4402	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.425006	0.059535	-4.365471	26607.615508
HLA B*5101	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.387182	0.021584	-4.365598	24388.303846
HLA B*5101	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.514185	0.148579	-4.365606	32672.725075
HLA A*1101	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.488346	0.122535	-4.365811	30785.465323
HLA A*2603	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.639429	0.273594	-4.365836	43594.264554
HLA A*0211	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.534299	0.168455	-4.365844	34221.520318
HLA A*3101	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.383272	0.017415	-4.365857	24169.744200
HLA A*2603	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.618850	0.252948	-4.365902	41576.719191
HLA B*4601	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.382788	0.016864	-4.365924	24142.823542
HLA A*2602	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.517594	0.151627	-4.365967	32930.207033
HLA A*0101	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.360769	-0.005447	-4.366216	22949.260025
HLA A*2603	1:264-272	9	QSNLFAHRD	1.146458	-0.869636	-4.643104	0.276822	-4.366282	43964.683390
HLA B*5401	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.459893	0.093574	-4.366320	28833.240799
HLA A*2403	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.441972	0.075603	-4.366369	27667.606311
HLA A*3201	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.606410	0.239809	-4.366601	40402.635290
HLA A*0211	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.537330	0.170588	-4.366742	34461.179280
HLA A*2601	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.383653	0.016864	-4.366788	24190.935898
HLA B*4403	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.636408	0.269593	-4.366815	43292.026708
HLA A*2602	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.622821	0.255887	-4.366934	41958.586178
HLA B*0802	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.489502	0.122535	-4.366967	30867.515079
HLA A*2601	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.384994	0.017995	-4.366999	24265.778365
HLA B*5101	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.384501	0.017415	-4.367086	24238.226233
HLA A*6802	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.426815	0.059535	-4.367280	26718.683754
HLA B*4002	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.652142	0.284825	-4.367318	44889.257173
HLA B*4001	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.384771	0.017415	-4.367356	24253.310428
HLA A*0203	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.213035	-0.154364	-4.367400	16331.851383
HLA B*5701	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.414372	0.046803	-4.367569	25964.035069
HLA B*1501	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.389503	0.021903	-4.367600	24519.007603
HLA B*4403	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.595184	0.227561	-4.367623	39371.671587
HLA A*2602	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.637352	0.269593	-4.367760	43386.279596
HLA A*0206	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.538364	0.170588	-4.367776	34543.306698
HLA B*5801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.362411	-0.005447	-4.367858	23036.207231
HLA A*3101	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.389827	0.021903	-4.367924	24537.319463
HLA B*1503	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.389841	0.021584	-4.368258	24538.115941
HLA A*0101	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.391500	0.023199	-4.368301	24632.015578
HLA B*4001	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.391601	0.023199	-4.368402	24637.746273
HLA A*3301	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.638614	0.269593	-4.369021	43512.504791
HLA A*6901	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.370317	0.001267	-4.369050	23459.405046
HLA B*4501	1:426-434	9	PLIEAALKD	1.179547	-0.891585	-4.657048	0.287962	-4.369086	45399.194085
HLA B*5101	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.492309	0.123142	-4.369168	31067.714360
HLA A*3001	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.244732	-0.124662	-4.369394	17568.404469
HLA A*0301	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.365926	-0.003611	-4.369537	23223.400202
HLA B*1503	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.506484	0.136944	-4.369539	32098.426739
HLA B*3901	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.387574	0.017995	-4.369579	24410.347452
HLA A*0203	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.421181	0.051538	-4.369643	26374.303203
HLA B*4403	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.616193	0.246392	-4.369801	41323.105187
HLA B*4501	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.604979	0.235091	-4.369888	40269.742894
HLA A*0212	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.393128	0.023199	-4.369930	24724.535637
HLA B*4501	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.638666	0.268538	-4.370128	43517.683852
HLA B*5701	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.421677	0.051538	-4.370139	26404.426306
HLA B*1509	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.534577	0.164416	-4.370160	34243.373178
HLA A*3301	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.493442	0.123142	-4.370300	31148.831206
HLA A*3002	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.452627	0.082100	-4.370527	28354.794353

HLA A*2602	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.631561	0.261006	-4.370555	42811.547862
HLA A*2601	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.394268	0.023199	-4.371069	24789.492961
HLA A*3201	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.598689	0.227561	-4.371129	39690.748174
HLA A*0201	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.393133	0.021903	-4.371230	24724.803153
HLA A*2301	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.543427	0.171999	-4.371428	34948.379961
HLA A*3201	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.535852	0.164416	-4.371436	34344.113371
HLA B*4402	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.350835	-0.020620	-4.371455	22430.299067
HLA B*4402	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.423411	0.051538	-4.371873	26510.056654
HLA B*4001	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.388739	0.016864	-4.371875	24475.935817
HLA A*0216	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.453999	0.082100	-4.371899	28444.519452
HLA A*2603	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.645094	0.273190	-4.371904	44166.599567
HLA A*6801	1:306-314	9	AFDVADVNS	1.123303	-0.850113	-4.645327	0.273190	-4.372137	44190.260606
HLA A*0219	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.440285	0.067914	-4.372370	27560.345468
HLA A*0211	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.509526	0.136944	-4.372582	32324.091663
HLA A*0219	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.448231	0.075603	-4.372628	28069.237514
HLA A*2403	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.454924	0.082100	-4.372824	28505.213502
HLA B*1509	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.530282	0.157454	-4.372828	33906.399921
HLA A*0212	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.419691	0.046803	-4.372889	26283.997735
HLA A*0201	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.390891	0.017995	-4.372896	24597.526320
HLA A*0202	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.541430	0.168455	-4.372975	34788.042060
HLA A*2402	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.570451	0.197447	-4.373004	37192.110649
HLA A*6801	1:65-73	9	LRWLGLDWD	0.855521	-0.555685	-4.672999	0.299836	-4.373162	47097.602192
HLA B*7301	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.553441	0.180214	-4.373227	35763.544412
HLA B*1509	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.543927	0.170588	-4.373339	34988.674413
HLA B*1801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.545354	0.171999	-4.373354	35103.759172
HLA B*1517	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.488987	0.115588	-4.373399	30830.965960
HLA B*0801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.367970	-0.005447	-4.373417	23332.961168
HLA A*0206	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.522108	0.148579	-4.373529	33274.215258
HLA A*2601	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.375131	0.001267	-4.373865	23720.895951
HLA A*2403	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.420671	0.046803	-4.373868	26343.359363
HLA A*2402	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.540765	0.166895	-4.373870	34734.822366
HLA A*3301	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.542419	0.168455	-4.373964	34867.364326
HLA B*4801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.442030	0.067914	-4.374116	27671.348531
HLA A*0206	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.480409	0.106226	-4.374184	30227.982492
HLA A*0201	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.397564	0.023199	-4.374365	24978.362920
HLA B*0702	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.450007	0.075603	-4.374404	28184.272299
HLA B*3501	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.351740	-0.022687	-4.374427	22477.065744
HLA B*4501	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.659254	0.284825	-4.374430	45630.403573
HLA B*5401	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.545032	0.170588	-4.374443	35077.751491
HLA A*3201	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.620645	0.245974	-4.374671	41748.917846
HLA A*8001	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.421515	0.046803	-4.374712	26394.571839
HLA B*1503	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.434263	0.059535	-4.374728	27180.843316
HLA A*3002	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.450348	0.075603	-4.374745	28206.389672
HLA B*4501	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.600047	0.225072	-4.374976	39815.052049
HLA A*2402	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.554275	0.178924	-4.375350	35832.294677
HLA B*7301	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.592428	0.217015	-4.375413	39122.617894
HLA B*4501	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.621881	0.246392	-4.375489	41867.887827
HLA B*4601	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.397658	0.021903	-4.375755	24983.768712
HLA A*0203	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.435447	0.059535	-4.375912	27255.055299
HLA A*0201	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.392778	0.016864	-4.375914	24704.613875
HLA B*5801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.353373	-0.022687	-4.376060	22561.735730
HLA B*0702	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.392985	0.016864	-4.376121	24716.377807
HLA B*4002	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.645735	0.269593	-4.376143	44231.877398
HLA A*0250	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.572229	0.196045	-4.376184	37344.735290
HLA A*1101	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.423089	0.046803	-4.376286	26490.415877
HLA B*4002	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.629242	0.252948	-4.376294	42583.562221
HLA A*2603	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.482714	0.106226	-4.376488	30388.831901
HLA B*4403	1:303-311	9	MVAAFDVAD	1.026583	-0.773635	-4.629519	0.252948	-4.376571	42610.754837
HLA B*0803	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.470177	0.093574	-4.376604	29524.133120
HLA A*2301	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.545208	0.168455	-4.376753	35091.986884
HLA A*0101	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.373233	-0.003611	-4.376844	23617.433690
HLA B*5301	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.555379	0.178488	-4.376890	35923.519513
HLA A*3201	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.555828	0.178924	-4.376903	35960.658068
HLA B*4403	1:31-39	9	WAYARHTGG	0.740729	-0.451864	-4.665805	0.288865	-4.376940	46323.852920
HLA A*0202	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.528708	0.151627	-4.377080	33783.724372

HLA A*2602	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.594216	0.217015	-4.377201	39284.014804
HLA B*4501	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.646840	0.269593	-4.377247	44344.486590
HLA A*3101	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.398854	0.021584	-4.377270	25052.659663
HLA B*3801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.549592	0.171999	-4.377593	35448.029413
HLA A*3301	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.612753	0.235091	-4.377663	40997.115619
HLA B*3801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.542116	0.164416	-4.377700	34843.039728
HLA A*2602	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.609060	0.231300	-4.377759	40649.940315
HLA B*5101	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.493465	0.115588	-4.377877	31150.516369
HLA B*1502	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.617694	0.239809	-4.377886	41466.203018
HLA A*0212	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.395351	0.017415	-4.377936	24851.394095
HLA B*0803	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.515802	0.137558	-4.378244	32794.559673
HLA A*2601	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.322434	-0.055990	-4.378425	21010.408165
HLA B*3501	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.401683	0.023199	-4.378484	25216.372920
HLA B*4403	1:341-349	9	TVRLRDHLD	1.047805	-0.762435	-4.664367	0.285370	-4.378997	46170.735107
HLA B*4001	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.400590	0.021584	-4.379006	25153.018372
HLA B*1801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.472668	0.093574	-4.379094	29693.925113
HLA A*2601	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.401239	0.021903	-4.379336	25190.603136
HLA A*2602	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.502689	0.122535	-4.380155	31819.205267
HLA A*0216	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.495772	0.115588	-4.380185	31316.444190
HLA B*5301	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.594923	0.214632	-4.380291	39348.036087
HLA A*6802	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.403541	0.023199	-4.380342	25324.510593
HLA A*3301	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.641570	0.261006	-4.380564	43809.645227
HLA B*3801	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.578058	0.197447	-4.380612	37849.352794
HLA A*8001	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.397482	0.016864	-4.380617	24973.633812
HLA A*3101	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.398711	0.017995	-4.380715	25044.393568
HLA B*1502	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.612020	0.231300	-4.380720	40927.975552
HLA A*3301	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.636695	0.255887	-4.380807	43320.609157
HLA B*7301	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.559939	0.178924	-4.381015	36302.725295
HLA B*4801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.404406	0.023199	-4.381207	25374.977841
HLA A*2603	1:369-377	9	VQTRIVVLG	0.809010	-0.540629	-4.649638	0.268381	-4.381257	44631.128460
HLA B*5401	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.553318	0.171999	-4.381319	35753.485033
HLA B*4601	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.404565	0.023199	-4.381367	25384.314314
HLA A*0219	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.432961	0.051538	-4.381424	27099.502147
HLA B*5701	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.398896	0.017415	-4.381481	25055.099360
HLA A*0201	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.398969	0.017415	-4.381554	25059.301617
HLA B*3901	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.492984	0.111406	-4.381578	31115.988746
HLA B*5301	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.579064	0.197447	-4.381617	37937.091955
HLA A*6801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.533315	0.151627	-4.381687	34144.036758
HLA B*5301	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.550269	0.168455	-4.381813	35503.302195
HLA A*0250	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.518971	0.136944	-4.382027	33034.767863
HLA A*3301	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.593957	0.211872	-4.382085	39260.644320
HLA A*2902	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.428911	0.046803	-4.382108	26847.929593
HLA B*0802	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.475999	0.093574	-4.382426	29922.589776
HLA A*2501	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.498049	0.115588	-4.382461	31481.041757
HLA B*1502	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.561398	0.178924	-4.382474	36424.890890
HLA B*4501	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.638365	0.255887	-4.382478	43487.559775
HLA B*5401	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.519784	0.136944	-4.382840	33096.660965
HLA A*0219	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.464985	0.082100	-4.382885	29173.248607
HLA B*5401	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.228645	-0.154364	-4.383010	16929.549347
HLA B*4402	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.404690	0.021584	-4.383106	25391.593653
HLA B*5401	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.563339	0.180214	-4.383125	36588.022217
HLA B*4402	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.401220	0.017995	-4.383225	25189.512933
HLA A*0212	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.310680	-0.072551	-4.383231	20449.373912
HLA B*2705	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.434916	0.051538	-4.383379	27221.752678
HLA A*3201	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.580892	0.197447	-4.383445	38097.101640
HLA B*4801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.430325	0.046803	-4.383522	26935.509211
HLA A*2902	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.405146	0.021584	-4.383562	25418.256589
HLA B*3801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.562124	0.178488	-4.383636	36485.831690
HLA B*3901	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.506253	0.122535	-4.383719	32081.413654
HLA B*1501	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.407225	0.023199	-4.384026	25540.244687
HLA A*2301	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.521011	0.136944	-4.384066	33190.256776
HLA B*0702	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.405660	0.021584	-4.384077	25448.389115
HLA B*0803	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.507245	0.123142	-4.384103	32154.738329
HLA A*0250	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.535765	0.151627	-4.384138	34337.239538
HLA A*0202	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.556175	0.171999	-4.384176	35989.461987

HLA B*4403	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.640165	0.255887	-4.384277	43668.145051
HLA A*2902	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.402491	0.017995	-4.384496	25263.344331
HLA A*0212	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.444037	0.059535	-4.384501	27799.487191
HLA A*3002	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.536209	0.151627	-4.384582	34372.366258
HLA B*1509	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.563637	0.178924	-4.384713	36613.168872
HLA A*3301	1:330-338	9	EHIRMLDVG	0.833919	-0.594110	-4.624590	0.239809	-4.384781	42129.859243
HLA B*7301	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.521751	0.136944	-4.384806	33246.865013
HLA B*4001	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.444530	0.059535	-4.384995	27831.087488
HLA A*0211	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.552003	0.166895	-4.385108	35645.332404
HLA B*5801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.364544	-0.020620	-4.385164	23149.643594
HLA A*3301	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.551439	0.166266	-4.385173	35599.081484
HLA B*0702	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.444918	0.059535	-4.385382	27855.941490
HLA B*3901	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.479166	0.093574	-4.385593	30141.598771
HLA B*3901	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.461256	0.075603	-4.385654	28923.853974
HLA A*2601	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.403102	0.017415	-4.385687	25298.904025
HLA A*3301	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.564812	0.178924	-4.385888	36712.339530
HLA B*3801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.492154	0.106226	-4.385929	31056.623529
HLA B*4601	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.403447	0.017415	-4.386032	25319.031074
HLA B*5801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.357327	-0.028903	-4.386230	22768.094809
HLA A*6801	1:398-406	9	AAKELGPDG	0.727431	-0.453837	-4.660070	0.273594	-4.386476	45716.142857
HLA A*6801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.535204	0.148579	-4.386625	34292.871430
HLA A*0219	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.408381	0.021584	-4.386797	25608.314823
HLA B*5801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.352752	-0.034117	-4.386870	22529.535816
HLA B*5701	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.408515	0.021584	-4.386931	25616.212715
HLA A*2301	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.535552	0.148579	-4.386972	34320.339479
HLA B*1501	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.405007	0.017995	-4.387012	25410.144797
HLA A*6802	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.433847	0.046803	-4.387044	27154.828747
HLA A*0301	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.364645	-0.022687	-4.387332	23155.029412
HLA A*0301	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.366779	-0.020620	-4.387398	23269.050887
HLA B*7301	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.553849	0.166266	-4.387584	35797.225227
HLA B*1502	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.471124	0.083388	-4.387736	29588.571420
HLA A*0211	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.510281	0.122535	-4.387746	32380.273621
HLA B*5101	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.494039	0.106226	-4.387813	31191.662604
HLA A*3101	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.411090	0.023199	-4.387891	25768.548521
HLA B*5701	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.411097	0.023199	-4.387898	25768.966740
HLA A*2603	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.622992	0.235091	-4.387902	41975.159815
HLA A*0202	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.525479	0.137558	-4.387921	33533.534614
HLA B*1502	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.525211	0.136944	-4.388267	33512.859942
HLA B*4601	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.382995	-0.005447	-4.388442	24154.319958
HLA A*1101	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.440029	0.051538	-4.388491	27544.098532
HLA B*1501	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.301764	-0.086740	-4.388503	20033.817831
HLA B*7301	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-3.983810	-0.404745	-4.388555	9634.080360
HLA B*3501	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.471460	0.082100	-4.389360	29611.470413
HLA B*2705	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.411081	0.021584	-4.389497	25767.990907
HLA A*6802	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.407382	0.017415	-4.389967	25549.503747
HLA B*4002	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.604685	0.214632	-4.390053	40242.520244
HLA B*1509	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.527622	0.137558	-4.390064	33699.391819
HLA A*8001	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.458145	0.067914	-4.390231	28717.421470
HLA B*1501	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.312541	-0.077849	-4.390390	20537.179932
HLA B*4801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.412159	0.021584	-4.390575	25832.055922
HLA B*5801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.318090	-0.072551	-4.390641	20801.291098
HLA B*4403	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.675548	0.284825	-4.390723	47374.865321
HLA B*1503	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-3.985986	-0.404745	-4.390731	9682.463927
HLA B*0801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.407667	0.016864	-4.390802	25566.233840
HLA A*0216	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.318464	-0.072551	-4.391015	20819.191492
HLA A*2603	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.652121	0.261006	-4.391115	44887.071613
HLA B*4403	1:12-20	9	CPSPTGTPH	0.697462	-0.428924	-4.659661	0.268538	-4.391123	45673.129552
HLA B*4402	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.438111	0.046803	-4.391309	27422.773937
HLA A*0101	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.370709	-0.020620	-4.391329	23480.609057
HLA A*0203	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.438243	0.046803	-4.391440	27431.083029
HLA B*4001	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.386047	-0.005447	-4.391494	24324.660967
HLA B*5301	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.608555	0.217015	-4.391540	40602.686792
HLA A*0201	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.388020	-0.003611	-4.391631	24435.451233
HLA A*2403	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.409636	0.017995	-4.391640	25682.401154
HLA A*2501	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.475076	0.083388	-4.391688	29859.039345

HLA B*3801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.570660	0.178924	-4.391736	37210.022223
HLA A*2603	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.638238	0.246392	-4.391846	43474.857435
HLA A*2902	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.408780	0.016864	-4.391916	25631.877141
HLA A*6901	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.371816	-0.020620	-4.392435	23540.515296
HLA A*6801	1:71-79	9	DWDEGPEVG	0.976127	-0.691302	-4.677592	0.284825	-4.392767	47598.365581
HLA B*5701	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.414715	0.021903	-4.392812	25984.550703
HLA B*1509	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.529941	0.136944	-4.392997	33879.813020
HLA A*6801	1:45-53	9	IEDTDAQRD	1.146721	-0.856788	-4.683059	0.289933	-4.393126	48201.359987
HLA A*0212	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.415039	0.021903	-4.393136	26003.957094
HLA A*6801	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.618441	0.225072	-4.393370	41537.600579
HLA A*2602	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.475546	0.082100	-4.393446	29891.363647
HLA A*8001	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.415258	0.021584	-4.393674	26017.043489
HLA B*0702	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.415669	0.021903	-4.393766	26041.686283
HLA B*1502	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.545398	0.151627	-4.393771	35107.367599
HLA B*1509	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.469649	0.075603	-4.394046	29488.217468
HLA A*0211	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.517352	0.123142	-4.394211	32911.862821
HLA A*2501	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.487899	0.093574	-4.394326	30753.837849
HLA B*4403	1:108-116	9	YHAFSTPEE	0.844648	-0.609557	-4.629500	0.235091	-4.394410	42608.910722
HLA B*5701	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.395783	0.001267	-4.394517	24876.143976
HLA B*4601	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.390960	-0.003611	-4.394571	24601.385649
HLA A*2902	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.454236	0.059535	-4.394701	28460.065750
HLA B*2705	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.470501	0.075603	-4.394899	29546.183025
HLA A*0203	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.416872	0.021903	-4.394969	26113.918183
HLA B*1503	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.532626	0.137558	-4.395069	34089.958001
HLA B*3801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.532652	0.137558	-4.395094	34091.986714
HLA A*8001	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.446800	0.051538	-4.395262	27976.912145
HLA B*4501	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.607302	0.211872	-4.395430	40485.778757
HLA A*3001	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.295096	-0.100479	-4.395575	19728.582485
HLA B*5401	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.562538	0.166895	-4.395643	36520.587871
HLA A*2402	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.518203	0.122535	-4.395668	32976.379904
HLA A*0201	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.396995	0.001267	-4.395729	24945.682815
HLA A*2301	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.518382	0.122535	-4.395847	32989.940983
HLA A*3301	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.641840	0.245974	-4.395866	43836.909319
HLA A*0301	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.366974	-0.028903	-4.395877	23279.501521
HLA B*0801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.397324	0.001267	-4.396058	24964.583445
HLA A*8001	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.417988	0.021903	-4.396085	26181.109342
HLA A*0219	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.419320	0.023199	-4.396122	26261.540759
HLA A*0250	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.533731	0.137558	-4.396173	34176.747052
HLA B*4402	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.419541	0.023199	-4.396342	26274.898926
HLA B*0801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.414438	0.017995	-4.396443	25967.968318
HLA A*3101	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.271787	-0.124662	-4.396448	18697.633435
HLA A*6801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.413331	0.016864	-4.396467	25901.884663
HLA B*4601	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.414525	0.017995	-4.396530	25973.166740
HLA A*2301	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.534189	0.137558	-4.396631	34212.820096
HLA B*5401	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.502861	0.106226	-4.396635	31831.773850
HLA A*0203	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.413531	0.016864	-4.396667	25913.798139
HLA B*4001	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.414868	0.017995	-4.396873	25993.689589
HLA B*5801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.350948	-0.046382	-4.397330	22436.124404
HLA B*0801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.374743	-0.022687	-4.397430	23699.731375
HLA A*3301	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.628737	0.231300	-4.397436	42534.060960
HLA A*6901	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.374833	-0.022687	-4.397520	23704.603967
HLA A*3101	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.393922	-0.003611	-4.397533	24769.786861
HLA A*3002	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.566104	0.168455	-4.397649	36821.737530
HLA A*3002	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.528933	0.131008	-4.397925	33801.274485
HLA B*3801	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.534999	0.136944	-4.398055	34276.734933
HLA A*6801	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.667727	0.269593	-4.398134	46529.303626
HLA A*3002	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.325881	-0.072551	-4.398432	21177.816646
HLA B*1801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.509846	0.111406	-4.398440	32347.882700
HLA B*0802	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.474110	0.075603	-4.398508	29792.722587
HLA B*5701	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.416517	0.017995	-4.398522	26092.594610
HLA A*0211	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.547151	0.148579	-4.398572	35249.339406
HLA A*2603	1:403-411	9	GPDGAAVLD	1.323933	-1.054340	-4.668185	0.269593	-4.398592	46578.414609
HLA A*0203	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.416867	0.017995	-4.398872	26113.635637
HLA A*0219	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.458611	0.059535	-4.399075	28748.198848
HLA B*0803	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.514679	0.115588	-4.399091	32709.864890

HLA B*1501	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.376637	-0.022687	-4.399324	23803.296615
HLA B*4801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.421247	0.021903	-4.399344	26378.298603
HLA B*2705	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.481488	0.082100	-4.399388	30303.136048
HLA A*0301	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.321673	-0.077849	-4.399523	20973.613292
HLA B*1501	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.396072	-0.003611	-4.399683	24892.702478
HLA B*5101	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.451323	0.051538	-4.399785	28269.787091
HLA B*1509	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.566800	0.166895	-4.399905	36880.748415
HLA B*4002	1:449-457	9	SPIRVAATG	0.976487	-0.730095	-4.646501	0.246392	-4.400109	44309.954622
HLA A*3002	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.597778	0.197447	-4.400331	39607.523202
HLA A*2601	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.377699	-0.022687	-4.400386	23861.573322
HLA A*2603	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.646379	0.245974	-4.400405	44297.491354
HLA B*3801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.566950	0.166266	-4.400685	36893.519955
HLA B*7301	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.565150	0.164416	-4.400734	36740.950468
HLA B*3801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.512158	0.111406	-4.400752	32520.540333
HLA A*3002	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.538615	0.137558	-4.401057	34563.308160
HLA A*2501	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.395649	-0.005447	-4.401096	24868.474259
HLA A*0216	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.476812	0.075603	-4.401210	29978.651980
HLA A*8001	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.461421	0.059535	-4.401885	28934.809287
HLA B*4601	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.403158	0.001267	-4.401892	25302.188981
HLA B*4402	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.418928	0.016864	-4.402064	26237.825446
HLA B*0802	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.484406	0.082100	-4.402306	30507.430882
HLA A*0301	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.368461	-0.034117	-4.402578	23359.357893
HLA B*5801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.361387	-0.041216	-4.402603	22981.935492
HLA B*1502	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.581167	0.178488	-4.402678	38121.223102
HLA B*0702	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.399084	-0.003611	-4.402695	25065.945332
HLA A*2403	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.426026	0.023199	-4.402827	26670.160709
HLA B*0803	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.478485	0.075603	-4.402882	30094.347661
HLA B*5101	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.514535	0.111406	-4.403130	32699.072310
HLA A*3002	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.496762	0.093574	-4.403188	31387.850661
HLA A*6802	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.421186	0.017995	-4.403190	26374.588568
HLA A*2603	1:132-140	9	YDNFDRHLT	0.730479	-0.502918	-4.631126	0.227561	-4.403566	42768.722236
HLA A*3201	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.572175	0.168455	-4.403720	37340.088868
HLA A*2601	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.374833	-0.028903	-4.403736	23704.603967
HLA A*3301	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.618735	0.214632	-4.404103	41565.699305
HLA A*0250	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.601675	0.197447	-4.404229	39964.600955
HLA B*7301	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.583053	0.178488	-4.404565	38287.187294
HLA A*6802	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.426543	0.021903	-4.404639	26701.921780
HLA A*6801	1:126-134	9	RNPKLGYDN	0.804444	-0.548557	-4.660539	0.255887	-4.404652	45765.633479
HLA B*4001	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.401264	-0.003611	-4.404875	25192.102243
HLA B*3801	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.573489	0.168455	-4.405033	37453.180994
HLA B*3801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.572079	0.166895	-4.405184	37331.807552
HLA B*1509	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.465166	0.059535	-4.405630	29185.403589
HLA A*0202	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.576496	0.170588	-4.405908	37713.431500
HLA B*5101	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.488068	0.082100	-4.405969	30765.819172
HLA A*6901	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.359747	-0.046382	-4.406129	22895.316988
HLA B*7301	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.557813	0.151627	-4.406185	36125.423363
HLA A*3301	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.563936	0.157454	-4.406482	36638.332810
HLA B*0803	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.529239	0.122535	-4.406704	33825.054795
HLA A*6801	1:66-74	9	RWLGLDWDE	0.694093	-0.436380	-4.664520	0.257713	-4.406806	46186.973568
HLA B*0802	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.490331	0.083388	-4.406943	30926.518812
HLA A*2402	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.555590	0.148579	-4.407011	35941.014575
HLA A*2601	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.386432	-0.020620	-4.407052	24346.251914
HLA B*2705	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.453905	0.046803	-4.407102	28438.364850
HLA A*1101	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.489379	0.082100	-4.407280	30858.832829
HLA B*5801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.355875	-0.051442	-4.407317	22692.101082
HLA A*1101	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.483177	0.075603	-4.407574	30421.236007
HLA A*0211	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.459116	0.051538	-4.407578	28781.656084
HLA A*3201	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.578315	0.170588	-4.407726	37871.678303
HLA B*5801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.351916	-0.055990	-4.407906	22486.187477
HLA B*4402	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.409224	0.001267	-4.407958	25658.098345
HLA A*3301	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.283299	-0.124662	-4.407961	19199.906676
HLA A*0301	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.367035	-0.041216	-4.408251	23282.776179
HLA A*2301	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.523882	0.115588	-4.408294	33410.400602
HLA A*2301	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.539325	0.131008	-4.408317	34619.823382
HLA B*0702	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.455234	0.046803	-4.408432	28525.576498

HLA B*5301	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.604624	0.196045	-4.408579	40236.860245
HLA A*0101	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.386319	-0.022687	-4.409006	24339.930630
HLA A*0203	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.432221	0.023199	-4.409023	27053.360803
HLA B*0802	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.477049	0.067914	-4.409135	29995.036756
HLA A*3301	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.560801	0.151627	-4.409174	36374.873388
HLA A*0301	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.363156	-0.046382	-4.409538	23075.746720
HLA B*1801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.491741	0.082100	-4.409641	31027.067333
HLA A*2402	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.546667	0.136944	-4.409723	35210.078114
HLA B*0702	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.433100	0.023199	-4.409901	27108.153240
HLA A*3001	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.301310	-0.108675	-4.409985	20012.911266
HLA B*3901	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.493414	0.083388	-4.410026	31146.809131
HLA A*0212	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.428140	0.017995	-4.410145	26800.331698
HLA B*2705	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.469898	0.059535	-4.410362	29505.132284
HLA B*3501	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.470078	0.059535	-4.410543	29517.425546
HLA A*2501	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.427976	0.017415	-4.410561	26790.184542
HLA A*0101	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.381909	-0.028903	-4.410812	24094.024786
HLA A*0101	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.412298	0.001267	-4.411031	25840.302403
HLA A*3301	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.608574	0.197447	-4.411127	40604.444079
HLA B*1509	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.522594	0.111406	-4.411188	33311.498162
HLA A*6801	1:192-200	9	GDPLYTLVN	1.024887	-0.763881	-4.672231	0.261006	-4.411224	47014.358596
HLA B*0801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.434613	0.023199	-4.411414	27202.761906
HLA B*5701	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.407845	-0.003611	-4.411456	25576.747599
HLA B*1503	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.527056	0.115588	-4.411468	33655.483745
HLA A*0201	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.391082	-0.020620	-4.411701	24608.307343
HLA B*1503	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.487397	0.075603	-4.411794	30718.254232
HLA B*1801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.495711	0.083388	-4.412323	31312.039619
HLA B*0801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.408813	-0.003611	-4.412424	25633.818533
HLA A*2902	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.429926	0.017415	-4.412511	26910.748518
HLA B*0801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.371527	-0.041216	-4.412743	23524.856262
HLA B*7301	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.581226	0.168455	-4.412770	38126.379240
HLA A*3002	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.519051	0.106226	-4.412826	33040.844713
HLA B*0801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.383923	-0.028903	-4.412826	24205.990663
HLA A*3002	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.536141	0.123142	-4.413000	34366.974111
HLA B*4801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.429881	0.016864	-4.413017	26907.982561
HLA A*2602	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.581853	0.168455	-4.413397	38181.490316
HLA A*2603	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.644734	0.231300	-4.413434	44130.057421
HLA B*5101	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.489706	0.075603	-4.414104	30882.046614
HLA B*0803	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.482352	0.067914	-4.414438	30363.524811
HLA B*5401	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.563055	0.148579	-4.414476	36564.079660
HLA A*0250	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.586479	0.171999	-4.414480	38590.376163
HLA B*1503	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.497901	0.083388	-4.414513	31470.314121
HLA A*0219	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.436521	0.021903	-4.414618	27322.521864
HLA B*3801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.585344	0.170588	-4.414756	38489.672045
HLA B*5301	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.572352	0.157454	-4.414898	37355.242373
HLA A*0219	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.432543	0.017415	-4.415128	27073.418963
HLA B*3501	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.461938	0.046803	-4.415135	28969.267293
HLA B*4501	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.632259	0.217015	-4.415244	42880.390054
HLA B*4601	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.392663	-0.022687	-4.415350	24698.065931
HLA B*3801	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.563966	0.148579	-4.415387	36640.909622
HLA A*6901	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.374203	-0.041216	-4.415419	23670.260742
HLA B*5101	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.498869	0.083388	-4.415481	31540.535725
HLA A*0211	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.437132	0.021584	-4.415548	27360.979977
HLA A*1101	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.483482	0.067914	-4.415568	30442.638348
HLA A*2403	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.343094	-0.072551	-4.415644	22034.008420
HLA A*3301	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.611717	0.196045	-4.415672	40899.422877
HLA B*4801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.433760	0.017995	-4.415765	27149.393820
HLA B*1501	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.343563	-0.072551	-4.416114	22057.861631
HLA A*0101	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.374934	-0.041216	-4.416150	23710.118897
HLA B*4001	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.417427	0.001267	-4.416160	26147.279998
HLA B*1509	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.364732	-0.051442	-4.416174	23159.664723
HLA A*0201	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.393612	-0.022687	-4.416299	24752.104938
HLA A*0101	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.360468	-0.055990	-4.416458	22933.373948
HLA B*4402	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.370293	-0.046382	-4.416675	23458.135953
HLA B*4001	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.396107	-0.020620	-4.416727	24894.722561
HLA A*3002	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.411633	-0.005447	-4.417080	25800.771204

HLA A*3001	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.281102	-0.136008	-4.417111	19103.034027
HLA B*5301	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.532709	0.115588	-4.417121	34096.413414
HLA A*0101	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.383004	-0.034117	-4.417122	24154.842653
HLA B*2705	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.485054	0.067914	-4.417140	30553.016448
HLA A*0203	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.434667	0.017415	-4.417252	27206.146887
HLA A*3101	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.396732	-0.020620	-4.417352	24930.572615
HLA A*3301	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.434695	0.016864	-4.417831	27207.913131
HLA A*6801	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.555525	0.137558	-4.417967	35935.570754
HLA B*5301	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.596930	0.178924	-4.418005	39530.246383
HLA A*6801	1:119-127	9	ARHVAAGRN	0.722813	-0.476839	-4.663998	0.245974	-4.418024	46131.536523
HLA B*0803	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.501552	0.083388	-4.418164	31735.999275
HLA B*1517	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.435684	0.017415	-4.418269	27269.951498
HLA A*0211	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.124526	-0.293904	-4.418429	13320.656224
HLA A*0206	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.440374	0.021903	-4.418471	27566.011791
HLA A*0250	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.586977	0.168455	-4.418522	38634.660721
HLA B*4601	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.389693	-0.028903	-4.418596	24529.754211
HLA A*6801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.486548	0.067914	-4.418634	30658.320947
HLA B*4402	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.436081	0.017415	-4.418666	27294.895032
HLA A*0216	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.465692	0.046803	-4.418889	29220.792342
HLA A*0301	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.367505	-0.051442	-4.418947	23307.981260
HLA A*2501	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.470647	0.051538	-4.419109	29556.094865
HLA B*5301	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.599650	0.180214	-4.419437	39778.666927
HLA A*0206	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.470999	0.051538	-4.419462	29580.088878
HLA B*1502	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.550880	0.131008	-4.419872	35553.275254
HLA B*3901	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.487859	0.067914	-4.419945	30751.009606
HLA B*5301	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.571633	0.151627	-4.420005	37293.454687
HLA A*2403	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.416461	-0.003611	-4.420072	26089.207037
HLA B*1801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.471620	0.051538	-4.420082	29622.365662
HLA B*4402	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.416529	-0.003611	-4.420140	26093.300409
HLA A*3002	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.590772	0.170588	-4.420183	38973.689515
HLA A*3301	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.637390	0.217015	-4.420375	43390.035198
HLA A*2601	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.333653	-0.086740	-4.420393	21560.224580
HLA B*1503	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.542971	0.122535	-4.420437	34911.720230
HLA B*1517	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.488355	0.067914	-4.420441	30786.131514
HLA A*0216	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.488454	0.067914	-4.420539	30793.127390
HLA B*3901	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.266254	-0.154364	-4.420618	18460.931212
HLA A*8001	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.386714	-0.034117	-4.420831	24362.062308
HLA B*4402	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.365024	-0.055990	-4.421014	23175.206047
HLA A*0211	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.527246	0.106226	-4.421021	33670.234844
HLA B*3801	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.572758	0.151627	-4.421131	37390.219914
HLA B*4002	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.638226	0.217015	-4.421212	43473.681480
HLA B*1501	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.392487	-0.028903	-4.421390	24688.046929
HLA A*0203	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.417901	-0.003611	-4.421512	26175.869302
HLA B*3801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.552799	0.131008	-4.421791	35710.764228
HLA A*0201	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.392912	-0.028903	-4.421815	24712.233055
HLA B*1509	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.537469	0.115588	-4.421881	34472.180474
HLA A*2602	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.619597	0.197447	-4.422150	41648.307042
HLA B*7301	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.589146	0.166895	-4.422251	38828.058689
HLA B*4002	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.634260	0.211872	-4.422388	43078.491640
HLA A*0206	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.545170	0.122535	-4.422636	35088.949516
HLA A*0202	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.571266	0.148579	-4.422687	37261.994425
HLA B*1517	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.474362	0.051538	-4.422824	29809.973339
HLA A*2501	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.498456	0.075603	-4.422853	31510.518996
HLA B*0802	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.482853	0.059535	-4.423317	30398.533061
HLA A*2902	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.298662	-0.124662	-4.423324	19891.264858
HLA B*1502	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.620774	0.197447	-4.423328	41761.341830
HLA A*2402	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.593936	0.170588	-4.423348	39258.732805
HLA A*0202	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.538972	0.115588	-4.423385	34591.741366
HLA B*3901	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.505544	0.082100	-4.423444	32029.042266
HLA A*6901	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.367462	-0.055990	-4.423453	23305.711685
HLA A*2603	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.635339	0.211872	-4.423467	43185.594448
HLA A*6801	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.602495	0.178924	-4.423571	40040.127448
HLA A*0250	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.588594	0.164416	-4.424177	38778.727013
HLA B*4403	1:455-463	9	ATGTTVSPP	0.121000	0.093632	-4.638847	0.214632	-4.424215	43535.815418
HLA B*7301	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.540056	0.115588	-4.424468	34678.119414

HLA A*0301	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.368576	-0.055990	-4.424566	23365.550919
HLA B*0702	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.419703	-0.005447	-4.425150	26284.708712
HLA A*0216	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.484817	0.059535	-4.425281	30536.326876
HLA A*3002	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.472404	0.046803	-4.425602	29675.938789
HLA B*1502	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.594091	0.168455	-4.425636	39272.752744
HLA A*6801	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.604443	0.178488	-4.425955	40220.102610
HLA A*2603	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.583493	0.157454	-4.426039	38325.940098
HLA B*5701	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.420678	-0.005447	-4.426125	26343.786911
HLA B*4402	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.392179	-0.034117	-4.426296	24670.556820
HLA B*5801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.348479	-0.077849	-4.426328	22308.919208
HLA B*5301	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.563313	0.136944	-4.426369	36585.844974
HLA A*2402	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.598379	0.171999	-4.426380	39662.414915
HLA A*2402	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.557468	0.131008	-4.426460	36096.705907
HLA A*3101	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.385575	-0.041216	-4.426791	24298.225006
HLA B*7301	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.510201	0.083388	-4.426813	32374.318263
HLA A*0219	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.397940	-0.028903	-4.426843	24999.993108
HLA A*0250	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.597512	0.170588	-4.426924	39583.317831
HLA A*3101	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.404298	-0.022687	-4.426985	25368.663939
HLA B*3501	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.448888	0.021903	-4.426985	28111.788143
HLA A*0212	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.444079	0.016864	-4.427215	27802.194382
HLA B*1517	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.510807	0.083388	-4.427419	32419.536313
HLA B*4601	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.393321	-0.034117	-4.427438	24735.506144
HLA B*4801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.444859	0.017415	-4.427444	27852.174306
HLA B*4402	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.276974	-0.150664	-4.427638	18922.316578
HLA B*1502	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.592104	0.164416	-4.427687	39093.421228
HLA A*0216	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.445127	0.017415	-4.427712	27869.356802
HLA A*2603	1:55-63	9	EESYLALLD	1.112493	-0.915046	-4.625253	0.197447	-4.427806	42194.181133
HLA B*3501	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.422405	-0.005447	-4.427852	26448.745414
HLA A*0206	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.124309	-0.303590	-4.427899	13314.028052
HLA A*0203	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.429268	0.001267	-4.428001	26870.015810
HLA A*2402	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.495937	0.067914	-4.428022	31328.305730
HLA A*2301	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.539440	0.111406	-4.428034	34629.001779
HLA B*1801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.503688	0.075603	-4.428085	31892.448244
HLA A*2601	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.387036	-0.041216	-4.428252	24380.125061
HLA A*8001	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.445688	0.017415	-4.428273	27905.414169
HLA B*0802	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.445489	0.016864	-4.428624	27892.585077
HLA A*2602	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.608893	0.180214	-4.428679	40634.329585
HLA A*6901	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.394564	-0.034117	-4.428681	24806.396381
HLA B*4601	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.341945	-0.086740	-4.428684	21975.795898
HLA A*2403	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.430039	0.001267	-4.428772	26917.737466
HLA A*3002	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.350941	-0.077849	-4.428790	22435.760276
HLA B*0801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.377633	-0.051442	-4.429075	23857.959119
HLA A*1101	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.512585	0.083388	-4.429197	32552.575820
HLA A*2602	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.608221	0.178924	-4.429297	40571.507613
HLA A*8001	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.351669	-0.077849	-4.429518	22473.418087
HLA A*6801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.523099	0.093574	-4.429526	33350.266178
HLA B*4601	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.409001	-0.020620	-4.429621	25644.915024
HLA A*0201	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.395550	-0.034117	-4.429668	24862.824402
HLA B*1801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.447115	0.017415	-4.429700	27997.200665
HLA B*2705	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.453061	0.023199	-4.429863	28383.186873
HLA B*5301	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.600632	0.170588	-4.430044	39868.721549
HLA A*0219	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.424745	-0.005447	-4.430192	26591.642493
HLA A*0203	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.343519	-0.086740	-4.430258	22055.594466
HLA A*3201	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.561302	0.131008	-4.430294	36416.812546
HLA A*2402	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.524133	0.093574	-4.430559	33429.746083
HLA A*2902	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.452471	0.021903	-4.430568	28344.672005
HLA A*0250	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.588056	0.157454	-4.430602	38730.715167
HLA B*4801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.432054	0.001267	-4.430788	27042.971545
HLA B*3901	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.490587	0.059535	-4.431052	30944.760875
HLA A*2301	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.537419	0.106226	-4.431194	34468.264392
HLA B*5401	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.127613	-0.303590	-4.431203	13415.684724
HLA A*1101	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.490998	0.059535	-4.431463	30974.071099
HLA B*7301	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.514094	0.082100	-4.431994	32665.832325
HLA A*6901	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.307367	-0.124662	-4.432029	20293.980658
HLA A*0219	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.359493	-0.072551	-4.432044	22881.943893

HLA B*3801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.589500	0.157454	-4.432047	38859.790027
HLA B*1501	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.411706	-0.020620	-4.432325	25805.098526
HLA B*2705	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.449828	0.017415	-4.432413	28172.686673
HLA A*8001	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.433953	0.001267	-4.432686	27161.440259
HLA B*0803	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.484368	0.051538	-4.432830	30504.790327
HLA B*0802	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.484624	0.051538	-4.433087	30522.783633
HLA B*7301	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.556328	0.123142	-4.433186	36002.119648
HLA A*6801	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.613764	0.180214	-4.433550	41092.596267
HLA A*0202	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.485174	0.051538	-4.433636	30561.447321
HLA B*5301	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.599909	0.166266	-4.433643	39802.345771
HLA B*4001	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.404775	-0.028903	-4.433677	25396.539300
HLA A*6801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.556314	0.122535	-4.433779	36000.951062
HLA A*0216	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.455697	0.021903	-4.433794	28555.993784
HLA A*0250	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.600738	0.166895	-4.433843	39878.428571
HLA B*0802	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.455819	0.021584	-4.434236	28564.028122
HLA A*3301	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.614487	0.180214	-4.434274	41161.123712
HLA A*0101	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.388096	-0.046382	-4.434477	24439.681778
HLA A*0219	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.481403	0.046803	-4.434600	30297.234905
HLA A*2603	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.659752	0.225072	-4.434681	45682.766945
HLA B*0702	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.412063	-0.022687	-4.434750	25826.326866
HLA A*0212	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.436018	0.001267	-4.434751	27290.908439
HLA B*4801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.431206	-0.003611	-4.434817	26990.208972
HLA B*4801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.357106	-0.077849	-4.434955	22756.519503
HLA A*0212	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.431361	-0.003611	-4.434972	26999.847619
HLA A*3301	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.517235	0.082100	-4.435135	32902.961548
HLA A*2501	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.457088	0.021903	-4.435185	28647.595369
HLA A*6802	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.414957	-0.020620	-4.435577	25999.033812
HLA B*4002	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.412930	-0.022687	-4.435617	25877.934141
HLA A*3001	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.284958	-0.150664	-4.435622	19273.378668
HLA B*1501	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.389320	-0.046382	-4.435701	24508.663467
HLA A*8001	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.453773	0.017995	-4.435778	28429.750645
HLA B*0802	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.457908	0.021903	-4.436005	28701.734591
HLA B*4403	1:241-249	9	IPKFAHLPT	0.597728	-0.372656	-4.661240	0.225072	-4.436168	45839.473910
HLA B*5701	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.415587	-0.020620	-4.436206	26036.755858
HLA B*1503	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.518384	0.082100	-4.436284	32990.119455
HLA A*0212	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.415728	-0.020620	-4.436347	26045.208587
HLA B*5301	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.600867	0.164416	-4.436451	39890.295920
HLA B*4501	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.358715	-0.077849	-4.436565	22841.006471
HLA B*5301	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.608592	0.171999	-4.436593	40606.201441
HLA B*1501	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.300918	-0.136008	-4.436926	19994.838736
HLA B*0702	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.385600	-0.051442	-4.437043	24299.671006
HLA A*3101	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.390673	-0.046382	-4.437055	24585.153932
HLA A*0211	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.552841	0.115588	-4.437254	35714.241840
HLA A*6802	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.381320	-0.055990	-4.437310	24061.330142
HLA A*3002	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.552940	0.115588	-4.437352	35722.357586
HLA A*6802	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.414765	-0.022687	-4.437452	25987.502915
HLA A*3002	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.594921	0.157454	-4.437467	39347.823219
HLA A*6802	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.438809	0.001267	-4.437543	27466.870541
HLA A*8001	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.433965	-0.003611	-4.437576	27162.174971
HLA A*0201	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.396432	-0.041216	-4.437648	24913.315021
HLA A*2902	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.461127	0.023199	-4.437928	28915.249138
HLA A*2601	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.365430	-0.072551	-4.437981	23196.906126
HLA A*2601	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.391848	-0.046382	-4.438230	24651.745434
HLA B*4403	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.586942	0.148579	-4.438363	38631.525709
HLA A*2602	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.587090	0.148579	-4.438511	38644.694466
HLA A*1101	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.460476	0.021903	-4.438573	28871.950951
HLA A*2402	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.360816	-0.077849	-4.438665	22951.743219
HLA A*2603	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.655775	0.217015	-4.438760	45266.271359
HLA B*5301	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.605665	0.166895	-4.438770	40333.406780
HLA A*0201	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.393098	-0.046382	-4.439479	24722.796857
HLA B*5801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.352860	-0.086740	-4.439600	22535.143100
HLA B*0801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.419043	-0.020620	-4.439662	26244.781610
HLA A*2403	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.411210	-0.028903	-4.440113	25775.659157
HLA A*1101	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.463413	0.023199	-4.440214	29067.855159
HLA A*1101	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.457718	0.017415	-4.440303	28689.160217

HLA A*0206	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.556124	0.115588	-4.440536	35985.178864
HLA A*2602	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.368278	-0.072551	-4.440828	23349.502993
HLA B*4001	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.399632	-0.041216	-4.440848	25097.560982
HLA B*2705	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.462863	0.021903	-4.440960	29031.081034
HLA A*6801	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.658263	0.217015	-4.441248	45526.349405
HLA B*7301	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.563952	0.122535	-4.441418	36639.720302
HLA A*0250	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.572641	0.131008	-4.441633	37380.107435
HLA B*2705	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.436204	-0.005447	-4.441651	27302.574554
HLA B*1502	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.613775	0.171999	-4.441776	41093.707814
HLA B*1503	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.493498	0.051538	-4.441961	31152.875750
HLA B*1517	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.463876	0.021903	-4.441973	29098.850686
HLA A*0219	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.438471	-0.003611	-4.442082	27445.481521
HLA A*0201	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.386117	-0.055990	-4.442108	24328.609099
HLA A*0101	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.369701	-0.072551	-4.442252	23426.177451
HLA A*2602	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.579811	0.137558	-4.442253	38002.413004
HLA B*0802	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.489154	0.046803	-4.442351	30842.810474
HLA A*6801	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.609025	0.166266	-4.442759	40646.641774
HLA B*4403	1:186-194	9	ALTRASGDP	0.162721	0.054294	-4.659933	0.217015	-4.442919	45701.800589
HLA B*0803	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.502454	0.059535	-4.442919	31801.996085
HLA A*2601	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.408950	-0.034117	-4.443067	25641.863010
HLA A*2301	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.536935	0.093574	-4.443362	34429.873074
HLA A*0216	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.466749	0.023199	-4.443551	29292.015563
HLA A*0203	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.420923	-0.022687	-4.443610	26358.612845
HLA B*5101	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.511547	0.067914	-4.443632	32474.830033
HLA A*2602	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.608390	0.164416	-4.443974	40587.313781
HLA A*2301	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.527476	0.083388	-4.444088	33688.090496
HLA B*5701	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.371576	-0.072551	-4.444127	23527.529018
HLA B*1517	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.503965	0.059535	-4.444430	31912.813827
HLA B*7301	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.504181	0.059535	-4.444646	31928.701101
HLA A*0206	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.526793	0.082100	-4.444693	33635.097809
HLA B*1801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.461656	0.016864	-4.444791	28950.466933
HLA B*3501	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.462793	0.017995	-4.444797	29026.369769
HLA A*3201	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.602385	0.157454	-4.444931	40029.947948
HLA B*7301	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.538632	0.093574	-4.445058	34564.617071
HLA B*1517	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.491929	0.046803	-4.445126	31040.498479
HLA A*6801	1:271-279	9	RDRGFIPEG	0.853110	-0.621810	-4.676781	0.231300	-4.445481	47509.610285
HLA B*5101	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.492333	0.046803	-4.445530	31069.395134
HLA B*0802	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.462955	0.017415	-4.445540	29037.206823
HLA B*1503	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.467607	0.021903	-4.445704	29349.913000
HLA A*0212	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.416945	-0.028903	-4.445848	26118.298026
HLA B*5701	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.417100	-0.028903	-4.446003	26127.625299
HLA B*4501	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.569267	0.123142	-4.446125	37090.841353
HLA A*2902	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.441001	-0.005447	-4.446448	27605.858022
HLA A*6901	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.395012	-0.051442	-4.446455	24832.041800
HLA B*1502	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.617330	0.170588	-4.446742	41431.446820
HLA B*3801	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.569906	0.123142	-4.446764	37145.460325
HLA B*4002	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.626996	0.180214	-4.446782	42363.894788
HLA B*4801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.441582	-0.005447	-4.447029	27642.770803
HLA B*5101	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.506589	0.059535	-4.447054	32106.241892
HLA B*5401	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.530477	0.083388	-4.447089	33921.628018
HLA A*0250	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.595809	0.148579	-4.447230	39428.369409
HLA B*4403	1:453-461	9	VAATGTTVS	1.073878	-0.862006	-4.659104	0.211872	-4.447232	45614.607561
HLA A*3101	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.395856	-0.051442	-4.447298	24880.316218
HLA B*1501	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.338331	-0.109399	-4.447730	21793.706856
HLA A*2403	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.413616	-0.034117	-4.447733	25918.845499
HLA A*0301	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.360997	-0.086740	-4.447736	22961.306022
HLA A*2601	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.396352	-0.051442	-4.447794	24908.732982
HLA B*1801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.494741	0.046803	-4.447938	31242.157720
HLA A*0212	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.425297	-0.022687	-4.447984	26625.470583
HLA B*4001	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.370235	-0.077849	-4.448084	23454.963519
HLA B*0801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.414133	-0.034117	-4.448250	25949.711841
HLA A*0219	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.465194	0.016864	-4.448330	29187.298329
HLA A*3002	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.516262	0.067914	-4.448348	32829.351442
HLA A*3101	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.419482	-0.028903	-4.448385	26271.345559
HLA A*1101	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.465549	0.016864	-4.448684	29211.150977

HLA A*2501	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.508288	0.059535	-4.448753	32232.066548
HLA B*0702	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.466801	0.017995	-4.448806	29295.502035
HLA B*3801	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.564760	0.115588	-4.449172	36707.970377
HLA B*1501	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.397806	-0.051442	-4.449248	24992.285207
HLA A*2402	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.560696	0.111406	-4.449290	36366.019185
HLA A*0219	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.467297	0.017995	-4.449301	29328.961551
HLA B*0802	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.420441	-0.028903	-4.449344	26329.396629
HLA A*8001	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.444027	-0.005447	-4.449475	27798.885629
HLA A*1101	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.467628	0.017995	-4.449633	29351.342053
HLA A*2402	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.325190	-0.124662	-4.449852	21144.159944
HLA B*3501	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.467038	0.016864	-4.450174	29311.513436
HLA B*1517	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.473466	0.023199	-4.450268	29748.593262
HLA A*3201	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.587236	0.136944	-4.450291	38657.658578
HLA B*4601	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.403985	-0.046382	-4.450367	25350.417364
HLA B*5701	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.416444	-0.034117	-4.450562	26088.219077
HLA B*3501	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.446969	-0.003611	-4.450580	27987.811611
HLA A*8001	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.473819	0.023199	-4.450620	29772.743548
HLA A*2603	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.602256	0.151627	-4.450628	40018.039053
HLA B*5401	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.532864	0.082100	-4.450764	34108.589803
HLA B*0803	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.452091	0.001267	-4.450824	28319.841559
HLA A*3301	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.588730	0.137558	-4.451172	38790.896662
HLA A*2603	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.619654	0.168455	-4.451198	41653.714898
HLA A*2301	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.519185	0.067914	-4.451271	33051.034880
HLA B*1502	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.618183	0.166895	-4.451288	41512.889413
HLA B*4601	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.378803	-0.072551	-4.451354	23922.322100
HLA B*1502	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.608867	0.157454	-4.451413	40631.911557
HLA B*4402	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.422513	-0.028903	-4.451416	26455.328133
HLA A*0201	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.400038	-0.051442	-4.451480	25121.061056
HLA B*3901	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.498517	0.046803	-4.451714	31514.951487
HLA A*0216	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.468673	0.016864	-4.451809	29422.087615
HLA B*5101	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.473831	0.021903	-4.451928	29773.548895
HLA A*8001	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.410773	-0.041216	-4.451989	25749.735718
HLA B*0803	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.473727	0.021584	-4.452144	29766.462588
HLA A*2602	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.630678	0.178488	-4.452189	42724.552617
HLA A*2501	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.469063	0.016864	-4.452199	29448.521742
HLA B*0801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.343126	-0.109399	-4.452525	22035.677305
HLA A*6802	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.406313	-0.046382	-4.452695	25486.690994
HLA B*4501	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.623354	0.170588	-4.452766	42010.144855
HLA A*6901	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.366039	-0.086740	-4.452778	23229.431514
HLA B*5701	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.430158	-0.022687	-4.452845	26925.165211
HLA B*0801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.375037	-0.077849	-4.452886	23715.763410
HLA B*0802	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.476772	0.023199	-4.453574	29975.895027
HLA A*2402	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.591389	0.137558	-4.453831	39029.180781
HLA A*0250	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.577004	0.123142	-4.453862	37757.526763
HLA B*5301	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.576691	0.122535	-4.454157	37730.369418
HLA B*4601	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.376336	-0.077849	-4.454186	23786.819352
HLA A*2902	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.431559	-0.022687	-4.454246	27012.119966
HLA A*2402	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.569901	0.115588	-4.454313	37145.058422
HLA B*4002	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.560541	0.106226	-4.454315	36353.036918
HLA A*2501	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.501296	0.046803	-4.454493	31717.290774
HLA A*0216	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.472494	0.017995	-4.454498	29682.040070
HLA B*1509	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.577074	0.122535	-4.454539	37763.655182
HLA B*5401	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.565954	0.111406	-4.454548	36808.990840
HLA B*0801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.318593	-0.136008	-4.454601	20825.387037
HLA B*1503	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.522524	0.067914	-4.454609	33306.092255
HLA B*0702	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.455885	0.001267	-4.454619	28568.355240
HLA A*2603	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.633300	0.178488	-4.454811	42983.279619
HLA B*1502	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.592733	0.137558	-4.455175	39150.141944
HLA A*3201	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.627224	0.171999	-4.455224	42386.131467
HLA A*2902	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.456604	0.001267	-4.455338	28615.687207
HLA A*3301	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.625953	0.170588	-4.455364	42262.259216
HLA A*2601	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.377546	-0.077849	-4.455396	23853.184047
HLA B*1801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.434874	-0.020620	-4.455493	27219.102008
HLA A*2902	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.452180	-0.003611	-4.455791	28325.664031
HLA B*7301	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.593530	0.137558	-4.455972	39222.007321

HLA A*2902	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.404537	-0.051442	-4.455979	25382.666452
HLA A*2501	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.479324	0.023199	-4.456125	30152.525953
HLA A*6901	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.378340	-0.077849	-4.456190	23896.840510
HLA A*3301	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.628262	0.171999	-4.456263	42487.605228
HLA B*4601	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.415213	-0.041216	-4.456429	26014.369389
HLA A*2602	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.627292	0.170588	-4.456704	42392.781813
HLA A*0203	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.436201	-0.020620	-4.456821	27302.426851
HLA A*2603	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.621460	0.164416	-4.457044	41827.363838
HLA A*3001	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.302783	-0.154364	-4.457148	20080.910332
HLA B*2705	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.453649	-0.003611	-4.457260	28421.600318
HLA A*2501	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.475278	0.017995	-4.457283	29872.934509
HLA A*2301	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.533498	0.075603	-4.457896	34158.447604
HLA B*4001	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.385492	-0.072551	-4.458043	24293.624666
HLA A*2403	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.416947	-0.041216	-4.458163	26118.439323
HLA A*2602	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.630356	0.171999	-4.458356	42692.898841
HLA B*4002	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.636880	0.178488	-4.458392	43339.127529
HLA B*4403	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.630426	0.171999	-4.458427	42699.828319
HLA A*0212	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.424508	-0.034117	-4.458625	26577.116820
HLA A*0202	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.581235	0.122535	-4.458700	38127.204287
HLA A*3101	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.424856	-0.034117	-4.458973	26598.404671
HLA B*5301	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.590008	0.131008	-4.459000	38905.225635
HLA B*1517	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.477190	0.017995	-4.459195	30004.774526
HLA A*0101	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.407803	-0.051442	-4.459245	25574.257108
HLA B*5801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.350593	-0.108675	-4.459268	22417.803969
HLA A*1101	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.480896	0.021584	-4.459312	30261.852170
HLA B*5801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.359150	-0.100479	-4.459629	22863.877867
HLA B*4501	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.639883	0.180214	-4.459669	43639.805472
HLA B*4801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.437228	-0.022687	-4.459915	27367.049464
HLA B*5301	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.608545	0.148579	-4.459966	40601.808178
HLA A*6801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.481753	0.021584	-4.460169	30321.666548
HLA A*2301	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.542337	0.082100	-4.460237	34860.762951
HLA B*4801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.419057	-0.041216	-4.460273	26245.633512
HLA A*0211	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.542414	0.082100	-4.460315	34866.987071
HLA B*5701	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.419264	-0.041216	-4.460480	26258.131252
HLA B*2705	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.461801	0.001267	-4.460535	28960.178928
HLA A*6802	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.419417	-0.041216	-4.460633	26267.366358
HLA B*3901	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.483983	0.023199	-4.460784	30477.737814
HLA B*5401	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.482728	0.021903	-4.460825	30389.818318
HLA B*1509	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.544367	0.083388	-4.460979	35024.088591
HLA A*3201	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.627903	0.166895	-4.461008	42452.452233
HLA B*4001	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.438353	-0.022687	-4.461040	27438.058674
HLA B*4002	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.633307	0.171999	-4.461307	42983.977229
HLA A*0101	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.351935	-0.109399	-4.461333	22487.160680
HLA A*2403	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.439072	-0.022687	-4.461759	27483.517969
HLA B*4001	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.415718	-0.046382	-4.462100	26044.644987
HLA A*8001	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.439566	-0.022687	-4.462253	27514.759097
HLA A*2603	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.641182	0.178924	-4.462258	43770.556797
HLA B*3901	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.484222	0.021903	-4.462319	30494.560336
HLA B*1801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.484058	0.021584	-4.462474	30483.014468
HLA A*2603	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.642719	0.180214	-4.462505	43925.694263
HLA A*0206	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.538235	0.075603	-4.462632	34533.030076
HLA B*1502	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.384893	-0.077849	-4.462743	24260.134189
HLA A*8001	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.390252	-0.072551	-4.462803	24561.357927
HLA A*2501	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.484439	0.021584	-4.462855	30509.741555
HLA B*5301	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.556669	0.093574	-4.463095	36030.372011
HLA B*4801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.434282	-0.028903	-4.463185	27182.019705
HLA A*2902	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.354519	-0.108675	-4.463194	22621.377991
HLA A*0250	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.585744	0.122535	-4.463209	38525.086553
HLA B*4001	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.429127	-0.034117	-4.463244	26861.295397
HLA B*4402	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.412011	-0.051442	-4.463453	25823.253263
HLA A*3101	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.407573	-0.055990	-4.463563	25560.702019
HLA A*2402	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.546961	0.083388	-4.463573	35233.896494
HLA B*1501	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.422508	-0.041216	-4.463724	26455.041894
HLA A*0202	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.485430	0.021584	-4.463846	30579.474046
HLA B*0702	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.429799	-0.034117	-4.463916	26902.888122

HLA B*4501	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.630208	0.166266	-4.463942	42678.350598
HLA B*2705	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.481121	0.016864	-4.464257	30277.572726
HLA B*4501	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.632757	0.168455	-4.464301	42929.597636
HLA B*4801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.443745	-0.020620	-4.464365	27780.844819
HLA B*4402	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.458940	-0.005447	-4.464387	28769.980535
HLA A*0203	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.386883	-0.077849	-4.464733	24371.553473
HLA A*2602	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.587992	0.123142	-4.464850	38725.058300
HLA B*1503	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.481720	0.016864	-4.464856	30319.370119
HLA B*4501	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.643825	0.178924	-4.464901	44037.762187
HLA A*0301	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.355543	-0.109399	-4.464942	22674.798276
HLA A*0201	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.387294	-0.077849	-4.465144	24394.637694
HLA B*1801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.524711	0.059535	-4.465176	33474.265100
HLA A*6801	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.576729	0.111406	-4.465323	37733.635433
HLA A*3301	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.629745	0.164416	-4.465328	42632.890453
HLA A*2603	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.613973	0.148579	-4.465394	41112.386300
HLA A*2402	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.571694	0.106226	-4.465468	37298.700646
HLA B*0801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.392959	-0.072551	-4.465510	24714.907009
HLA B*4601	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.414111	-0.051442	-4.465554	25948.448406
HLA A*0203	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.436739	-0.028903	-4.465642	27336.271822
HLA B*0801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.419334	-0.046382	-4.465716	26262.393205
HLA B*4501	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.637820	0.171999	-4.465821	43433.013025
HLA B*2705	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.387980	-0.077849	-4.465830	24433.204054
HLA B*1501	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.431916	-0.034117	-4.466033	27034.341253
HLA A*0101	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.273925	-0.192252	-4.466176	18789.908818
HLA B*5701	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.419849	-0.046382	-4.466231	26293.526428
HLA A*8001	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.445839	-0.020620	-4.466458	27915.077614
HLA B*0802	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.484744	0.017995	-4.466749	30531.206163
HLA B*1502	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.573176	0.106226	-4.466951	37426.242552
HLA B*5401	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.542574	0.075603	-4.466972	34879.816035
HLA B*0801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.380253	-0.086740	-4.466993	24002.305872
HLA B*7301	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.542788	0.075603	-4.467185	34896.991592
HLA A*8001	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.438386	-0.028903	-4.467289	27440.136869
HLA B*4002	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.646229	0.178924	-4.467305	44282.156760
HLA A*0203	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.421056	-0.046382	-4.467438	26366.742138
HLA A*6801	1:142-150	9	AQRAAYLAE	0.818142	-0.622097	-4.663613	0.196045	-4.467567	46090.625768
HLA B*1502	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.561161	0.093574	-4.467587	36404.993809
HLA B*4403	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.636117	0.168455	-4.467661	43262.995018
HLA B*4001	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.358410	-0.109399	-4.467808	22824.948368
HLA A*0301	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.367331	-0.100479	-4.467810	23298.652201
HLA B*7301	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.484699	0.016864	-4.467835	30528.068086
HLA A*0216	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.174180	-0.293904	-4.468083	14934.119987
HLA B*1503	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.514947	0.046803	-4.468144	32730.044181
HLA A*2402	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.486226	0.017995	-4.468231	30635.606803
HLA A*2501	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.395987	-0.072551	-4.468538	24887.854946
HLA B*4801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.434493	-0.034117	-4.468611	27195.257581
HLA A*3201	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.544357	0.075603	-4.468755	35023.330693
HLA B*1801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.465269	-0.003611	-4.468880	29192.351567
HLA A*2403	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.448404	-0.020620	-4.469024	28080.476772
HLA A*3301	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.635922	0.166895	-4.469027	43243.573394
HLA B*1509	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.562632	0.093574	-4.469058	36528.491619
HLA B*0702	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.391662	-0.077849	-4.469511	24641.211991
HLA B*4501	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.575869	0.106226	-4.469643	37658.996020
HLA B*4403	1:286-294	9	LLGWSIADD	0.960771	-0.781847	-4.648717	0.178924	-4.469793	44536.580561
HLA B*4501	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.648440	0.178488	-4.469951	44508.158954
HLA A*2501	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.334175	-0.136008	-4.470183	21586.133865
HLA A*0202	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.576649	0.106226	-4.470423	37726.695489
HLA B*4001	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.419125	-0.051442	-4.470567	26249.751428
HLA B*3801	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.593241	0.122535	-4.470706	39195.917037
HLA B*5401	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.530355	0.059535	-4.470819	33912.086724
HLA A*2603	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.637510	0.166266	-4.471244	43402.008349
HLA A*0203	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.430067	-0.041216	-4.471283	26919.484986
HLA A*0202	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.530846	0.059535	-4.471310	33950.451680
HLA A*3201	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.620114	0.148579	-4.471535	41697.905351
HLA A*2403	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.384846	-0.086740	-4.471586	24257.509438
HLA B*1517	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.362282	-0.109399	-4.471680	23029.353968

HLA A*3301	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.565352	0.093574	-4.471779	36758.048189
HLA A*2602	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.583265	0.111406	-4.471859	38305.833483
HLA B*5401	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.518685	0.046803	-4.471882	33012.971896
HLA A*3002	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.362512	-0.109399	-4.471911	23041.566658
HLA A*0301	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.347297	-0.124662	-4.471958	22248.295273
HLA A*2602	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.638922	0.166895	-4.472027	43543.352836
HLA A*0211	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.547832	0.075603	-4.472230	35304.684365
HLA A*2301	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.519138	0.046803	-4.472335	33047.459025
HLA B*4002	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.636892	0.164416	-4.472476	43340.299845
HLA B*5401	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.540413	0.067914	-4.472498	34706.647068
HLA A*2602	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.578777	0.106226	-4.472552	37912.061490
HLA A*2902	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.443762	-0.028903	-4.472665	27781.896878
HLA B*5801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.363273	-0.109399	-4.472672	23081.989426
HLA A*0219	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.438711	-0.034117	-4.472828	27460.630355
HLA A*0211	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.490308	0.017415	-4.472893	30924.845767
HLA A*0206	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.532525	0.059535	-4.472990	34082.028739
HLA A*0206	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.520036	0.046803	-4.473233	33115.824783
HLA A*2501	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.450622	-0.022687	-4.473309	28224.248756
HLA A*0212	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.432242	-0.041216	-4.473458	27054.678036
HLA A*3001	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.259330	-0.214129	-4.473459	18168.943390
HLA A*2902	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.417485	-0.055990	-4.473475	26150.816585
HLA B*4601	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.417520	-0.055990	-4.473511	26152.938766
HLA A*2602	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.631056	0.157454	-4.473602	42761.781578
HLA B*5301	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.596993	0.123142	-4.473851	39536.020869
HLA B*1502	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.495455	0.021584	-4.473872	31293.581044
HLA B*0803	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.497107	0.023199	-4.473908	31412.821893
HLA A*6901	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.364589	-0.109399	-4.473988	23152.023220
HLA B*4002	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.625624	0.151627	-4.473996	42230.262555
HLA B*5701	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.422809	-0.051442	-4.474251	26473.367450
HLA A*0101	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.387555	-0.086740	-4.474295	24409.291016
HLA A*0301	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.365620	-0.108675	-4.474295	23207.073261
HLA A*6801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.549912	0.075603	-4.474309	35474.119718
HLA A*3201	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.580587	0.106226	-4.474361	38070.317917
HLA A*0250	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.590001	0.115588	-4.474413	38904.594221
HLA B*4002	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.640874	0.166266	-4.474609	43739.547790
HLA B*3501	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.454024	-0.020620	-4.474644	28446.212201
HLA B*4002	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.623307	0.148579	-4.474728	42005.599696
HLA A*6801	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.645533	0.170588	-4.474945	44211.303283
HLA B*5101	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.492004	0.016864	-4.475140	31045.872565
HLA A*0250	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.581493	0.106226	-4.475268	38149.900074
HLA A*0216	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.471674	-0.003611	-4.475285	29626.051727
HLA B*3801	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.550974	0.075603	-4.475371	35560.969657
HLA A*0201	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.388662	-0.086740	-4.475401	24471.566608
HLA A*6802	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.441401	-0.034117	-4.475518	27631.258288
HLA B*0702	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.429256	-0.046382	-4.475638	26869.289001
HLA A*0206	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.543838	0.067914	-4.475924	34981.482328
HLA B*4002	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.643268	0.166895	-4.476374	43981.335628
HLA A*2902	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.455892	-0.020620	-4.476512	28568.818899
HLA A*0203	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.442662	-0.034117	-4.476780	27711.646858
HLA B*5801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.352282	-0.124662	-4.476944	22505.172541
HLA B*4002	1:411-419	9	DAALAALTS	1.231227	-1.062772	-4.645505	0.168455	-4.477050	44208.433237
HLA A*6802	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.390372	-0.086740	-4.477112	24568.135447
HLA B*3901	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.399401	-0.077849	-4.477251	25084.258556
HLA B*1501	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.421268	-0.055990	-4.477258	26379.582967
HLA B*0702	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.456964	-0.020620	-4.477583	28639.382589
HLA B*0802	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.478854	0.001267	-4.477587	30119.919231
HLA A*2301	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.537215	0.059535	-4.477680	34452.045364
HLA A*0219	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.478971	0.001267	-4.477705	30128.067604
HLA A*2902	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.436495	-0.041216	-4.477711	27320.895983
HLA B*1503	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.495770	0.017995	-4.477775	31316.274772
HLA A*6901	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.258853	-0.219267	-4.478120	18149.001072
HLA B*2705	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.496242	0.017995	-4.478247	31350.346226
HLA A*0203	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.353669	-0.124662	-4.478330	22577.120090
HLA A*2301	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.353739	-0.124662	-4.478401	22580.784579
HLA B*5401	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.501674	0.023199	-4.478476	31744.928319

HLA A*8001	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.432341	-0.046382	-4.478723	27060.825972
HLA A*0216	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.480501	0.001267	-4.479234	30234.360837
HLA B*4501	1:320-328	9	DQKKADALN	0.868989	-0.720410	-4.627830	0.148579	-4.479251	42445.333275
HLA B*5101	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.475701	-0.003611	-4.479312	29902.038345
HLA B*4501	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.644044	0.164416	-4.479627	44059.924027
HLA B*0803	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.526713	0.046803	-4.479910	33628.911665
HLA B*1509	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.501829	0.021903	-4.479926	31756.264955
HLA A*0101	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.402096	-0.077849	-4.479945	25240.393884
HLA A*2603	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.477059	-0.003611	-4.480670	29995.685842
HLA B*5101	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.439474	-0.041216	-4.480690	27508.954489
HLA A*2301	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.532272	0.051538	-4.480734	34062.121516
HLA A*0219	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.460126	-0.020620	-4.480746	28848.687414
HLA A*6901	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.372150	-0.108675	-4.480824	23558.606168
HLA B*4402	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.403031	-0.077849	-4.480881	25294.798431
HLA B*1503	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.261712	-0.219267	-4.480979	18268.885318
HLA A*0212	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.434730	-0.046382	-4.481112	27210.121098
HLA A*1101	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.477573	-0.003611	-4.481184	30031.244763
HLA A*0211	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.549517	0.067914	-4.481602	35441.893307
HLA B*1801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.373026	-0.108675	-4.481701	23606.192808
HLA A*0101	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.373127	-0.108675	-4.481802	23611.684843
HLA B*3801	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.575479	0.093574	-4.481905	37625.191856
HLA A*3301	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.588206	0.106226	-4.481980	38744.127337
HLA A*2403	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.435656	-0.046382	-4.482038	27268.181226
HLA A*3201	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.619745	0.137558	-4.482187	41662.504163
HLA A*1101	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.483494	0.001267	-4.482228	30443.461816
HLA B*4801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.430873	-0.051442	-4.482315	26969.482940
HLA A*0216	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.459924	-0.022687	-4.482611	28835.268671
HLA B*4402	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.441443	-0.041216	-4.482659	27633.949096
HLA B*4001	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.426947	-0.055990	-4.482937	26726.779507
HLA B*0803	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.505351	0.021903	-4.483448	32014.836984
HLA B*4501	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.650592	0.166895	-4.483697	44729.264674
HLA B*3501	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.397073	-0.086740	-4.483813	24950.136674
HLA A*2501	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.442820	-0.041216	-4.484036	27721.693114
HLA A*2501	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.291854	-0.192252	-4.484105	19581.844281
HLA B*4801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.428187	-0.055990	-4.484177	26803.231591
HLA B*5101	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.502403	0.017995	-4.484407	31798.211315
HLA B*4801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.438208	-0.046382	-4.484590	27428.857132
HLA B*5101	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.507849	0.023199	-4.484650	32199.475489
HLA A*3201	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.600294	0.115588	-4.484706	39837.674951
HLA A*6901	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.292594	-0.192252	-4.484845	19615.242446
HLA A*2501	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.486229	0.001267	-4.484962	30635.772539
HLA A*0202	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.560794	0.075603	-4.485192	36374.283041
HLA B*3501	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.486478	0.001267	-4.485211	30653.345607
HLA A*3301	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.412723	-0.072551	-4.485274	25865.617359
HLA B*3901	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.479928	-0.005447	-4.485375	30194.477418
HLA B*1509	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.462776	-0.022687	-4.485463	29025.270583
HLA B*0802	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.481882	-0.003611	-4.485493	30330.689917
HLA B*0802	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.462866	-0.022687	-4.485553	29031.238090
HLA A*2403	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.429595	-0.055990	-4.485585	26890.228978
HLA B*1517	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.398915	-0.086740	-4.485655	25056.183746
HLA A*0202	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.553657	0.067914	-4.485742	35781.348709
HLA A*0202	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.376412	-0.109399	-4.485810	23790.937598
HLA B*0803	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.502769	0.016864	-4.485905	31825.058510
HLA A*2603	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.658098	0.171999	-4.486099	45509.112194
HLA B*1509	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.568207	0.082100	-4.486107	37000.455202
HLA B*4403	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.653047	0.166895	-4.486152	44982.850281
HLA A*0211	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.545866	0.059535	-4.486330	35145.183417
HLA A*0250	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.568473	0.082100	-4.486373	37023.081142
HLA B*4403	1:61-69	9	LLDALRWLG	0.782557	-0.604069	-4.664931	0.178488	-4.486442	46230.720895
HLA B*3801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.568559	0.082100	-4.486460	37030.492642
HLA A*2402	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.435299	-0.051442	-4.486741	27245.767732
HLA A*3201	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.598377	0.111406	-4.486971	39662.200347
HLA B*5301	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.593217	0.106226	-4.486992	39193.796638
HLA A*1101	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.441175	-0.046382	-4.487557	27616.911738
HLA B*4403	1:257-265	9	KLSKRDPQS	1.059741	-0.879527	-4.667912	0.180214	-4.487698	46549.193628

HLA A*2402	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.569812	0.082100	-4.487712	37137.423082
HLA A*2601	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.387334	-0.100479	-4.487814	24396.881326
HLA A*2602	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.556337	0.067914	-4.488423	36002.898726
HLA A*0219	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.465805	-0.022687	-4.488492	29228.381227
HLA B*1502	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.564251	0.075603	-4.488648	36664.902488
HLA B*0803	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.506221	0.017415	-4.488806	32078.983949
HLA B*1501	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.334525	-0.154364	-4.488889	21603.540890
HLA B*4601	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.334955	-0.154364	-4.489319	21624.939196
HLA B*5701	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.411684	-0.077849	-4.489534	25803.842132
HLA B*4403	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.641201	0.151627	-4.489573	43772.451188
HLA A*3101	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.345864	-0.143836	-4.489699	22174.996189
HLA A*6901	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.389296	-0.100479	-4.489776	24507.337611
HLA A*0301	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.345962	-0.143836	-4.489798	22180.035261
HLA A*3301	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.621139	0.131008	-4.490131	41796.374771
HLA A*2902	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.443926	-0.046382	-4.490308	27792.419659
HLA B*4501	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.601847	0.111406	-4.490441	39980.386968
HLA B*3901	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.507346	0.016864	-4.490482	32162.219203
HLA A*2902	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.456560	-0.034117	-4.490677	28612.746012
HLA A*0301	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.354820	-0.136008	-4.490828	22637.047946
HLA B*5801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.347052	-0.143836	-4.490888	22235.781269
HLA A*3001	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.298723	-0.192252	-4.490975	19894.062902
HLA A*3201	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.613618	0.122535	-4.491083	41078.815582
HLA A*6901	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.347254	-0.143836	-4.491090	22246.128884
HLA B*1517	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.470513	-0.020620	-4.491133	29546.982244
HLA A*0216	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.413371	-0.077849	-4.491221	25904.266920
HLA A*2501	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.439791	-0.051442	-4.491233	27529.052580
HLA B*5701	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.404530	-0.086740	-4.491270	25382.254503
HLA B*1801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.509320	0.017995	-4.491324	32308.706787
HLA A*1101	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.485961	-0.005447	-4.491408	30616.884445
HLA B*5701	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.435489	-0.055990	-4.491480	27257.709471
HLA B*7301	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.559695	0.067914	-4.491780	36282.306093
HLA A*0211	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.515083	0.023199	-4.491884	32740.315615
HLA A*0101	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.391488	-0.100479	-4.491968	24631.349305
HLA A*3002	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.509583	0.017415	-4.492168	32328.288809
HLA A*1101	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.384090	-0.109399	-4.493488	24215.290021
HLA B*0702	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.437538	-0.055990	-4.493528	27386.599401
HLA B*4501	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.631239	0.137558	-4.493681	42779.829633
HLA B*0802	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.488256	-0.005447	-4.493704	30779.137227
HLA B*3501	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.415892	-0.077849	-4.493742	26055.073573
HLA A*1101	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.415906	-0.077849	-4.493756	26055.919317
HLA B*4001	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.385217	-0.108675	-4.493892	24278.252711
HLA A*0201	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.369530	-0.124662	-4.494191	23416.927767
HLA B*1503	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.511709	0.017415	-4.494294	32486.954577
HLA B*5301	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.605714	0.111406	-4.494308	40337.989225
HLA A*2601	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.385142	-0.109399	-4.494541	24274.050110
HLA A*2603	1:338-346	9	GDFTVRLRD	1.102016	-0.931428	-4.665231	0.170588	-4.494643	46262.745175
HLA A*0202	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.416799	-0.077849	-4.494649	26109.539075
HLA A*1101	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.474169	-0.020620	-4.494788	29796.752242
HLA A*2902	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.385469	-0.109399	-4.494867	24292.310444
HLA A*6901	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.340523	-0.154364	-4.494888	21903.987072
HLA A*6802	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.417264	-0.077849	-4.495114	26137.521502
HLA B*4402	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.340906	-0.154364	-4.495271	21923.310788
HLA B*4002	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.618458	0.123142	-4.495316	41539.173605
HLA A*3101	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.408691	-0.086740	-4.495431	25626.608390
HLA B*1502	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.618084	0.122535	-4.495550	41503.458119
HLA A*0201	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.395083	-0.100479	-4.495562	24836.072285
HLA A*0212	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.417725	-0.077849	-4.495574	26165.250815
HLA B*1503	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.466735	-0.028903	-4.495638	29291.064779
HLA B*0702	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.423148	-0.072551	-4.495698	26493.998875
HLA B*1503	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.444441	-0.051442	-4.495883	27825.366678
HLA B*7301	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.607326	0.111406	-4.495920	40487.969052
HLA B*5401	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.360252	-0.136008	-4.496260	22921.962623
HLA A*2301	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.514559	0.017995	-4.496564	32700.841341
HLA A*0203	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.440574	-0.055990	-4.496564	27578.690676
HLA A*0201	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.387431	-0.109399	-4.496829	24402.293287

HLA B*1509	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.543681	0.046803	-4.496878	34968.805148
HLA B*1801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.520097	0.023199	-4.496898	33120.483087
HLA A*0206	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.520235	0.023199	-4.497037	33131.056284
HLA A*6801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.468236	-0.028903	-4.497139	29392.496842
HLA A*2601	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.388521	-0.108675	-4.497195	24463.624589
HLA B*5401	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.410458	-0.086740	-4.497198	25731.075852
HLA B*5101	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.491877	-0.005447	-4.497324	31036.804335
HLA B*1801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.468634	-0.028903	-4.497536	29419.381846
HLA A*2402	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.573296	0.075603	-4.497693	37436.570039
HLA B*1517	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.475088	-0.022687	-4.497775	29859.847026
HLA B*3901	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.475179	-0.022687	-4.497866	29866.147691
HLA A*0212	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.442148	-0.055990	-4.498138	27678.834490
HLA B*0801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.442582	-0.055990	-4.498573	27706.550151
HLA B*4403	1:97-105	9	VLARLLAAG	0.788969	-0.622703	-4.665231	0.166266	-4.498966	46262.745175
HLA A*0212	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.447535	-0.051442	-4.498977	28024.325450
HLA A*0216	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.465300	-0.034117	-4.499417	29194.404696
HLA A*1101	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.476782	-0.022687	-4.499469	29976.543699
HLA A*0211	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.546298	0.046803	-4.499495	35180.185039
HLA A*0203	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.390137	-0.109399	-4.499536	24554.847953
HLA B*5401	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.516443	0.016864	-4.499579	32843.029734
HLA A*6801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.476970	-0.022687	-4.499657	29989.520089
HLA B*3901	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.496212	-0.003611	-4.499823	31348.141479
HLA B*1517	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.494464	-0.005447	-4.499911	31222.220125
HLA A*6802	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.448510	-0.051442	-4.499952	28087.313656
HLA B*3801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.518168	0.017995	-4.500172	32973.704035
HLA B*4601	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.399763	-0.100479	-4.500242	25105.165535
HLA A*0219	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.453881	-0.046382	-4.500263	28436.826408
HLA B*3901	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.459210	-0.041216	-4.500426	28787.884981
HLA A*0201	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.391958	-0.108675	-4.500633	24658.014301
HLA B*0803	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.518870	0.017995	-4.500875	33027.084037
HLA A*6802	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.391629	-0.109399	-4.501028	24639.345775
HLA B*4402	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.400750	-0.100479	-4.501229	25162.273177
HLA A*8001	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.449835	-0.051442	-4.501277	28173.143910
HLA B*1502	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.518816	0.017415	-4.501401	33022.974816
HLA A*2603	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.578110	0.075603	-4.502508	37853.857800
HLA B*7301	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.554157	0.051538	-4.502620	35822.603550
HLA A*6801	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.669533	0.166895	-4.502638	46723.278263
HLA B*0802	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.482035	-0.020620	-4.502655	30341.357361
HLA B*4402	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.430177	-0.072551	-4.502728	26926.330534
HLA B*5301	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.586155	0.083388	-4.502767	38561.576702
HLA B*5301	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.524615	0.021584	-4.503031	33466.841149
HLA A*0216	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.474286	-0.028903	-4.503189	29804.813189
HLA A*6801	1:125-133	9	GRNPKLGYD	0.923015	-0.751016	-4.675205	0.171999	-4.503206	47337.461350
HLA B*5101	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.482658	-0.020620	-4.503277	30384.886552
HLA A*0211	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.499858	-0.003611	-4.503469	31612.453160
HLA B*1502	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.619167	0.115588	-4.503580	41607.095217
HLA B*0702	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.200282	-0.303590	-4.503872	15859.241581
HLA A*6801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.311716	-0.192252	-4.503968	20498.219476
HLA B*0702	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.463049	-0.041216	-4.504265	29043.491025
HLA B*4801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.431805	-0.072551	-4.504356	27027.468246
HLA A*0211	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.526351	0.021903	-4.504448	33600.906315
HLA B*3501	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.279688	-0.224761	-4.504449	19040.921357
HLA B*3501	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.470335	-0.034117	-4.504452	29534.836453
HLA B*0801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.360654	-0.143836	-4.504489	22943.177337
HLA A*8001	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.395196	-0.109399	-4.504594	24842.522422
HLA B*3801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.556314	0.051538	-4.504776	36000.951062
HLA B*4001	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.418512	-0.086740	-4.505252	26212.713431
HLA A*3002	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.588669	0.083388	-4.505281	38785.440830
HLA B*4501	1:196-204	9	YTLVNPCDD	0.929562	-0.777935	-4.656987	0.151627	-4.505360	45392.808815
HLA A*2603	1:288-296	9	GWSIADDHD	0.907843	-0.740948	-4.672275	0.166895	-4.505380	47019.191351
HLA B*1517	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.459438	-0.046382	-4.505820	28802.995654
HLA A*0206	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.522836	0.016864	-4.505972	33330.065120
HLA B*1801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.483353	-0.022687	-4.506040	30433.581675
HLA B*5801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.370124	-0.136008	-4.506133	23449.000506
HLA B*1517	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.465109	-0.041216	-4.506325	29181.614480

HLA A*0203	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.455364	-0.051442	-4.506806	28534.065372
HLA A*0212	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.352480	-0.154364	-4.506844	22515.401906
HLA A*0216	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.486266	-0.020620	-4.506886	30638.424432
HLA A*6901	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.282533	-0.224369	-4.506902	19166.075104
HLA B*2705	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.478086	-0.028903	-4.506988	30066.683180
HLA A*2603	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.630320	0.123142	-4.507179	42689.434524
HLA A*6801	1:380-388	9	WELLKFFND	0.942251	-0.784797	-4.664818	0.157454	-4.507364	46218.717506
HLA B*3801	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.575880	0.067914	-4.507966	37660.014689
HLA B*5301	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.583836	0.075603	-4.508233	38356.223563
HLA B*4403	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.673180	0.164416	-4.508763	47117.225325
HLA A*0250	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.560310	0.051538	-4.508773	36333.768768
HLA A*1101	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.467583	-0.041216	-4.508799	29348.325245
HLA A*0216	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.467663	-0.041216	-4.508879	29353.723962
HLA B*5301	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.560426	0.051538	-4.508888	36343.401566
HLA A*8001	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.400240	-0.108675	-4.508915	25132.751361
HLA A*0202	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.591051	0.082100	-4.508951	38998.787951
HLA A*0206	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.526436	0.017415	-4.509021	33607.450931
HLA A*6802	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.289770	-0.219267	-4.509037	19488.104486
HLA A*2603	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.631702	0.122535	-4.509167	42825.446461
HLA B*0803	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.431368	-0.077849	-4.509218	27000.285821
HLA B*0803	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.488621	-0.020620	-4.509240	30804.957368
HLA B*4402	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.400625	-0.108675	-4.509300	25155.059581
HLA A*2601	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.365559	-0.143836	-4.509395	23203.809251
HLA B*3501	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.463030	-0.046382	-4.509412	29042.234076
HLA A*8001	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.453559	-0.055990	-4.509549	28415.758125
HLA A*6801	1:172-180	9	RGPVTFAAG	0.765569	-0.601153	-4.674026	0.164416	-4.509609	47209.078368
HLA B*3901	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.475600	-0.034117	-4.509717	29895.083185
HLA B*3901	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.511044	0.001267	-4.509778	32437.255149
HLA B*3501	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.400383	-0.109399	-4.509782	25141.046619
HLA A*2601	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.385457	-0.124662	-4.510119	24291.653359
HLA B*1801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.504830	-0.005447	-4.510277	31976.410393
HLA B*5101	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.511601	0.001267	-4.510334	32478.871045
HLA B*3801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.593915	0.083388	-4.510527	39256.821383
HLA B*4002	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.648247	0.137558	-4.510689	44488.419028
HLA B*4002	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.647634	0.136944	-4.510689	44425.646550
HLA A*3201	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.592982	0.082100	-4.510882	39172.598963
HLA A*2301	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.532845	0.021903	-4.510942	34107.113646
HLA A*3002	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.507374	-0.003611	-4.510985	32164.307199
HLA B*0802	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.438701	-0.072551	-4.511252	27460.036126
HLA A*2501	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.482730	-0.028903	-4.511633	30389.982724
HLA B*4403	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.649490	0.137558	-4.511932	44615.919736
HLA B*1503	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.506507	-0.005447	-4.511954	32100.163275
HLA A*0202	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.558783	0.046803	-4.511981	36206.228063
HLA B*7301	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.530063	0.017995	-4.512068	33889.345234
HLA B*4601	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.376442	-0.136008	-4.512450	23792.610839
HLA B*1509	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.478429	-0.034117	-4.512546	30090.440544
HLA A*0202	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.530580	0.017995	-4.512585	33929.703518
HLA B*4601	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.403555	-0.109399	-4.512954	25325.332623
HLA A*0301	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.362378	-0.150664	-4.513042	23034.462571
HLA B*4501	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.650023	0.136944	-4.513079	44670.743742
HLA B*5801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.362463	-0.150664	-4.513126	23038.949108
HLA A*6802	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.369297	-0.143836	-4.513133	23404.389510
HLA A*6802	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.388500	-0.124662	-4.513161	24462.433509
HLA B*1503	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.467304	-0.046382	-4.513686	29329.437554
HLA B*1503	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.514977	0.001267	-4.513711	32732.346118
HLA B*1501	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.413522	-0.100479	-4.514001	25913.237382
HLA B*3501	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.462664	-0.051442	-4.514106	29017.734434
HLA B*1801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.436258	-0.077849	-4.514107	27305.971955
HLA A*2501	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.493695	-0.020620	-4.514315	31167.035790
HLA A*2301	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.532234	0.017415	-4.514819	34059.173287
HLA B*3901	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.442317	-0.072551	-4.514868	27689.617829
HLA A*8001	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.428222	-0.086740	-4.514962	26805.406717
HLA B*5101	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.486226	-0.028903	-4.515129	30635.606803
HLA A*0211	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.532046	0.016864	-4.515182	34044.435968
HLA A*0203	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.414823	-0.100479	-4.515303	25991.017890

HLA B*4402	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.428659	-0.086740	-4.515399	26832.392948
HLA A*0101	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.379471	-0.136008	-4.515479	23959.104809
HLA A*3001	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.291245	-0.224369	-4.515614	19554.426172
HLA A*6901	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.365068	-0.150664	-4.515732	23177.588300
HLA A*0250	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.591342	0.075603	-4.515740	39024.958138
HLA B*5101	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.481643	-0.034117	-4.515760	30313.957796
HLA B*0803	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.510313	-0.005447	-4.515761	32382.726146
HLA B*1517	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.481715	-0.034117	-4.515833	30319.042072
HLA B*5701	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.415507	-0.100479	-4.515986	26031.967195
HLA B*0702	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.487209	-0.028903	-4.516112	30704.962521
HLA B*1517	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.487350	-0.028903	-4.516252	30714.930765
HLA B*0801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.391747	-0.124662	-4.516408	24646.011483
HLA A*3301	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.512816	-0.003611	-4.516427	32569.838767
HLA A*0211	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.534584	0.017995	-4.516588	34243.928942
HLA A*0203	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.213082	-0.303590	-4.516672	16333.618549
HLA A*0202	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.496755	-0.020620	-4.517374	31387.341250
HLA B*4801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.430732	-0.086740	-4.517471	26960.730246
HLA A*0206	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.392947	-0.124662	-4.517609	24714.238493
HLA A*0219	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.476631	-0.041216	-4.517847	29966.166630
HLA B*5801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.363701	-0.154364	-4.518065	23104.727141
HLA A*2402	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.577666	0.059535	-4.518131	37815.173182
HLA A*2603	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.649142	0.131008	-4.518134	44580.211691
HLA A*2603	1:160-168	9	MPDDDLAWN	0.837377	-0.699819	-4.655754	0.137558	-4.518196	45264.067443
HLA A*0101	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.363915	-0.154364	-4.518279	23116.104396
HLA A*0206	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.536997	0.017995	-4.519001	34434.716221
HLA B*1502	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.587083	0.067914	-4.519168	38644.067281
HLA B*0802	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.467764	-0.051442	-4.519206	29360.553173
HLA B*7301	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.515818	-0.003611	-4.519429	32795.801601
HLA A*3101	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.410918	-0.108675	-4.519593	25758.373966
HLA B*0803	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.468213	-0.051442	-4.519655	29390.906784
HLA A*0206	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.516352	-0.003611	-4.519963	32836.101056
HLA A*0206	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.497633	-0.022687	-4.520320	31450.911501
HLA B*0803	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.497650	-0.022687	-4.520337	31452.102545
HLA B*3901	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.500046	-0.020620	-4.520666	31626.137710
HLA A*3001	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.301407	-0.219267	-4.520674	20017.350731
HLA B*3801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.567528	0.046803	-4.520725	36942.651744
HLA B*4403	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.636377	0.115588	-4.520789	43288.982149
HLA B*5401	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.517289	-0.003611	-4.520900	32907.055835
HLA B*4601	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.396300	-0.124662	-4.520961	24905.768581
HLA A*2301	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.469522	-0.051442	-4.520964	29479.604215
HLA B*1503	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.544271	0.023199	-4.521072	35016.320918
HLA A*2301	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.537955	0.016864	-4.521091	34510.805667
HLA B*3801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.580735	0.059535	-4.521199	38083.295369
HLA A*2403	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.411811	-0.109399	-4.521210	25811.381413
HLA B*5701	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.412782	-0.108675	-4.521456	25869.115849
HLA B*5301	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.480496	-0.041216	-4.521712	30234.033709
HLA A*0101	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.397099	-0.124662	-4.521760	24951.621470
HLA A*2603	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.302525	-0.219267	-4.521792	20068.963982
HLA A*0216	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.475454	-0.046382	-4.521836	29885.057663
HLA A*2501	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.465988	-0.055990	-4.521978	29240.717369
HLA A*0301	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.367636	-0.154364	-4.522001	23315.043571
HLA A*0212	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.435283	-0.086740	-4.522022	27244.735975
HLA A*3201	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.539031	0.016864	-4.522167	34596.420120
HLA A*2301	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.545429	0.023199	-4.522230	35109.836736
HLA A*0250	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.543878	0.021584	-4.522294	34984.699657
HLA B*5701	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.413108	-0.109399	-4.522507	25888.576082
HLA B*2705	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.481629	-0.041216	-4.522845	30312.973841
HLA A*0101	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.379031	-0.143836	-4.522867	23934.878854
HLA A*3101	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.386893	-0.136008	-4.522901	24372.080868
HLA B*1502	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.605136	0.082100	-4.523036	40284.341814
HLA B*4001	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.387440	-0.136008	-4.523448	24402.821348
HLA B*1502	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.518020	-0.005447	-4.523467	32962.467752
HLA B*5101	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.500923	-0.022687	-4.523610	31690.020167
HLA B*0702	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.414215	-0.109399	-4.523613	25954.625784
HLA B*0802	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.482507	-0.041216	-4.523723	30374.368125

HLA B*4403	1:373-381	9	IVVLGDAWE	0.654011	-0.517067	-4.660669	0.136944	-4.523724	45779.252790
HLA B*4403	1:176-184	9	TFAAGSVPD	0.820748	-0.697606	-4.646964	0.123142	-4.523822	44357.203047
HLA B*1517	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.445996	-0.077849	-4.523846	27925.197619
HLA B*4501	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.639580	0.115588	-4.523992	43609.360937
HLA A*2301	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.545621	0.021584	-4.524038	35125.415298
HLA A*2602	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.639648	0.115588	-4.524060	43616.203206
HLA B*2705	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.503686	-0.020620	-4.524305	31892.275710
HLA A*2403	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.423993	-0.100479	-4.524473	26545.647808
HLA A*0250	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.592621	0.067914	-4.524706	39139.976964
HLA A*2402	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.576362	0.051538	-4.524825	37701.803841
HLA B*0702	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.438163	-0.086740	-4.524903	27426.037923
HLA B*1801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.526184	0.001267	-4.524918	33588.002614
HLA B*4002	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.647530	0.122535	-4.524996	44415.072944
HLA B*0802	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.491003	-0.034117	-4.525120	30974.406234
HLA B*4403	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.647979	0.122535	-4.525445	44460.990261
HLA B*1509	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.547132	0.021584	-4.525549	35247.813879
HLA A*1101	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.496708	-0.028903	-4.525610	31383.945393
HLA A*6801	1:117-125	9	VEARHVAAG	0.833789	-0.702781	-4.656710	0.131008	-4.525702	45363.840794
HLA B*3501	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.469869	-0.055990	-4.525860	29503.216913
HLA A*3002	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.401396	-0.124662	-4.526058	25199.735442
HLA B*5301	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.608437	0.082100	-4.526337	40591.705476
HLA A*2603	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.638560	0.111406	-4.527154	43507.090978
HLA A*3001	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.302586	-0.224761	-4.527347	20071.787023
HLA B*1501	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.383516	-0.143836	-4.527352	24183.346612
HLA B*5401	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.545469	0.017995	-4.527473	35113.065870
HLA B*0801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.373407	-0.154364	-4.527771	23626.890392
HLA A*3101	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.427670	-0.100479	-4.528150	26771.350015
HLA A*3201	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.611619	0.083388	-4.528231	40890.130956
HLA B*4002	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.639742	0.111406	-4.528336	43625.642580
HLA B*7301	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.549940	0.021584	-4.528356	35476.422725
HLA B*5101	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.456012	-0.072551	-4.528563	28576.702247
HLA B*5101	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.304109	-0.224761	-4.528869	20142.274322
HLA B*3901	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.500225	-0.028903	-4.529128	31639.143520
HLA B*4002	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.644951	0.115588	-4.529363	44152.026850
HLA A*0219	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.473441	-0.055990	-4.529431	29746.823012
HLA A*2601	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.375298	-0.154364	-4.529662	23730.008948
HLA B*4001	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.405132	-0.124662	-4.529793	25417.431543
HLA B*1503	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.457314	-0.072551	-4.529865	28662.477343
HLA A*2301	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.496057	-0.034117	-4.530174	31336.950539
HLA A*2402	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.577029	0.046803	-4.530227	37759.773734
HLA B*4501	1:63-71	9	DALRWLGLD	0.996990	-0.874455	-4.652843	0.122535	-4.530308	44961.683618
HLA A*1101	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.496456	-0.034117	-4.530573	31365.783798
HLA B*1801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.394573	-0.136008	-4.530581	24806.933186
HLA A*6901	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.305965	-0.224761	-4.530725	20228.542840
HLA A*2501	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.311580	-0.219267	-4.530847	20491.788686
HLA A*0202	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.444124	-0.086740	-4.530863	27805.052257
HLA A*0212	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.421999	-0.109399	-4.531397	26424.003327
HLA A*2902	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.387924	-0.143836	-4.531760	24430.031918
HLA A*0203	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.395785	-0.136008	-4.531794	24876.278553
HLA B*3801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.549214	0.017415	-4.531799	35417.167900
HLA A*0219	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.454015	-0.077849	-4.531864	28445.596644
HLA B*0702	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.407521	-0.124662	-4.532183	25557.660028
HLA A*3301	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.554035	0.021584	-4.532451	35812.527559
HLA B*5101	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.486083	-0.046382	-4.532465	30625.498622
HLA B*2705	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.460476	-0.072551	-4.533027	28871.950951
HLA B*0803	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.529694	-0.003611	-4.533305	33860.573451
HLA A*0202	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.556568	0.023199	-4.533369	36021.991413
HLA B*3501	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.382727	-0.150664	-4.533391	24139.427921
HLA B*1509	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.556664	0.023199	-4.533465	36029.982173
HLA B*1801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.460920	-0.072551	-4.533471	28901.486724
HLA A*0201	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.379125	-0.154364	-4.533490	23940.058816
HLA B*4002	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.477571	-0.055990	-4.533561	30031.082298
HLA B*5301	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.593100	0.059535	-4.533564	39183.196367
HLA A*6802	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.433375	-0.100479	-4.533854	27125.316968
HLA A*8001	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.409314	-0.124662	-4.533975	25663.373571

HLA B*1509	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.550847	0.016864	-4.533982	35550.582606
HLA B*1801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.493251	-0.041216	-4.534467	31135.184746
HLA A*0206	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.425116	-0.109399	-4.534515	26614.381748
HLA B*7301	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.581571	0.046803	-4.534768	38156.711444
HLA B*2705	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.488592	-0.046382	-4.534974	30802.957616
HLA B*4801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.434554	-0.100479	-4.535034	27199.083057
HLA B*1503	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.512411	-0.022687	-4.535099	32539.546597
HLA B*4601	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.426608	-0.108675	-4.535283	26705.966811
HLA A*0101	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.384757	-0.150664	-4.535421	24252.523194
HLA B*0801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.435076	-0.100479	-4.535555	27231.768654
HLA A*0201	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.399831	-0.136008	-4.535840	25109.104513
HLA B*3901	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.400038	-0.136008	-4.536046	25121.061056
HLA B*4001	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.435680	-0.100479	-4.536159	27269.656445
HLA A*0250	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.595752	0.059535	-4.536217	39423.250467
HLA B*0802	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.459022	-0.077849	-4.536871	28775.428535
HLA B*0801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.428309	-0.108675	-4.536984	26810.772783
HLA A*0202	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.317747	-0.219267	-4.537014	20784.867814
HLA A*0212	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.436720	-0.100479	-4.537200	27335.088758
HLA B*2705	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.514557	-0.022687	-4.537244	32700.664434
HLA B*4002	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.612941	0.075603	-4.537339	41014.862647
HLA B*5301	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.605627	0.067914	-4.537713	40329.915743
HLA B*4801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.428427	-0.109399	-4.537825	26818.025929
HLA B*1509	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.509047	-0.028903	-4.537950	32288.437911
HLA A*6801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.534642	-0.003611	-4.538253	34248.560651
HLA B*4801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.429792	-0.108675	-4.538466	26902.451500
HLA B*5701	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.413933	-0.124662	-4.538594	25937.781854
HLA A*0211	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.540135	0.001267	-4.538869	34684.498563
HLA A*3002	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.487483	-0.051442	-4.538926	30724.403595
HLA B*4403	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.632588	0.093574	-4.539014	42912.879298
HLA B*1801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.492645	-0.046382	-4.539027	31091.758082
HLA A*2603	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.606981	0.067914	-4.539066	40455.783645
HLA A*2402	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.560733	0.021584	-4.539150	36369.167099
HLA A*2602	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.632851	0.093574	-4.539277	42938.888415
HLA A*0206	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.452608	-0.086740	-4.539347	28353.567210
HLA B*0702	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.403435	-0.136008	-4.539444	25318.346218
HLA B*2705	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.430046	-0.109399	-4.539444	26918.174335
HLA B*1502	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.591333	0.051538	-4.539795	39024.113665
HLA A*6801	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.646114	0.106226	-4.539888	44270.419799
HLA A*3201	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.608066	0.067914	-4.540152	40557.024033
HLA A*1101	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.484262	-0.055990	-4.540253	30497.364992
HLA B*3901	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.431613	-0.108675	-4.540287	27015.481225
HLA A*3301	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.623702	0.083388	-4.540314	42043.794317
HLA A*0201	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.389677	-0.150664	-4.540341	24528.825306
HLA A*2601	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.390227	-0.150664	-4.540890	24559.896354
HLA A*2501	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.506803	-0.034117	-4.540921	32122.051683
HLA A*0201	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.397150	-0.143836	-4.540986	24954.591328
HLA B*3901	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.431923	-0.109399	-4.541321	27034.780015
HLA B*4403	1:270-278	9	HRDRGFIPE	0.743898	-0.637672	-4.647617	0.106226	-4.541392	44423.964217
HLA B*1501	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.432841	-0.108675	-4.541516	27092.026308
HLA A*0219	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.490101	-0.051442	-4.541543	30910.126872
HLA B*5401	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.521036	-0.020620	-4.541656	33192.231946
HLA B*4002	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.625269	0.083388	-4.541881	42195.779025
HLA B*4801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.405891	-0.136008	-4.541899	25461.884642
HLA A*2603	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.624061	0.082100	-4.541961	42078.608920
HLA B*5401	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.543333	0.001267	-4.542067	34940.818104
HLA B*4402	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.406508	-0.136008	-4.542517	25498.137618
HLA B*4601	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.392038	-0.150664	-4.542702	24662.550221
HLA A*2301	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.544021	0.001267	-4.542755	34996.246627
HLA A*2402	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.560073	0.016864	-4.543209	36313.921463
HLA B*1503	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.539649	-0.003611	-4.543260	34645.678970
HLA B*2705	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.487444	-0.055990	-4.543434	30721.578059
HLA A*0203	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.392846	-0.150664	-4.543510	24708.490007
HLA B*0802	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.497161	-0.046382	-4.543543	31416.730754
HLA B*4402	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.434178	-0.109399	-4.543577	27175.550199
HLA A*3002	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.561666	0.017995	-4.543671	36447.362045

HLA B*3901	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.497426	-0.046382	-4.543808	31435.942222
HLA B*4402	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.419200	-0.124662	-4.543862	26254.296085
HLA A*2403	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.389505	-0.154364	-4.543870	24519.140248
HLA B*4002	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.637665	0.093574	-4.544091	43417.507919
HLA A*0212	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.435562	-0.108675	-4.544237	27262.281151
HLA A*2301	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.540645	-0.003611	-4.544256	34725.240199
HLA A*2602	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.561739	0.017415	-4.544324	36453.475019
HLA A*2602	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.627712	0.083388	-4.544324	42433.853601
HLA A*8001	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.400684	-0.143836	-4.544520	25158.461963
HLA B*1801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.420145	-0.124662	-4.544806	26311.455415
HLA B*0803	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.516016	-0.028903	-4.544919	32810.708407
HLA B*0802	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.489459	-0.055990	-4.545450	30864.509408
HLA A*0202	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.541935	-0.003611	-4.545546	34828.528483
HLA A*0212	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.409560	-0.136008	-4.545569	25677.955493
HLA B*5101	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.489699	-0.055990	-4.545689	30881.545412
HLA A*0202	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.562575	0.016864	-4.545711	36523.749165
HLA A*2603	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.494306	-0.051442	-4.545749	31210.905289
HLA A*2902	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.459081	-0.086740	-4.545820	28779.320595
HLA A*2301	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.540439	-0.005447	-4.545886	34708.712480
HLA B*4403	1:441-449	9	ALKPRKAFS	0.996463	-0.885057	-4.657314	0.111406	-4.545908	45426.955891
HLA A*6802	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.437611	-0.108675	-4.546285	27391.192698
HLA A*2902	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.410352	-0.136008	-4.546360	25724.812512
HLA A*3201	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.540915	-0.005447	-4.546363	34746.850786
HLA B*1509	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.468615	-0.077849	-4.546464	29418.108629
HLA B*5401	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.541042	-0.005447	-4.546489	34757.003006
HLA A*3201	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.547797	0.001267	-4.546531	35301.819565
HLA B*1501	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.422133	-0.124662	-4.546794	26432.152787
HLA B*0801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.396293	-0.150664	-4.546957	24905.364372
HLA A*6802	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.396307	-0.150664	-4.546971	24906.172797
HLA B*1801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.495537	-0.051442	-4.546980	31299.506923
HLA B*5701	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.411015	-0.136008	-4.547023	25764.087948
HLA A*3002	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.548330	0.001267	-4.547064	35345.198412
HLA B*0803	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.500878	-0.046382	-4.547260	31686.762984
HLA B*1501	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.396838	-0.150664	-4.547502	24936.642577
HLA B*3801	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.564399	0.016864	-4.547534	36677.400861
HLA B*0803	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.513506	-0.034117	-4.547624	32621.682555
HLA A*0206	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.527079	-0.020620	-4.547699	33657.304519
HLA A*2603	1:328-336	9	NAEHIRMLD	0.906949	-0.791361	-4.663319	0.115588	-4.547731	46059.468157
HLA A*0216	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.423131	-0.124662	-4.547793	26492.995587
HLA A*0216	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.491861	-0.055990	-4.547851	31035.629017
HLA A*3301	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.623505	0.075603	-4.547902	42024.692668
HLA B*2705	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.461174	-0.086740	-4.547914	28918.377873
HLA A*0212	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.423401	-0.124662	-4.548063	26509.482994
HLA A*3002	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.461876	-0.086740	-4.548616	28965.192846
HLA B*1801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.397959	-0.150664	-4.548623	25001.075109
HLA A*0211	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.519895	-0.028903	-4.548798	33105.077351
HLA A*2501	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.470981	-0.077849	-4.548830	29578.808706
HLA B*0803	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.507654	-0.041216	-4.548870	32185.020501
HLA B*4801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.424238	-0.124662	-4.548899	26560.587348
HLA A*0219	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.462356	-0.086740	-4.549095	28997.176982
HLA A*2402	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.566729	0.017415	-4.549314	36874.763278
HLA B*1509	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.476767	-0.072551	-4.549318	29975.570696
HLA A*0202	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.571221	0.021903	-4.549318	37258.164540
HLA B*3801	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.571167	0.021584	-4.549584	37253.528890
HLA B*1517	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.498305	-0.051442	-4.549747	31499.610906
HLA A*3002	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.609356	0.059535	-4.549821	40677.658632
HLA B*4501	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.643936	0.093574	-4.550362	44048.960863
HLA A*3002	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.572446	0.021903	-4.550542	37363.326757
HLA A*0250	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.597425	0.046803	-4.550623	39575.395393
HLA A*3101	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.400064	-0.150664	-4.550728	25122.556024
HLA A*1101	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.464087	-0.086740	-4.550827	29113.022076
HLA A*0250	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.568261	0.017415	-4.550846	37005.059361
HLA B*3801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.574285	0.023199	-4.551087	37521.931369
HLA A*3002	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.602625	0.051538	-4.551087	40052.042917
HLA B*4403	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.626775	0.075603	-4.551172	42342.356971

HLA B*2705	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.426961	-0.124662	-4.551622	26727.647054
HLA B*4601	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.408235	-0.143836	-4.552071	25599.726899
HLA B*5701	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.408261	-0.143836	-4.552097	25601.250353
HLA B*2705	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.500937	-0.051442	-4.552379	31691.048820
HLA A*0216	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.500939	-0.051442	-4.552381	31691.220266
HLA A*2501	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.506115	-0.046382	-4.552497	32071.175431
HLA A*3002	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.574210	0.021584	-4.552626	37515.436268
HLA B*1509	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.547285	-0.005447	-4.552732	35260.210698
HLA A*2602	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.547346	-0.005447	-4.552793	35265.170647
HLA A*0219	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.444157	-0.108675	-4.552831	27807.158249
HLA B*3801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.574978	0.021903	-4.553075	37581.861077
HLA B*4501	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.443804	-0.109399	-4.553203	27784.602355
HLA B*0702	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.444955	-0.108675	-4.553630	27858.352756
HLA A*2501	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.399575	-0.154364	-4.553940	25094.302593
HLA A*8001	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.453700	-0.100479	-4.554180	28424.983189
HLA B*4801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.403574	-0.150664	-4.554238	25326.428705
HLA A*2602	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.629860	0.075603	-4.554257	42644.193273
HLA A*0206	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.476692	-0.077849	-4.554542	29970.381881
HLA A*3002	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.261148	-0.293904	-4.555052	18245.180876
HLA B*1502	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.577187	0.021903	-4.555284	37773.462720
HLA A*2403	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.411494	-0.143836	-4.555330	25792.537339
HLA B*5301	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.602141	0.046803	-4.555338	40007.432294
HLA A*0203	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.446666	-0.108675	-4.555340	27968.286412
HLA B*1503	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.469249	-0.086740	-4.555989	29461.110177
HLA B*1517	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.455526	-0.100479	-4.556005	28544.718623
HLA B*3501	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.447357	-0.108675	-4.556031	28012.805573
HLA B*1517	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.500293	-0.055990	-4.556283	31644.107673
HLA A*2902	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.456050	-0.100479	-4.556529	28579.175903
HLA A*0206	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.522453	-0.034117	-4.556571	33300.687225
HLA A*2301	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.534140	-0.022687	-4.556827	34208.933478
HLA A*2402	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.551850	-0.005447	-4.557297	35632.800183
HLA B*1502	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.616968	0.059535	-4.557433	41396.943706
HLA B*4501	1:351-359	9	HGHHIALDE	0.892348	-0.816745	-4.633363	0.075603	-4.557760	42989.558517
HLA A*3301	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.480101	-0.077849	-4.557951	30206.567647
HLA A*0301	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.365707	-0.192252	-4.557959	23211.718991
HLA A*0216	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.457518	-0.100479	-4.557997	28675.970810
HLA A*0250	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.581376	0.023199	-4.558177	38139.582133
HLA A*0216	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.471763	-0.086740	-4.558503	29632.142752
HLA B*1502	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.535869	-0.022687	-4.558556	34345.413980
HLA B*5101	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.507365	-0.051442	-4.558807	32163.611185
HLA B*1502	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.605630	0.046803	-4.558827	40330.133924
HLA A*0219	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.449530	-0.109399	-4.558928	28153.337110
HLA B*5801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.366812	-0.192252	-4.559063	23270.813315
HLA A*0211	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.538890	-0.020620	-4.559510	34585.192174
HLA B*4001	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.415986	-0.143836	-4.559822	26060.712386
HLA A*2301	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.531026	-0.028903	-4.559929	33964.597076
HLA B*5401	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.487444	-0.072551	-4.559994	30721.578059
HLA B*3901	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.335681	-0.224369	-4.560050	21661.118881
HLA A*3201	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.577652	0.017415	-4.560237	37813.945747
HLA B*1502	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.583481	0.023199	-4.560282	38324.903417
HLA A*3002	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.519227	-0.041216	-4.560443	33054.253481
HLA A*2601	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.368409	-0.192252	-4.560661	23356.577885
HLA B*4002	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.643003	0.082100	-4.560903	43954.457285
HLA B*4403	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.505072	-0.055990	-4.561062	31994.233208
HLA B*7301	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.562430	0.001267	-4.561163	36511.500674
HLA B*4501	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.644591	0.083388	-4.561203	44115.496762
HLA A*2501	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.460951	-0.100479	-4.561430	28903.519396
HLA B*7301	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.585119	0.023199	-4.561920	38469.687648
HLA A*0219	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.461496	-0.100479	-4.561975	28939.818812
HLA A*2603	1:280-288	9	LLNYLALLG	0.742104	-0.648530	-4.655552	0.093574	-4.561978	45243.013212
HLA A*0219	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.426333	-0.136008	-4.562342	26689.068430
HLA B*1503	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.521206	-0.041216	-4.562422	33205.163238
HLA B*3501	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.438187	-0.124662	-4.562848	27427.521681
HLA B*1503	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.412443	-0.150664	-4.563107	25848.971033
HLA B*3901	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.511702	-0.051442	-4.563144	32486.427329

HLA A*2301	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.542929	-0.020620	-4.563548	34908.320762
HLA A*3201	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.615164	0.051538	-4.563626	41225.304707
HLA A*0212	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.269733	-0.293904	-4.563637	18609.435155
HLA A*2501	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.476918	-0.086740	-4.563658	29985.951022
HLA A*0206	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.565369	0.001267	-4.564102	36759.440214
HLA A*2602	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.439636	-0.124662	-4.564298	27519.225013
HLA B*3801	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.541686	-0.022687	-4.564373	34808.561850
HLA B*3901	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.508572	-0.055990	-4.564563	32253.172456
HLA A*3301	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.428561	-0.136008	-4.564569	26826.296909
HLA B*1503	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.543974	-0.020620	-4.564594	34992.460315
HLA A*3002	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.518283	-0.046382	-4.564665	32982.446013
HLA A*3201	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.611609	0.046803	-4.564806	40889.246121
HLA B*5701	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.410521	-0.154364	-4.564886	25734.834587
HLA A*2402	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.587069	0.021903	-4.565166	38642.812941
HLA A*0216	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.456764	-0.108675	-4.565439	28626.216067
HLA B*0802	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.456099	-0.109399	-4.565498	28582.422901
HLA A*2902	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.414953	-0.150664	-4.565616	25998.752510
HLA B*1509	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.519483	-0.046382	-4.565865	33073.750592
HLA B*0702	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.465711	-0.100479	-4.566190	29222.057020
HLA A*0206	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.537450	-0.028903	-4.566353	34470.688581
HLA A*3301	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.617932	0.051538	-4.566394	41488.866293
HLA A*0202	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.583913	0.017415	-4.566498	38363.071770
HLA A*2603	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.649892	0.083388	-4.566504	44657.212621
HLA A*0250	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.588443	0.021903	-4.566540	38765.302866
HLA A*2602	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.626688	0.059535	-4.567153	42333.882323
HLA A*2602	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.584061	0.016864	-4.567197	38376.149017
HLA A*2501	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.442587	-0.124662	-4.567249	27706.849931
HLA B*5301	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.589174	0.021903	-4.567271	38830.579437
HLA B*3801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.568597	0.001267	-4.567331	37033.698075
HLA A*0203	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.423711	-0.143836	-4.567547	26528.420319
HLA A*8001	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.431556	-0.136008	-4.567565	27011.973834
HLA B*4501	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.650366	0.082100	-4.568266	44706.040591
HLA A*0301	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.264694	-0.303590	-4.568283	18394.735440
HLA A*2403	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.460081	-0.108675	-4.568756	28845.722271
HLA B*7301	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.586359	0.017415	-4.568944	38579.730379
HLA A*2402	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.570270	0.001267	-4.569003	37176.621075
HLA A*0219	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.444380	-0.124662	-4.569041	27821.453118
HLA B*4801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.425455	-0.143836	-4.569291	26635.123069
HLA A*6802	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.377147	-0.192252	-4.569399	23831.256808
HLA A*0206	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.528625	-0.041216	-4.569841	33777.328161
HLA A*3201	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.629587	0.059535	-4.570052	42617.440426
HLA A*6801	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.617105	0.046803	-4.570302	41409.935011
HLA B*1801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.536484	-0.034117	-4.570602	34394.129376
HLA B*4801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.345955	-0.224761	-4.570716	22179.675290
HLA A*0219	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.416515	-0.154364	-4.570879	26092.453452
HLA A*3001	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.314063	-0.257009	-4.571072	20609.301578
HLA A*0250	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.588288	0.016864	-4.571424	38751.464081
HLA B*4002	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.594660	0.023199	-4.571461	39324.202035
HLA B*0802	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.484725	-0.086740	-4.571465	30529.884828
HLA B*5701	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.420970	-0.150664	-4.571633	26361.464943
HLA B*4403	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.551239	-0.020620	-4.571859	35582.715345
HLA B*5801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.352637	-0.219267	-4.571904	22523.564376
HLA B*0702	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.421437	-0.150664	-4.572101	26389.860133
HLA A*0211	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.549719	-0.022687	-4.572406	35458.386501
HLA A*0250	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.590605	0.017995	-4.572609	38958.722513
HLA A*3201	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.500117	-0.072551	-4.572667	31631.270944
HLA A*0211	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.538615	-0.034117	-4.572733	34563.308160
HLA B*0702	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.429118	-0.143836	-4.572953	26860.714137
HLA B*1509	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.531865	-0.041216	-4.573081	34030.257321
HLA A*2902	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.418719	-0.154364	-4.573083	26225.195495
HLA B*4403	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.569485	-0.003611	-4.573096	37109.507181
HLA B*5401	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.539125	-0.034117	-4.573242	34603.907442
HLA B*7301	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.567819	-0.005447	-4.573267	36967.442159
HLA B*5101	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.472999	-0.100479	-4.573478	29716.584113
HLA B*5301	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.591575	0.017995	-4.573580	39045.864685

HLA B*5301	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.596906	0.023199	-4.573707	39528.107898
HLA B*3501	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.473473	-0.100479	-4.573953	29749.076076
HLA A*3101	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.420058	-0.154364	-4.574422	26306.189286
HLA A*2402	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.571085	-0.003611	-4.574696	37246.475747
HLA A*0216	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.465762	-0.109399	-4.575161	29225.535164
HLA A*6801	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.657278	0.082100	-4.575178	45423.269718
HLA B*4002	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.626759	0.051538	-4.575221	42340.753529
HLA B*3801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.541221	-0.034117	-4.575338	34771.296341
HLA A*2403	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.439411	-0.136008	-4.575419	27504.936632
HLA B*5801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.350788	-0.224761	-4.575549	22427.872289
HLA B*4002	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.643569	0.067914	-4.575655	44011.801746
HLA B*1509	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.577600	0.001267	-4.576334	37809.445491
HLA A*0301	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.357437	-0.219267	-4.576704	22773.884670
HLA B*0803	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.504167	-0.072551	-4.576718	31927.664733
HLA B*3901	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.490265	-0.086740	-4.577005	30921.834513
HLA A*6801	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.660396	0.083388	-4.577008	45750.533163
HLA A*2602	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.548488	-0.028903	-4.577391	35358.012046
HLA B*5801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.353229	-0.224369	-4.577598	22554.291513
HLA A*3002	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.442049	-0.136008	-4.578057	27672.546149
HLA B*4501	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.646041	0.067914	-4.578126	44262.995982
HLA A*0212	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.427550	-0.150664	-4.578214	26763.964702
HLA A*2603	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.595257	0.016864	-4.578392	39378.275029
HLA A*2402	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.601598	0.023199	-4.578399	39957.466858
HLA B*0803	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.522627	-0.055990	-4.578617	33314.021218
HLA B*5101	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.492091	-0.086740	-4.578831	31052.087512
HLA A*3301	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.625683	0.046803	-4.578880	42235.974467
HLA A*0301	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.364765	-0.214129	-4.578894	23161.418867
HLA A*0202	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.580227	0.001267	-4.578961	38038.819656
HLA A*0211	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.532718	-0.046382	-4.579100	34097.151253
HLA A*8001	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.428493	-0.150664	-4.579156	26822.088548
HLA A*2602	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.601584	0.021903	-4.579681	39956.169886
HLA B*4801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.425497	-0.154364	-4.579861	26637.716871
HLA B*4001	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.425664	-0.154364	-4.580028	26647.950440
HLA B*5401	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.557348	-0.022687	-4.580035	36086.748043
HLA B*4001	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.388471	-0.192252	-4.580723	24460.845491
HLA B*7301	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.529368	-0.051442	-4.580810	33835.120731
HLA A*0211	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.502971	-0.077849	-4.580821	31839.868578
HLA B*0802	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.480654	-0.100479	-4.581133	30244.994401
HLA B*1502	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.598083	0.016864	-4.581219	39635.388400
HLA A*6801	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.633267	0.051538	-4.581729	42980.024256
HLA B*4001	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.431112	-0.150664	-4.581776	26984.369042
HLA B*5301	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.598734	0.016864	-4.581870	39694.828112
HLA A*1101	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.530439	-0.051442	-4.581881	33918.691949
HLA B*5801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.367822	-0.214129	-4.581951	23325.010112
HLA A*3301	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.553058	-0.028903	-4.581961	35732.021593
HLA A*3201	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.603597	0.021584	-4.582014	40141.847771
HLA A*3201	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.578573	-0.003611	-4.582184	37894.221984
HLA A*2603	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.390121	-0.192252	-4.582373	24553.918097
HLA B*3501	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.438812	-0.143836	-4.582647	27467.019134
HLA A*2301	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.510342	-0.072551	-4.582892	32384.828457
HLA A*0216	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.428594	-0.154364	-4.582958	26828.328768
HLA A*0211	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.473629	-0.109399	-4.583027	29759.699960
HLA B*1509	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.358412	-0.224761	-4.583173	22825.071848
HLA B*5401	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.554401	-0.028903	-4.583304	35842.764038
HLA B*4501	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.630337	0.046803	-4.583534	42691.051170
HLA A*0216	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.364373	-0.219267	-4.583640	23140.503098
HLA A*3301	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.643224	0.059535	-4.583688	43976.815111
HLA B*7301	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.561140	-0.022687	-4.583827	36403.221329
HLA B*5101	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.506122	-0.077849	-4.583971	32071.695940
HLA A*2602	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.635557	0.051538	-4.584020	43207.327438
HLA A*0206	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.537671	-0.046382	-4.584053	34488.222404
HLA A*2501	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.475482	-0.108675	-4.584157	29886.997824
HLA B*1801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.429806	-0.154364	-4.584170	26903.324750
HLA B*3501	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.261916	-0.322910	-4.584826	18277.485782
HLA A*3002	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.562331	-0.022687	-4.585018	36503.205644

HLA B*3801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.533933	-0.051442	-4.585375	34192.651499
HLA B*4402	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.328487	-0.257009	-4.585496	21305.256286
HLA B*4403	1:67-75	9	WLGLDWDEG	0.705252	-0.621864	-4.668925	0.083388	-4.585537	46657.857258
HLA B*1503	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.282056	-0.303590	-4.585646	19145.038330
HLA A*0301	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.360971	-0.224761	-4.585731	22959.939663
HLA A*3002	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.557068	-0.028903	-4.585971	36063.523708
HLA B*0801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.393732	-0.192252	-4.585984	24758.935093
HLA B*1501	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.366748	-0.219267	-4.586015	23267.414466
HLA B*4402	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.442251	-0.143836	-4.586087	27685.423809
HLA A*0101	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.367310	-0.219267	-4.586577	23297.517841
HLA A*2602	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.633567	0.046803	-4.586765	43009.796760
HLA B*1801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.500058	-0.086740	-4.586798	31626.993191
HLA A*1101	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.486584	-0.100479	-4.587063	30660.808919
HLA B*5301	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.558386	-0.028903	-4.587289	36173.140877
HLA A*2402	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.514909	-0.072551	-4.587460	32727.211249
HLA B*1509	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.584052	-0.003611	-4.587663	38375.318583
HLA B*4403	1:155-163	9	VVRLRMPDD	0.825831	-0.743731	-4.669935	0.082100	-4.587835	46766.521548
HLA B*4002	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.510024	-0.077849	-4.587874	32361.185317
HLA B*4403	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.605919	0.017995	-4.587923	40356.979186
HLA A*2602	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.609586	0.021584	-4.588003	40699.230389
HLA B*4002	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.634834	0.046803	-4.588031	43135.393354
HLA B*3801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.582645	-0.005447	-4.588092	38251.163729
HLA A*0211	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.546954	-0.041216	-4.588170	35233.324664
HLA A*2301	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.510377	-0.077849	-4.588226	32387.456539
HLA A*2603	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.611548	0.023199	-4.588349	40883.495162
HLA B*5101	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.434028	-0.154364	-4.588392	27166.142758
HLA A*2402	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.554430	-0.034117	-4.588547	35845.090978
HLA B*4403	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.640092	0.051538	-4.588554	43660.822230
HLA A*2301	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.547560	-0.041216	-4.588776	35282.535961
HLA A*6801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.547774	-0.041216	-4.588990	35299.909827
HLA B*0802	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.453052	-0.136008	-4.589060	28382.572680
HLA B*4002	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.648597	0.059535	-4.589062	44524.294420
HLA A*0301	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.365092	-0.224369	-4.589461	23178.842215
HLA A*2603	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.611395	0.021584	-4.589812	40869.121303
HLA A*0203	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.365580	-0.224369	-4.589949	23204.939049
HLA A*0250	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.591413	0.001267	-4.590146	39031.292273
HLA B*4002	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.607192	0.016864	-4.590328	40475.485958
HLA B*4501	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.650000	0.059535	-4.590464	44668.327170
HLA B*5401	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.534565	-0.055990	-4.590555	34242.446927
HLA A*3301	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.608590	0.017995	-4.590595	40605.981767
HLA A*0101	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.376581	-0.214129	-4.590710	23800.206259
HLA B*3901	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.466075	-0.124662	-4.590736	29246.570950
HLA B*1801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.490709	-0.100479	-4.591189	30953.467301
HLA A*2301	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.544940	-0.046382	-4.591322	35070.351368
HLA B*1503	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.482192	-0.109399	-4.591591	30352.356961
HLA A*3201	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.613858	0.021903	-4.591955	41101.489485
HLA B*0802	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.483785	-0.108675	-4.592460	30463.890941
HLA B*3801	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.588930	-0.003611	-4.592541	38808.738392
HLA A*0201	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.400332	-0.192252	-4.592583	25138.054571
HLA B*4501	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.610103	0.017415	-4.592688	40747.698457
HLA A*0211	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.438476	-0.154364	-4.592840	27445.778476
HLA B*3801	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.563957	-0.028903	-4.592860	36640.116738
HLA A*2602	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.541519	-0.051442	-4.592961	34795.194375
HLA B*5401	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.449645	-0.143836	-4.593481	28160.801114
HLA A*0202	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.570949	-0.022687	-4.593636	37234.790621
HLA A*2601	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.374732	-0.219267	-4.593999	23699.090319
HLA A*3002	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.617264	0.023199	-4.594066	41425.171388
HLA A*0212	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.369842	-0.224369	-4.594211	23433.782667
HLA B*1801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.450627	-0.143836	-4.594463	28224.554138
HLA A*3301	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.589078	-0.005447	-4.594525	38821.967558
HLA B*0801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.380770	-0.214129	-4.594899	24030.889838
HLA A*2402	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.553692	-0.041216	-4.594908	35784.252424
HLA B*7301	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.539203	-0.055990	-4.595193	34610.085702
HLA A*0211	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.470703	-0.124662	-4.595365	29559.932599
HLA B*4501	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.647093	0.051538	-4.595556	44370.403227

HLA B*0803	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.486894	-0.108675	-4.595568	30682.711787
HLA A*2602	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.618947	0.023199	-4.595748	41585.942157
HLA B*1801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.486459	-0.109399	-4.595858	30652.018986
HLA B*4403	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.655932	0.059535	-4.596397	45282.681662
HLA A*3301	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.618474	0.021903	-4.596571	41540.746691
HLA B*3801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.576000	-0.020620	-4.596620	37670.406684
HLA A*0202	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.567723	-0.028903	-4.596626	36959.243488
HLA B*4403	1:184-192	9	DFALTRASG	0.793377	-0.725463	-4.664555	0.067914	-4.596640	46190.721717
HLA B*5301	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.593309	-0.003611	-4.596920	39202.066840
HLA B*1509	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.576416	-0.020620	-4.597036	37706.495272
HLA A*6802	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.372704	-0.224369	-4.597073	23588.703447
HLA A*0250	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.593675	-0.003611	-4.597286	39235.165103
HLA A*2301	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.541313	-0.055990	-4.597303	34778.633360
HLA A*3301	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.545880	-0.051442	-4.597322	35146.324225
HLA B*1502	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.615646	0.017995	-4.597650	41271.050056
HLA B*4501	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.620866	0.023199	-4.597667	41770.153804
HLA B*0802	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.473321	-0.124662	-4.597982	29738.616866
HLA A*3002	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.577408	-0.020620	-4.598027	37792.676528
HLA A*2601	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.373773	-0.224369	-4.598142	23646.838550
HLA B*2705	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.497687	-0.100479	-4.598167	31454.825101
HLA B*1517	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.473650	-0.124662	-4.598311	29761.148965
HLA A*2602	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.616729	0.017995	-4.598733	41374.106814
HLA A*0212	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.454924	-0.143836	-4.598760	28505.213502
HLA A*3002	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.564652	-0.034117	-4.598770	36698.836555
HLA A*3101	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.384654	-0.214129	-4.598783	24246.750929
HLA A*2402	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.569892	-0.028903	-4.598795	37144.254628
HLA A*3201	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.616794	0.017995	-4.598799	41380.374510
HLA A*1101	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.490150	-0.108675	-4.598825	30913.638699
HLA A*6901	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.385095	-0.214129	-4.599225	24271.423854
HLA B*1502	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.601067	0.001267	-4.599800	39908.643315
HLA A*3001	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.305988	-0.293904	-4.599892	20229.637212
HLA A*0219	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.456158	-0.143836	-4.599994	28586.288856
HLA B*0803	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.490658	-0.109399	-4.600056	30949.783514
HLA B*1503	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.464245	-0.136008	-4.600253	29123.576370
HLA A*2602	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.513706	-0.086740	-4.600446	32636.686777
HLA A*3201	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.623885	0.023199	-4.600687	42061.539338
HLA A*2403	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.450310	-0.150664	-4.600974	28203.948283
HLA B*5101	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.465112	-0.136008	-4.601120	29181.772350
HLA B*3801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.554820	-0.046382	-4.601202	35877.295819
HLA A*0216	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.457382	-0.143836	-4.601218	28666.974460
HLA A*8001	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.447197	-0.154364	-4.601561	28002.502329
HLA A*2402	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.579080	-0.022687	-4.601768	37938.528631
HLA B*5401	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.550447	-0.051442	-4.601889	35517.902435
HLA A*0206	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.545908	-0.055990	-4.601898	35148.605951
HLA B*2705	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.458355	-0.143836	-4.602190	28731.251667
HLA B*4403	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.649217	0.046803	-4.602415	44587.929927
HLA A*2603	1:386-394	9	FNDDQYVID	1.069129	-1.017591	-4.653989	0.051538	-4.602452	45080.540451
HLA A*3301	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.603924	0.001267	-4.602657	40172.044773
HLA A*6801	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.662546	0.059535	-4.603011	45977.561962
HLA A*0216	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.467017	-0.136008	-4.603025	29310.086322
HLA B*3801	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.530589	-0.072551	-4.603140	33930.437750
HLA B*5401	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.557155	-0.046382	-4.603537	36070.743118
HLA A*0250	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.574659	-0.028903	-4.603562	37554.220583
HLA B*4501	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.621571	0.017995	-4.603576	41838.000416
HLA A*6901	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.346785	-0.257009	-4.603794	22222.072082
HLA B*7301	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.557656	-0.046382	-4.604037	36112.331622
HLA B*3801	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.562883	-0.041216	-4.604099	36549.642555
HLA B*0702	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.412032	-0.192252	-4.604284	25824.510602
HLA A*0211	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.548321	-0.055990	-4.604311	35344.433566
HLA B*2705	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.496052	-0.108675	-4.604727	31336.611482
HLA A*0211	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.553506	-0.051442	-4.604948	35768.962173
HLA A*2603	1:395-403	9	PKAAAKELG	0.905113	-0.845578	-4.664928	0.059535	-4.605393	46230.470792
HLA B*1502	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.533099	-0.072551	-4.605650	34127.047165
HLA B*5301	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.607380	0.001267	-4.606114	40493.007181
HLA B*3901	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.505805	-0.100479	-4.606284	32048.281408

HLA B*4002	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.585673	-0.020620	-4.606293	38518.834567
HLA B*2705	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.452298	-0.154364	-4.606662	28333.327003
HLA A*2501	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.497610	-0.109399	-4.607008	31449.210088
HLA B*1501	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.414873	-0.192252	-4.607124	25993.970837
HLA A*3101	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.414898	-0.192252	-4.607150	25995.517752
HLA A*2402	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.587163	-0.020620	-4.607782	38651.175979
HLA B*5701	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.415617	-0.192252	-4.607869	26038.587050
HLA B*1517	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.499313	-0.108675	-4.607988	31572.801439
HLA B*5301	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.603337	-0.005447	-4.608784	40117.749920
HLA A*0101	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.384567	-0.224369	-4.608936	24241.898042
HLA B*1509	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.553614	-0.055990	-4.609605	35777.864563
HLA A*0219	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.459003	-0.150664	-4.609667	28774.183187
HLA B*5801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.352921	-0.257009	-4.609931	22538.313051
HLA A*2603	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.587275	-0.022687	-4.609963	38661.214014
HLA A*0211	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.523409	-0.086740	-4.610149	33374.090288
HLA A*1101	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.474223	-0.136008	-4.610231	29800.460007
HLA A*1101	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.455970	-0.154364	-4.610334	28573.919641
HLA B*3501	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.418637	-0.192252	-4.610888	26220.230326
HLA B*1502	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.559573	-0.051442	-4.611015	36272.100799
HLA A*6801	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.605592	-0.005447	-4.611039	40326.643170
HLA A*0201	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.386754	-0.224369	-4.611123	24364.302944
HLA B*1509	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.475442	-0.136008	-4.611451	29884.249300
HLA B*0801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.387163	-0.224369	-4.611532	24387.248365
HLA A*2403	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.392616	-0.219267	-4.611883	24695.393800
HLA A*3301	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.629343	0.017415	-4.611928	42593.469385
HLA B*7301	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.591321	-0.020620	-4.611941	39023.058098
HLA B*1503	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.512111	-0.100479	-4.612590	32517.021873
HLA A*2601	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.398490	-0.214129	-4.612619	25031.660991
HLA A*6901	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.309543	-0.303590	-4.613133	20395.899589
HLA B*4001	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.399171	-0.214129	-4.613300	25070.963181
HLA A*0250	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.319671	-0.293904	-4.613575	20877.163628
HLA B*1502	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.584771	-0.028903	-4.613674	38438.898697
HLA B*1503	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.557916	-0.055990	-4.613907	36134.023506
HLA A*2603	1:38-46	9	GGTFVFRIE	0.930381	-0.883578	-4.660763	0.046803	-4.613960	45789.160289
HLA A*2602	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.591418	-0.022687	-4.614105	39031.714585
HLA A*0212	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.421980	-0.192252	-4.614232	26422.859745
HLA B*0801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.389557	-0.224761	-4.614318	24522.058630
HLA B*5101	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.489713	-0.124662	-4.614375	30882.547823
HLA A*0201	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.400339	-0.214129	-4.614468	25138.462556
HLA A*6801	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.632498	0.017995	-4.614503	42904.058355
HLA A*0202	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.568280	-0.046382	-4.614662	37006.660942
HLA A*0203	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.389985	-0.224761	-4.614745	24546.214935
HLA B*4601	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.422508	-0.192252	-4.614760	26455.041894
HLA B*0802	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.471509	-0.143836	-4.615345	29614.834695
HLA B*4501	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.592712	-0.022687	-4.615399	39148.235809
HLA A*3001	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.292932	-0.322910	-4.615842	19630.529145
HLA B*5301	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.595283	-0.020620	-4.615902	39380.618452
HLA A*0101	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.391197	-0.224761	-4.615958	24614.831490
HLA B*1502	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.569636	-0.046382	-4.616017	37122.357938
HLA A*2501	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.472205	-0.143836	-4.616041	29662.295725
HLA B*1517	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.461891	-0.154364	-4.616255	28966.133052
HLA A*2602	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.617774	0.001267	-4.616508	41473.830856
HLA A*2601	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.391772	-0.224761	-4.616533	24647.478180
HLA B*0702	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.462245	-0.154364	-4.616610	28989.804958
HLA B*4601	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.402507	-0.214129	-4.616637	25264.301052
HLA B*4001	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.391902	-0.224761	-4.616662	24654.812978
HLA B*4002	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.634660	0.017995	-4.616665	43118.128341
HLA B*1502	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.613063	-0.003611	-4.616674	41026.402335
HLA A*0206	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.565261	-0.051442	-4.616703	36750.293585
HLA A*2902	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.424484	-0.192252	-4.616736	26575.679066
HLA A*0250	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.596225	-0.020620	-4.616844	39466.142141
HLA B*4801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.425175	-0.192252	-4.617427	26617.981513
HLA A*0250	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.594890	-0.022687	-4.617577	39345.056040
HLA B*4403	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.594935	-0.022687	-4.617622	39349.100444
HLA A*3301	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.561687	-0.055990	-4.617677	36449.136674

HLA A*3101	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.398814	-0.219267	-4.618081	25050.355723
HLA B*0802	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.467600	-0.150664	-4.618264	29349.436664
HLA B*0803	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.517804	-0.100479	-4.618283	32946.066091
HLA B*5301	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.595809	-0.022687	-4.618496	39428.369409
HLA A*3101	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.393871	-0.224761	-4.618631	24766.838997
HLA A*3301	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.641993	0.023199	-4.618794	43852.326963
HLA B*5101	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.509446	-0.109399	-4.618845	32318.146638
HLA A*0201	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.324974	-0.293904	-4.618878	21133.638907
HLA A*3301	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.426669	-0.192252	-4.618921	26709.723460
HLA A*3201	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.584881	-0.034117	-4.618999	38448.673599
HLA A*0206	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.519014	-0.100479	-4.619493	33037.984880
HLA A*0201	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.394759	-0.224761	-4.619519	24817.537470
HLA B*4001	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.401037	-0.219267	-4.620304	25178.885922
HLA B*1501	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.406391	-0.214129	-4.620520	25491.241445
HLA A*6801	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.599932	-0.020620	-4.620552	39804.499092
HLA A*1101	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.317122	-0.303590	-4.620712	20754.979265
HLA B*4002	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.642300	0.021584	-4.620717	43883.415924
HLA B*4601	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.402171	-0.219267	-4.621438	25244.763789
HLA B*5101	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.513022	-0.108675	-4.621697	32585.347989
HLA B*4001	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.397367	-0.224369	-4.621736	24967.014564
HLA B*1503	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.513452	-0.108675	-4.622127	32617.623774
HLA B*1503	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.478487	-0.143836	-4.622323	30094.510468
HLA B*4403	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.644168	0.021584	-4.622585	44072.558881
HLA B*1502	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.582158	-0.041216	-4.623374	38208.352252
HLA B*4501	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.620084	-0.003611	-4.623695	41694.972900
HLA A*6801	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.641260	0.017415	-4.623845	43778.371692
HLA B*0803	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.537304	-0.086740	-4.624044	34459.128598
HLA B*1501	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.399942	-0.224369	-4.624311	25115.489686
HLA A*2603	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.618928	-0.005447	-4.624375	41584.142394
HLA B*4002	1:466-474	9	ESLELLGRD	0.894117	-0.897728	-4.620918	-0.003611	-4.624529	41775.125482
HLA A*0201	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.406172	-0.219267	-4.625440	25478.419526
HLA B*4002	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.643036	0.017415	-4.625621	43957.786454
HLA B*5701	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.411626	-0.214129	-4.625755	25800.352470
HLA B*0702	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.406633	-0.219267	-4.625900	25505.449597
HLA A*2603	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.647836	0.021903	-4.625933	44446.320411
HLA A*2402	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.579557	-0.046382	-4.625939	37980.215894
HLA A*0301	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.369051	-0.257009	-4.626060	23391.098694
HLA A*1101	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.482582	-0.143836	-4.626418	30379.626883
HLA A*0212	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.407547	-0.219267	-4.626814	25559.180978
HLA B*4501	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.643997	0.016864	-4.627132	44055.157099
HLA A*1101	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.503260	-0.124662	-4.627922	31861.062399
HLA A*8001	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.408891	-0.219267	-4.628158	25638.395254
HLA B*5401	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.550602	-0.077849	-4.628452	35530.586461
HLA B*5301	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.594390	-0.034117	-4.628507	39299.744592
HLA B*4002	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.630067	0.001267	-4.628800	42664.499737
HLA B*7301	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.599923	-0.028903	-4.628826	39803.637750
HLA A*0250	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.594726	-0.034117	-4.628843	39330.159194
HLA B*4501	1:185-193	9	FALTRASGD	0.880898	-0.859314	-4.650759	0.021584	-4.629175	44746.448580
HLA B*5701	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.404965	-0.224369	-4.629334	25407.670528
HLA B*5701	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.404721	-0.224761	-4.629481	25393.379470
HLA A*3201	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.600689	-0.028903	-4.629592	39873.898333
HLA B*4403	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.653059	0.023199	-4.629860	44984.067058
HLA B*4601	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.406198	-0.224369	-4.630567	25479.935761
HLA B*0802	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.476220	-0.154364	-4.630584	29937.810168
HLA B*4403	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.632033	0.001267	-4.630767	42858.125933
HLA A*3301	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.610232	-0.020620	-4.630852	40759.824490
HLA B*4801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.406584	-0.224369	-4.630953	25502.552147
HLA A*8001	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.439075	-0.192252	-4.631326	27483.666652
HLA A*2603	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.648834	0.017415	-4.631419	44548.629089
HLA A*2602	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.553605	-0.077849	-4.631454	35777.090354
HLA B*0702	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.407429	-0.224369	-4.631798	25552.268297
HLA A*3002	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.440022	-0.192252	-4.632273	27543.651504
HLA A*0202	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.598170	-0.034117	-4.632287	39643.322847
HLA A*2602	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.591277	-0.041216	-4.632493	39019.047207
HLA A*0206	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.481847	-0.150664	-4.632511	30328.228732

HLA A*2902	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.407946	-0.224761	-4.632707	25582.698088
HLA B*2705	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.496715	-0.136008	-4.632723	31384.454748
HLA A*2301	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.545983	-0.086740	-4.632723	35154.691280
HLA A*2501	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.482061	-0.150664	-4.632725	30343.162992
HLA B*1517	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.488912	-0.143836	-4.632748	30825.629075
HLA A*0202	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.591662	-0.041216	-4.632878	39053.681118
HLA B*4402	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.440771	-0.192252	-4.633023	27591.226128
HLA B*1517	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.440966	-0.192252	-4.633218	27603.617944
HLA A*2403	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.441062	-0.192252	-4.633314	27609.741256
HLA B*1501	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.408560	-0.224761	-4.633320	25618.845887
HLA B*4402	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.409676	-0.224761	-4.634436	25684.763225
HLA A*0219	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.410326	-0.224369	-4.634695	25723.281705
HLA B*0803	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.498839	-0.136008	-4.634847	31538.317603
HLA A*2603	1:350-358	9	THGHHIALD	0.944144	-0.926149	-4.652861	0.017995	-4.634866	44963.629562
HLA B*4403	1:209-217	9	ITHVLRGED	0.748602	-0.731738	-4.651788	0.016864	-4.634923	44852.602415
HLA A*0211	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.416475	-0.219267	-4.635742	26090.053889
HLA B*4601	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.410982	-0.224761	-4.635743	25762.136690
HLA A*3101	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.411626	-0.224369	-4.635995	25800.352470
HLA A*2902	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.416912	-0.219267	-4.636179	26116.319941
HLA A*0212	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.411478	-0.224761	-4.636238	25791.560614
HLA A*0250	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.595099	-0.041216	-4.636315	39364.004464
HLA B*2705	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.485865	-0.150664	-4.636528	30610.094206
HLA A*6802	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.422497	-0.214129	-4.636626	26454.326310
HLA A*0216	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.486370	-0.150664	-4.637034	30645.718321
HLA B*5401	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.487220	-0.150664	-4.637884	30705.793084
HLA B*4403	1:14-22	9	SPTGTPHVG	0.810850	-0.793435	-4.655448	0.017415	-4.638033	45232.245068
HLA A*2301	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.537605	-0.100479	-4.638084	34482.998630
HLA B*3901	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.487599	-0.150664	-4.638262	30732.549239
HLA B*5301	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.565841	-0.072551	-4.638392	36799.433718
HLA A*6801	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.640078	0.001267	-4.638811	43659.405052
HLA A*0202	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.582938	-0.055990	-4.638929	38277.039297
HLA A*0206	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.502938	-0.136008	-4.638947	31837.457168
HLA B*1509	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.488454	-0.150664	-4.639118	30793.127390
HLA A*6801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.561424	-0.077849	-4.639273	36427.058555
HLA B*1801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.447112	-0.192252	-4.639364	27997.049204
HLA B*1517	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.488745	-0.150664	-4.639409	30813.791159
HLA A*0219	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.420201	-0.219267	-4.639468	26314.871847
HLA A*6801	1:468-476	9	LELLGRDRS	1.024128	-1.002225	-4.661491	0.021903	-4.639588	45866.016144
HLA B*3801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.539137	-0.100479	-4.639616	34604.843471
HLA A*2603	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.584158	-0.055990	-4.640148	38384.662000
HLA A*0250	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.562319	-0.077849	-4.640169	36502.218266
HLA B*5701	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.420981	-0.219267	-4.640248	26362.178016
HLA B*5101	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.416083	-0.224369	-4.640452	26066.493435
HLA A*1101	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.490004	-0.150664	-4.640668	30903.271597
HLA B*3801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.532323	-0.108675	-4.640998	34066.175748
HLA A*6801	1:72-80	9	WDEGPEVGG	0.897034	-0.873835	-4.664465	0.023199	-4.641267	46181.226999
HLA A*0201	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.384353	-0.257009	-4.641362	24229.966695
HLA B*3801	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.563694	-0.077849	-4.641543	36617.922937
HLA A*0101	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.384564	-0.257009	-4.641573	24241.766896
HLA B*4801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.427778	-0.214129	-4.641908	26778.013025
HLA B*4501	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.643198	0.001267	-4.641931	43974.198182
HLA B*0803	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.517315	-0.124662	-4.641976	32909.014152
HLA A*2402	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.586167	-0.055990	-4.642157	38562.619786
HLA A*2601	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.338669	-0.303590	-4.642259	21810.691292
HLA A*2301	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.533101	-0.109399	-4.642500	34127.231789
HLA B*0802	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.450688	-0.192252	-4.642940	28228.524402
HLA B*4402	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.418679	-0.224369	-4.643048	26222.783724
HLA A*3301	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.620434	-0.022687	-4.643121	41728.595662
HLA B*4501	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.622605	-0.020620	-4.643224	41937.708174
HLA A*0203	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.429360	-0.214129	-4.643489	26875.685597
HLA A*0250	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.597507	-0.046382	-4.643889	39582.889550
HLA B*1502	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.623573	-0.020620	-4.644192	42031.286304
HLA B*1502	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.419807	-0.224761	-4.644567	26290.966141
HLA A*3201	1:48-56	9	TDAQRDSEE	0.851414	-0.874101	-4.622128	-0.022687	-4.644815	41891.677149
HLA B*5101	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.494248	-0.150664	-4.644911	31206.684386

HLA A*2902	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.420580	-0.224369	-4.644949	26337.801878
HLA A*0301	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.351242	-0.293904	-4.645145	22451.301653
HLA A*0203	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.452923	-0.192252	-4.645174	28374.128875
HLA A*0216	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.453637	-0.192252	-4.645889	28420.831540
HLA A*0250	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.594526	-0.051442	-4.645968	39312.077748
HLA A*3201	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.625603	-0.020620	-4.646222	42228.206456
HLA A*2601	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.389273	-0.257009	-4.646282	24506.011827
HLA B*5301	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.600003	-0.046382	-4.646385	39810.959754
HLA B*3901	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.503178	-0.143836	-4.647014	31855.030201
HLA B*4402	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.427858	-0.219267	-4.647125	26782.938925
HLA B*1502	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.613249	-0.034117	-4.647366	41043.939997
HLA B*4001	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.353499	-0.293904	-4.647403	22568.327743
HLA B*4403	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.613331	-0.034117	-4.647449	41051.712243
HLA A*0211	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.547043	-0.100479	-4.647522	35240.568527
HLA B*7301	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.569899	-0.077849	-4.647748	37144.857471
HLA A*2403	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.423241	-0.224761	-4.648002	26499.732679
HLA B*5801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.354209	-0.293904	-4.648113	22605.229710
HLA A*2402	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.547731	-0.100479	-4.648211	35296.472560
HLA A*6802	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.423563	-0.224761	-4.648324	26519.380364
HLA B*5101	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.504592	-0.143836	-4.648428	31958.943293
HLA B*3801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.592520	-0.055990	-4.648510	39130.873076
HLA A*3201	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.505175	-0.143836	-4.649011	32001.849865
HLA B*1517	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.424790	-0.224369	-4.649159	26594.375932
HLA B*7301	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.608177	-0.041216	-4.649393	40567.337567
HLA A*8001	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.425025	-0.224369	-4.649394	26608.767087
HLA B*5401	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.549397	-0.100479	-4.649876	35432.116084
HLA A*2602	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.629472	-0.020620	-4.650092	42606.144698
HLA A*0202	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.499454	-0.150664	-4.650118	31583.051424
HLA A*3002	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.549773	-0.100479	-4.650252	35462.798772
HLA B*2705	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.436373	-0.214129	-4.650502	27313.211307
HLA A*3301	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.609572	-0.041216	-4.650788	40697.909340
HLA B*5301	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.426423	-0.224369	-4.650792	26694.555620
HLA A*3201	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.431624	-0.219267	-4.650892	27016.211988
HLA B*1509	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.496614	-0.154364	-4.650978	31377.154781
HLA B*7301	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.550703	-0.100479	-4.651183	35538.852734
HLA B*1517	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.347706	-0.303590	-4.651295	22269.247914
HLA B*1503	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.527180	-0.124662	-4.651842	33665.134968
HLA A*3301	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.432844	-0.219267	-4.652111	27092.172873
HLA A*3002	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.596302	-0.055990	-4.652292	39473.188516
HLA B*0803	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.498164	-0.154364	-4.652529	31489.388001
HLA B*4801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.433382	-0.219267	-4.652649	27125.757206
HLA B*4002	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.647406	-0.005447	-4.652853	44402.339897
HLA A*0203	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.434176	-0.219267	-4.653443	27175.403183
HLA A*2603	1:254-262	9	GTKKLSKRD	0.951078	-0.949811	-4.654713	0.001267	-4.653446	45155.718329
HLA B*1509	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.566783	-0.086740	-4.653523	36879.351796
HLA A*0212	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.439535	-0.214129	-4.653664	27512.824091
HLA A*0250	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.597996	-0.055990	-4.653986	39627.455541
HLA A*2602	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.620187	-0.034117	-4.654304	41704.898950
HLA A*2403	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.440318	-0.214129	-4.654447	27562.432925
HLA B*1509	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.545137	-0.109399	-4.654536	35086.292034
HLA A*2603	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.500272	-0.154364	-4.654636	31642.566990
HLA A*0202	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.603203	-0.051442	-4.654645	40105.380971
HLA A*2301	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.546366	-0.108675	-4.655041	35185.704778
HLA A*2603	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.577485	-0.077849	-4.655335	37799.424119
HLA B*4002	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.621439	-0.034117	-4.655557	41825.327355
HLA A*2902	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.442115	-0.214129	-4.656244	27676.738218
HLA A*0219	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.431669	-0.224761	-4.656430	27018.989071
HLA A*0219	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.442326	-0.214129	-4.656456	27690.217026
HLA A*0206	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.548368	-0.108675	-4.657043	35348.257962
HLA B*0803	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.514162	-0.143836	-4.657998	32670.957564
HLA A*0212	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.354794	-0.303590	-4.658384	22635.700883
HLA A*2602	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.612448	-0.046382	-4.658830	40968.293075
HLA A*3201	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.617636	-0.041216	-4.658852	41460.595208
HLA B*1503	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.434197	-0.224761	-4.658958	27176.726358
HLA B*5801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.355656	-0.303590	-4.659246	22680.687111

HLA A*3201	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.607904	-0.051442	-4.659346	40541.887637
HLA A*0219	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.467536	-0.192252	-4.659788	29345.149993
HLA A*0211	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.435236	-0.224761	-4.659996	27241.788314
HLA B*7301	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.509385	-0.150664	-4.660049	32313.601180
HLA B*7301	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.516399	-0.143836	-4.660234	32839.654041
HLA B*5301	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.604344	-0.055990	-4.660335	40210.965024
HLA A*3201	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.509912	-0.150664	-4.660575	32352.783028
HLA B*3801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.551267	-0.109399	-4.660666	35585.025403
HLA B*5301	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.610315	-0.051442	-4.661757	40767.542936
HLA B*4403	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.615998	-0.046382	-4.662380	41304.554419
HLA B*3501	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.448327	-0.214129	-4.662456	28075.464115
HLA B*1517	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.448576	-0.214129	-4.662705	28091.568558
HLA A*0250	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.553405	-0.109399	-4.662804	35760.642378
HLA A*2402	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.576068	-0.086740	-4.662808	37676.317137
HLA B*1509	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.562702	-0.100479	-4.663182	36534.420553
HLA B*4501	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.658080	-0.005447	-4.663527	45507.142643
HLA B*5301	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.509214	-0.154364	-4.663578	32300.842351
HLA B*5401	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.538996	-0.124662	-4.663657	34593.612792
HLA B*5301	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.577053	-0.086740	-4.663793	37761.816552
HLA A*2602	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.519970	-0.143836	-4.663806	33110.808880
HLA B*4402	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.449760	-0.214129	-4.663889	28168.267098
HLA B*7301	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.577154	-0.086740	-4.663894	37770.601925
HLA A*8001	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.450068	-0.214129	-4.664197	28188.236897
HLA A*0202	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.528318	-0.136008	-4.664326	33753.398801
HLA A*0211	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.555670	-0.108675	-4.664345	35947.626037
HLA A*6801	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.608381	-0.055990	-4.664371	40586.435499
HLA B*0803	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.513767	-0.150664	-4.664431	32641.277683
HLA A*8001	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.440860	-0.224761	-4.665621	27596.898799
HLA A*3201	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.619384	-0.046382	-4.665765	41627.808630
HLA A*8001	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.408802	-0.257009	-4.665811	25633.125162
HLA B*3901	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.441911	-0.224761	-4.666671	27663.714939
HLA B*2705	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.442364	-0.224369	-4.666733	27692.613946
HLA B*4501	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.530848	-0.136008	-4.666856	33950.635349
HLA A*0211	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.516312	-0.150664	-4.666975	32833.081320
HLA A*2403	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.443099	-0.224369	-4.667468	27739.545442
HLA A*0206	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.448273	-0.219267	-4.667540	28071.970974
HLA B*7301	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.543190	-0.124662	-4.667851	34929.289424
HLA B*1801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.448642	-0.219267	-4.667909	28095.824104
HLA A*2603	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.364403	-0.303590	-4.667993	23142.130594
HLA B*5401	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.558858	-0.109399	-4.668257	36212.496500
HLA B*0802	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.364871	-0.303590	-4.668461	23167.058085
HLA B*7301	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.596375	-0.072551	-4.668926	39479.808984
HLA B*1517	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.444333	-0.224761	-4.669094	27818.443061
HLA B*1501	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.375300	-0.293904	-4.669204	23730.137325
HLA B*4501	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.640317	-0.028903	-4.669220	43683.503340
HLA A*2601	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.375378	-0.293904	-4.669282	23734.374158
HLA A*0212	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.412432	-0.257009	-4.669441	25848.271842
HLA B*2705	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.450192	-0.219267	-4.669460	28196.320303
HLA B*3501	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.450449	-0.219267	-4.669716	28212.951953
HLA B*1509	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.545102	-0.124662	-4.669764	35083.444955
HLA A*0219	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.412854	-0.257009	-4.669864	25873.454633
HLA A*0206	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.445646	-0.224369	-4.670015	27902.696928
HLA A*0250	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.583342	-0.086740	-4.670082	38312.672693
HLA B*5401	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.561424	-0.108675	-4.670099	36427.058555
HLA A*2301	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.526351	-0.143836	-4.670187	33600.906315
HLA A*6801	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.623888	-0.046382	-4.670269	42061.766887
HLA A*2902	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.413921	-0.257009	-4.670930	25937.080261
HLA A*0211	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.535166	-0.136008	-4.671175	34289.903229
HLA A*2602	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.517482	-0.154364	-4.671846	32921.657002
HLA B*4501	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.599617	-0.072551	-4.672168	39775.654266
HLA A*2603	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.548243	-0.124662	-4.672905	35338.124217
HLA B*4601	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.369962	-0.303590	-4.673552	23440.249041
HLA B*3801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.587193	-0.086740	-4.673933	38653.894356
HLA B*0702	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.380479	-0.293904	-4.674382	24014.774692
HLA A*3301	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.640672	-0.034117	-4.674790	43719.202678

HLA A*1101	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.450416	-0.224761	-4.675176	28210.815229
HLA B*4002	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.646283	-0.028903	-4.675186	44287.667018
HLA B*0702	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.461256	-0.214129	-4.675385	28923.853974
HLA B*5801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.352482	-0.322910	-4.675392	22515.523712
HLA B*3901	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.483788	-0.192252	-4.676039	30464.055748
HLA B*1502	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.620323	-0.055990	-4.676314	41717.986898
HLA A*2301	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.540478	-0.136008	-4.676487	34711.904722
HLA A*1101	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.484488	-0.192252	-4.676740	30513.207892
HLA A*0216	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.452450	-0.224369	-4.676819	28343.291965
HLA A*0202	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.576832	-0.100479	-4.677311	37742.618433
HLA B*7301	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.452570	-0.224761	-4.677331	28351.113081
HLA A*2603	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.604824	-0.072551	-4.677375	40255.367041
HLA B*0802	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.452704	-0.224761	-4.677465	28359.856883
HLA B*1503	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.453559	-0.224369	-4.677928	28415.758125
HLA B*4501	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.643844	-0.034117	-4.677961	44039.668144
HLA B*3501	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.374424	-0.303590	-4.678014	23682.300831
HLA A*3301	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.631678	-0.046382	-4.678060	42823.129714
HLA A*3301	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.534400	-0.143836	-4.678236	34229.482033
HLA B*4501	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.622358	-0.055990	-4.678348	41913.892712
HLA A*1101	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.465088	-0.214129	-4.679217	29180.193691
HLA A*0216	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.454487	-0.224761	-4.679248	28476.544860
HLA A*0101	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.376531	-0.303590	-4.680121	23797.502527
HLA B*5301	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.602350	-0.077849	-4.680199	40026.699716
HLA A*2402	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.571532	-0.108675	-4.680206	37284.780298
HLA B*4403	1:246-254	9	HLPTVLGEG	0.570249	-0.575696	-4.675024	-0.005447	-4.680471	47317.746495
HLA B*7301	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.571947	-0.108675	-4.680622	37320.499452
HLA A*6901	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.386984	-0.293904	-4.680888	24377.223570
HLA B*4601	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.424630	-0.257009	-4.681639	26584.594393
HLA A*2603	1:300-308	9	LDEMVAAFD	0.975559	-0.996179	-4.661244	-0.020620	-4.681864	45839.969886
HLA A*2603	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.640792	-0.041216	-4.682008	43731.266661
HLA A*2603	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.653125	-0.028903	-4.682027	44990.881621
HLA B*2705	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.457537	-0.224761	-4.682298	28677.211907
HLA A*3201	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.490728	-0.192252	-4.682980	30954.806969
HLA B*1801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.458756	-0.224369	-4.683125	28757.842988
HLA B*4402	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.228030	-0.455159	-4.683188	16905.570554
HLA A*3201	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.627301	-0.055990	-4.683292	42393.699184
HLA A*0206	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.539463	-0.143836	-4.683299	34630.875220
HLA A*0211	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.539572	-0.143836	-4.683407	34639.494356
HLA B*4002	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.642197	-0.041216	-4.683413	43872.971373
HLA B*1502	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.558896	-0.124662	-4.683558	36215.631125
HLA A*2402	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.574297	-0.109399	-4.683695	37522.946330
HLA B*3501	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.390826	-0.293904	-4.684729	24593.800645
HLA A*0216	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.470983	-0.214129	-4.685112	29578.968725
HLA A*3002	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.576635	-0.108675	-4.685309	37725.470925
HLA A*0203	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.391547	-0.293904	-4.685451	24634.680852
HLA A*0101	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.391686	-0.293904	-4.685589	24642.545089
HLA B*4403	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.535324	-0.150664	-4.685988	34302.334288
HLA B*1801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.461291	-0.224761	-4.686052	28926.201192
HLA A*3101	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.429233	-0.257009	-4.686242	26867.835441
HLA B*4001	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.429674	-0.257009	-4.686684	26895.175520
HLA B*1502	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.577309	-0.109399	-4.686708	37784.090428
HLA A*2301	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.536068	-0.150664	-4.686732	34361.211027
HLA A*6802	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.430074	-0.257009	-4.687083	26919.921884
HLA B*5701	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.430518	-0.257009	-4.687527	26947.460747
HLA A*2602	1:293-301	9	DDHDLFGLD	0.923893	-0.979883	-4.631685	-0.055990	-4.687676	42823.824725
HLA B*1509	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.495592	-0.192252	-4.687843	31303.401683
HLA A*2602	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.578723	-0.109399	-4.688122	37907.344482
HLA B*7301	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.552130	-0.136008	-4.688138	35655.747139
HLA A*6901	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.365482	-0.322910	-4.688392	23199.667129
HLA B*4501	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.601840	-0.086740	-4.688580	39979.738105
HLA A*3002	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.469454	-0.219267	-4.688721	29474.979617
HLA A*0201	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.385323	-0.303590	-4.688913	24284.163850
HLA A*3201	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.602263	-0.086740	-4.689003	40018.688538
HLA B*3801	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.553288	-0.136008	-4.689296	35750.970631
HLA A*0250	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.470873	-0.219267	-4.690140	29571.448790

HLA B*1801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.386980	-0.303590	-4.690569	24376.959816
HLA B*4002	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.644189	-0.046382	-4.690571	44074.704782
HLA B*1502	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.603879	-0.086740	-4.690619	40167.915786
HLA B*4002	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.639192	-0.051442	-4.690634	43570.451207
HLA B*1501	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.433824	-0.257009	-4.690833	27153.359740
HLA B*4501	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.644669	-0.046382	-4.691051	44123.373244
HLA A*2603	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.582424	-0.108675	-4.691098	38231.716826
HLA A*0301	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.368252	-0.322910	-4.691162	23348.113533
HLA A*2301	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.536848	-0.154364	-4.691213	34422.982077
HLA B*1502	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.536924	-0.154364	-4.691288	34428.941778
HLA A*1101	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.466921	-0.224369	-4.691290	29303.585906
HLA B*4403	1:49-57	9	DAQRDSEES	1.072008	-1.100911	-4.662506	-0.028903	-4.691409	45973.333687
HLA B*4501	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.650322	-0.041216	-4.691538	44701.445587
HLA A*2603	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.657885	-0.034117	-4.692002	45486.713576
HLA B*5701	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.388713	-0.303590	-4.692303	24474.479327
HLA A*0203	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.435327	-0.257009	-4.692336	27247.536548
HLA B*0803	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.388953	-0.303590	-4.692543	24487.988285
HLA B*4801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.435560	-0.257009	-4.692569	27262.133666
HLA A*3001	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.288207	-0.404745	-4.692952	19418.120506
HLA B*0803	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.501054	-0.192252	-4.693306	31699.622233
HLA B*5301	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.559152	-0.136008	-4.695160	36236.992980
HLA A*0250	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.595073	-0.100479	-4.695553	39361.662030
HLA A*1101	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.476384	-0.219267	-4.695652	29949.149531
HLA A*0250	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.571017	-0.124662	-4.695679	37240.632725
HLA B*4001	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.372878	-0.322910	-4.695788	23598.148645
HLA A*2902	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.401990	-0.293904	-4.695894	25234.249984
HLA B*3801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.545462	-0.150664	-4.696126	35112.496001
HLA B*1509	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.553231	-0.143836	-4.697067	35746.329121
HLA B*5301	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.472412	-0.224761	-4.697172	29676.420423
HLA B*4501	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.646109	-0.051442	-4.697551	44269.940805
HLA A*0250	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.543615	-0.154364	-4.697979	34963.508583
HLA B*4001	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.394467	-0.303590	-4.698057	24800.894797
HLA A*2501	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.394759	-0.303590	-4.698348	24817.537470
HLA B*5101	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.484739	-0.214129	-4.698869	30530.875824
HLA B*3801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.574400	-0.124662	-4.699062	37531.879173
HLA A*2402	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.555299	-0.143836	-4.699135	35916.912484
HLA B*5101	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.481055	-0.219267	-4.700322	30272.986720
HLA B*4403	1:107-115	9	AYHAFSTPE	0.482563	-0.560412	-4.622607	-0.077849	-4.700456	41937.935053
HLA A*0202	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.592240	-0.108675	-4.700915	39105.689635
HLA B*5301	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.600837	-0.100479	-4.701316	39887.490592
HLA B*0802	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.487629	-0.214129	-4.701758	30734.710691
HLA B*5101	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.509559	-0.192252	-4.701811	32326.539932
HLA A*2601	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.379386	-0.322910	-4.702296	23954.439084
HLA B*4601	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.408973	-0.293904	-4.702877	25643.250244
HLA B*0803	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.483696	-0.219267	-4.702963	30457.628946
HLA B*0802	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.479124	-0.224369	-4.703493	30138.663785
HLA B*0802	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.484478	-0.219267	-4.703746	30512.547607
HLA A*2402	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.567758	-0.136008	-4.703767	36962.242791
HLA A*6801	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.617163	-0.086740	-4.703903	41415.535969
HLA A*0216	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.447599	-0.257009	-4.704608	28028.419179
HLA A*2403	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.447671	-0.257009	-4.704681	28033.120123
HLA A*3201	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.569027	-0.136008	-4.705035	37070.379950
HLA B*1502	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.605329	-0.100479	-4.705808	40302.216352
HLA A*6801	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.581172	-0.124662	-4.705833	38121.635567
HLA B*4002	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.633372	-0.072551	-4.705923	42990.488802
HLA B*4002	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.605498	-0.100479	-4.705977	40317.917608
HLA B*2705	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.513814	-0.192252	-4.706066	32644.809587
HLA A*2603	1:312-320	9	VNSSPARFD	0.843613	-0.889995	-4.659785	-0.046382	-4.706167	45686.227018
HLA A*2501	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.481913	-0.224761	-4.706674	30332.823106
HLA A*6801	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.597569	-0.109399	-4.706967	39588.457557
HLA A*8001	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.413261	-0.293904	-4.707165	25897.681214
HLA A*2602	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.515085	-0.192252	-4.707337	32740.492737
HLA B*5301	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.599542	-0.108675	-4.708217	39768.769042
HLA B*0702	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.451713	-0.257009	-4.708722	28295.185938
HLA A*3101	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.386900	-0.322910	-4.709809	24372.476422

HLA A*0250	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.601448	-0.108675	-4.710122	39943.634662
HLA B*3901	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.491088	-0.219267	-4.710355	30980.439273
HLA B*4403	1:461-469	9	SPPLFESLE	0.732367	-0.773583	-4.669233	-0.041216	-4.710449	46690.935190
HLA A*3201	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.601964	-0.109399	-4.711363	39991.202904
HLA A*2603	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.575570	-0.136008	-4.711579	37633.131070
HLA A*0202	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.568036	-0.143836	-4.711871	36985.845797
HLA B*3801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.568336	-0.143836	-4.712172	37011.466100
HLA B*4801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.418533	-0.293904	-4.712437	26213.989733
HLA B*1801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.498620	-0.214129	-4.712749	31522.454045
HLA B*5301	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.603513	-0.109399	-4.712911	40134.030667
HLA A*0206	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.488226	-0.224761	-4.712987	30776.972651
HLA A*2403	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.390276	-0.322910	-4.713186	24562.686705
HLA B*1502	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.577441	-0.136008	-4.713449	37795.538995
HLA B*3901	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.500739	-0.214129	-4.714869	31676.650707
HLA A*2501	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.490601	-0.224369	-4.714970	30945.765338
HLA A*0219	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.421080	-0.293904	-4.714984	26368.168588
HLA A*3002	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.560806	-0.154364	-4.715171	36375.266959
HLA A*3101	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.421851	-0.293904	-4.715754	26414.998953
HLA B*1502	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.607105	-0.108675	-4.715780	40467.384957
HLA A*0216	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.412784	-0.303590	-4.716374	25869.255798
HLA B*5701	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.422602	-0.293904	-4.716506	26460.767267
HLA B*4403	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.665260	-0.051442	-4.716702	46265.748588
HLA A*3201	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.616282	-0.100479	-4.716762	41331.601090
HLA A*8001	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.413284	-0.303590	-4.716874	25899.082288
HLA A*3301	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.607509	-0.109399	-4.716908	40505.057421
HLA B*1801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.460006	-0.257009	-4.717015	28840.729034
HLA B*4501	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.592543	-0.124662	-4.717205	39132.990070
HLA A*3201	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.608712	-0.108675	-4.717387	40617.406414
HLA A*2602	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.616964	-0.100479	-4.717443	41396.495803
HLA B*4002	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.630703	-0.086740	-4.717443	42727.095179
HLA A*6801	1:156-164	9	VRLRMPDDD	0.610006	-0.644123	-4.683421	-0.034117	-4.717538	48241.534378
HLA A*3301	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.631032	-0.086740	-4.717772	42759.468276
HLA A*0101	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.394904	-0.322910	-4.717814	24825.862994
HLA B*0702	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.394914	-0.322910	-4.717824	24826.400220
HLA B*3801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.563590	-0.154364	-4.717955	36609.207623
HLA A*6801	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.618056	-0.100479	-4.718535	41500.763857
HLA B*5401	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.504423	-0.214129	-4.718553	31946.497324
HLA A*2501	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.504644	-0.214129	-4.718773	31962.747194
HLA B*0801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.425013	-0.293904	-4.718917	26608.047344
HLA A*0250	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.575220	-0.143836	-4.719056	37602.808224
HLA B*1517	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.499865	-0.219267	-4.719132	31612.966223
HLA A*6801	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.564974	-0.154364	-4.719339	36726.046156
HLA B*1502	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.569384	-0.150664	-4.720048	37100.875577
HLA A*2603	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.620633	-0.100479	-4.721113	41747.788576
HLA A*0201	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.398231	-0.322910	-4.721141	25016.769386
HLA A*3201	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.596532	-0.124662	-4.721194	39494.121531
HLA A*0212	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.398830	-0.322910	-4.721740	25051.304379
HLA B*1501	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.399890	-0.322910	-4.722800	25112.500679
HLA B*0801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.318950	-0.404745	-4.723695	20842.518861
HLA A*0250	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.587687	-0.136008	-4.723695	38697.833100
HLA A*3301	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.616033	-0.108675	-4.724708	41307.906351
HLA A*2301	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.505617	-0.219267	-4.724884	32034.414197
HLA A*2403	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.431046	-0.293904	-4.724950	26980.281843
HLA A*2603	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.574337	-0.150664	-4.725001	37526.397404
HLA A*6801	1:84-92	9	PYRQSQRAE	0.712462	-0.763904	-4.673774	-0.051442	-4.725216	47181.758917
HLA B*0801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.403428	-0.322910	-4.726338	25317.935313
HLA B*0803	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.512209	-0.214129	-4.726339	32524.411079
HLA B*4002	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.617058	-0.109399	-4.726456	41405.454790
HLA B*5301	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.601906	-0.124662	-4.726567	39985.794570
HLA B*5101	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.404138	-0.322910	-4.727048	25359.333223
HLA A*6801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.424386	-0.303590	-4.727975	26569.641350
HLA A*3002	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.586037	-0.143836	-4.729873	38551.147420
HLA B*1502	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.510781	-0.219267	-4.730048	32417.607123
HLA A*0212	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.325576	-0.404745	-4.730320	21162.927829
HLA B*5401	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.511103	-0.219267	-4.730370	32441.642494

HLA B*3501	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.473452	-0.257009	-4.730462	29747.627658
HLA B*4403	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.644051	-0.086740	-4.730791	44060.639111
HLA B*4801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.427506	-0.303590	-4.731096	26761.213832
HLA A*0206	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.516986	-0.214129	-4.731115	32884.098812
HLA B*0801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.474117	-0.257009	-4.731126	29793.206117
HLA B*0803	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.506573	-0.224761	-4.731334	32105.026076
HLA A*0206	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.539160	-0.192252	-4.731412	34606.715605
HLA B*4601	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.408952	-0.322910	-4.731862	25642.001730
HLA A*0202	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.438311	-0.293904	-4.732215	27435.386941
HLA B*4403	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.607636	-0.124662	-4.732298	40516.892054
HLA A*1101	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.475893	-0.257009	-4.732903	29915.306158
HLA B*1503	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.540974	-0.192252	-4.733226	34751.550520
HLA B*4403	1:459-467	9	TVSPPLFES	0.850861	-0.923412	-4.662701	-0.072551	-4.735252	45993.981305
HLA B*7301	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.625974	-0.109399	-4.735372	42264.316973
HLA A*3301	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.635088	-0.100479	-4.735567	43160.603349
HLA A*0211	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.511678	-0.224369	-4.736047	32484.669897
HLA B*5301	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.592247	-0.143836	-4.736083	39106.324312
HLA A*2403	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.432555	-0.303590	-4.736145	27074.151294
HLA A*2902	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.432604	-0.303590	-4.736194	27077.227300
HLA A*0211	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.544653	-0.192252	-4.736905	35047.212346
HLA B*4002	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.628474	-0.108675	-4.737148	42508.297056
HLA B*2705	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.433572	-0.303590	-4.737162	27137.646345
HLA B*1503	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.523475	-0.214129	-4.737605	33379.146074
HLA B*1509	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.523788	-0.214129	-4.737917	33403.171521
HLA A*2402	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.583688	-0.154364	-4.738052	38343.153107
HLA B*4403	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.638085	-0.100479	-4.738565	43459.572502
HLA B*2705	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.481737	-0.257009	-4.738746	30320.518312
HLA A*1101	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.445106	-0.293904	-4.739010	27867.999904
HLA A*2602	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.630551	-0.108675	-4.739225	42712.073145
HLA B*1509	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.435844	-0.303590	-4.739434	27279.985207
HLA A*2301	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.549033	-0.192252	-4.741285	35402.417545
HLA A*0211	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.527354	-0.214129	-4.741484	33678.614890
HLA A*6801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.522860	-0.219267	-4.742127	33331.868288
HLA B*4403	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.632766	-0.109399	-4.742165	42930.526623
HLA A*6801	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.598882	-0.143836	-4.742718	39708.359329
HLA A*2402	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.592383	-0.150664	-4.743047	39118.596769
HLA A*0203	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.339630	-0.404745	-4.744375	21859.004031
HLA A*2603	1:397-405	9	AAAKELGPD	0.565511	-0.652251	-4.657882	-0.086740	-4.744622	45486.467499
HLA B*4403	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.635971	-0.108675	-4.744645	43248.486475
HLA B*3801	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.552428	-0.192252	-4.744680	35680.253048
HLA A*2602	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.526342	-0.219267	-4.745609	33600.179214
HLA A*2301	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.531898	-0.214129	-4.746027	34032.834818
HLA A*3002	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.595663	-0.150664	-4.746327	39415.146834
HLA A*0206	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.452932	-0.293904	-4.746836	28374.742885
HLA B*5301	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.596192	-0.150664	-4.746856	39463.153150
HLA A*6802	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.453019	-0.293904	-4.746923	28380.423110
HLA B*4403	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.592830	-0.154364	-4.747194	39158.826623
HLA A*2501	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.490864	-0.257009	-4.747874	30964.521293
HLA A*2902	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.425029	-0.322910	-4.747939	26609.054990
HLA A*0250	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.597562	-0.150664	-4.748225	39587.815055
HLA B*0803	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.524194	-0.224369	-4.748563	33434.448545
HLA B*7301	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.594448	-0.154364	-4.748813	39305.060133
HLA B*4501	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.595447	-0.154364	-4.749811	39395.534410
HLA A*2402	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.531001	-0.219267	-4.750268	33962.575944
HLA B*5101	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.493508	-0.257009	-4.750517	31153.549891
HLA A*2603	1:104-112	9	AGEAYHAFS	0.915833	-1.025232	-4.641436	-0.109399	-4.750834	43796.138006
HLA B*0803	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.494109	-0.257009	-4.751118	31196.725318
HLA B*2705	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.457314	-0.293904	-4.751217	28662.477343
HLA B*4403	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.615751	-0.136008	-4.751760	41281.098510
HLA B*4501	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.601365	-0.150664	-4.752029	39936.072206
HLA B*5701	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.429176	-0.322910	-4.752086	26864.347220
HLA B*4501	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.644326	-0.108675	-4.753000	44088.536430
HLA B*3801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.528534	-0.224761	-4.753294	33770.202380
HLA B*4002	1:282-290	9	NYLALLGWS	0.691708	-0.816370	-4.628812	-0.124662	-4.753474	42541.424943
HLA B*5801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.349153	-0.404745	-4.753898	22343.583791

HLA A*2603	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.610089	-0.143836	-4.753925	40746.375835
HLA B*4501	1:393-401	9	IDPKAAAKE	0.687509	-0.787988	-4.653874	-0.100479	-4.754353	45068.591879
HLA B*4402	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.460478	-0.293904	-4.754382	28872.107145
HLA B*3801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.530994	-0.224369	-4.755363	33962.024748
HLA B*3901	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.499123	-0.257009	-4.756132	31558.969236
HLA B*4402	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.452725	-0.303590	-4.756315	28361.237730
HLA A*2301	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.531861	-0.224761	-4.756621	34029.889123
HLA B*5401	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.564443	-0.192252	-4.756695	36681.171047
HLA B*3901	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.463474	-0.293904	-4.757378	29071.944048
HLA B*0802	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.500800	-0.257009	-4.757810	31681.106567
HLA B*4402	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.435365	-0.322910	-4.758275	27249.895148
HLA B*5301	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.435696	-0.322910	-4.758606	27270.689145
HLA A*3201	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.605371	-0.154364	-4.759736	40306.141093
HLA B*1502	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.616249	-0.143836	-4.760085	41328.470818
HLA A*0216	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.437435	-0.322910	-4.760345	27380.081204
HLA B*1502	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.458059	-0.303590	-4.761648	28711.673797
HLA A*2501	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.469056	-0.293904	-4.762960	29448.043806
HLA B*1517	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.469522	-0.293904	-4.763425	29479.604215
HLA B*4601	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.359507	-0.404745	-4.764252	22882.686638
HLA B*3801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.550743	-0.214129	-4.764873	35542.121325
HLA B*5101	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.461327	-0.303590	-4.764916	28928.548600
HLA A*0101	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.360360	-0.404745	-4.765105	22927.667576
HLA A*3001	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.310382	-0.455159	-4.765540	20435.328874
HLA B*1517	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.508615	-0.257009	-4.765624	32256.313358
HLA A*6801	1:294-302	9	DHDLFGLDE	0.840446	-0.949121	-4.657008	-0.108675	-4.765683	45395.018999
HLA B*1501	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.361196	-0.404745	-4.765941	22971.866990
HLA B*7301	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.546827	-0.219267	-4.766094	35223.033315
HLA A*2602	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.615970	-0.150664	-4.766634	41301.873069
HLA A*0219	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.463124	-0.303590	-4.766714	29048.519367
HLA A*6901	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.362500	-0.404745	-4.767245	23040.943405
HLA A*6802	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.444605	-0.322910	-4.767515	27835.905924
HLA B*4801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.445881	-0.322910	-4.768791	27917.796061
HLA A*0203	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.446788	-0.322910	-4.769698	27976.155396
HLA A*0219	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.447046	-0.322910	-4.769956	27992.808619
HLA A*0301	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.366567	-0.404745	-4.771312	23257.724176
HLA A*2301	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.546998	-0.224369	-4.771367	35236.946409
HLA B*3901	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.450009	-0.322910	-4.772919	28184.424773
HLA A*0211	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.518111	-0.257009	-4.775121	32969.423095
HLA A*3002	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.551653	-0.224369	-4.776022	35616.611224
HLA B*4002	1:359-367	9	EAAFAAAAE	0.661129	-0.797137	-4.640014	-0.136008	-4.776023	43653.028319
HLA A*0206	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.371426	-0.404745	-4.776171	23519.384424
HLA A*0202	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.584146	-0.192252	-4.776398	38383.623730
HLA A*3301	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.625915	-0.150664	-4.776579	42258.601228
HLA A*0201	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.372044	-0.404745	-4.776789	23552.871641
HLA B*1509	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.552994	-0.224369	-4.777363	35726.802705
HLA B*0802	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.484086	-0.293904	-4.777990	30484.993449
HLA B*7301	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.585786	-0.192252	-4.778038	38528.838232
HLA A*3002	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.564276	-0.214129	-4.778406	36667.084437
HLA A*0202	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.564979	-0.214129	-4.779108	36726.443526
HLA A*0202	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.556258	-0.224369	-4.780627	35996.277098
HLA B*3901	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.477073	-0.303590	-4.780663	29996.659498
HLA A*2402	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.589505	-0.192252	-4.781757	38860.210484
HLA B*1509	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.564211	-0.219267	-4.783478	36661.530641
HLA A*0206	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.527108	-0.257009	-4.784117	33659.489577
HLA A*0250	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.592261	-0.192252	-4.784513	39107.593698
HLA B*1502	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.560193	-0.224369	-4.784562	36323.942014
HLA B*4002	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.642836	-0.143836	-4.786672	43937.577527
HLA A*0250	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.574748	-0.214129	-4.788877	37561.941615
HLA B*5401	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.532885	-0.257009	-4.789894	34110.250557
HLA A*8001	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.467017	-0.322910	-4.789927	29310.086322
HLA B*5301	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.576961	-0.214129	-4.791091	37753.850190
HLA A*3301	1:307-315	9	FDVADVNSS	0.895996	-1.050360	-4.636765	-0.154364	-4.791129	43327.640518
HLA A*8001	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.386890	-0.404745	-4.791635	24371.949018
HLA B*5301	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.600148	-0.192252	-4.792400	39824.315112
HLA B*1517	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.469627	-0.322910	-4.792537	29486.781751

HLA B*2705	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.470027	-0.322910	-4.792937	29513.912663
HLA A*2601	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.388535	-0.404745	-4.793280	24464.418675
HLA B*0802	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.472738	-0.322910	-4.795648	29698.744730
HLA A*2602	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.571351	-0.224369	-4.795720	37269.252129
HLA A*1101	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.473349	-0.322910	-4.796259	29740.547521
HLA A*2501	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.473694	-0.322910	-4.796604	29764.208208
HLA B*1502	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.583340	-0.214129	-4.797469	38312.465427
HLA A*2301	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.540523	-0.257009	-4.797532	34715.472869
HLA B*1502	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.606161	-0.192252	-4.798412	40379.473111
HLA B*3801	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.579414	-0.219267	-4.798681	37967.684367
HLA B*4501	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.655039	-0.143836	-4.798875	45189.687052
HLA A*0219	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.394679	-0.404745	-4.799424	24812.973045
HLA A*0216	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.397778	-0.404745	-4.802522	24990.662793
HLA B*4403	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.545967	-0.257009	-4.802976	35153.360024
HLA A*0211	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.499597	-0.303590	-4.803187	31593.475653
HLA A*2402	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.589080	-0.214129	-4.803209	38822.177581
HLA B*4001	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.399077	-0.404745	-4.803822	25065.538523
HLA B*4501	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.584602	-0.219267	-4.803869	38423.929200
HLA B*1801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.510189	-0.293904	-4.804093	32373.442568
HLA B*3501	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.399563	-0.404745	-4.804308	25093.623815
HLA A*0250	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.580547	-0.224761	-4.805307	38066.816823
HLA A*2402	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.580972	-0.224761	-4.805733	38104.109722
HLA A*2403	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.402756	-0.404745	-4.807501	25278.792976
HLA B*4403	1:154-162	9	PVVRLRMPD	0.781042	-0.924878	-4.664583	-0.143836	-4.808419	46193.720454
HLA A*2602	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.505786	-0.303590	-4.809376	32046.894417
HLA B*5301	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.590450	-0.219267	-4.809717	38944.814679
HLA B*5801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.355478	-0.455159	-4.810636	22671.363828
HLA A*2902	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.406064	-0.404745	-4.810809	25472.079885
HLA A*6801	1:183-191	9	PDFALTRAS	1.098999	-1.249663	-4.661209	-0.150664	-4.811873	45836.250200
HLA A*0250	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.587922	-0.224369	-4.812291	38718.773862
HLA B*5101	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.518530	-0.293904	-4.812433	33001.186630
HLA A*0202	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.557237	-0.257009	-4.814247	36077.573620
HLA A*0250	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.510710	-0.303590	-4.814300	32412.346280
HLA B*5701	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.410200	-0.404745	-4.814944	25715.768157
HLA A*0202	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.590403	-0.224761	-4.815163	38940.601165
HLA B*0803	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.524145	-0.293904	-4.818049	33430.650351
HLA B*1503	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.562928	-0.257009	-4.819937	36553.399609
HLA B*4002	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.563574	-0.257009	-4.820583	36607.821287
HLA A*2402	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.596232	-0.224369	-4.820601	39466.782669
HLA B*1509	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.564124	-0.257009	-4.821133	36654.192988
HLA B*3801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.564187	-0.257009	-4.821196	36659.547347
HLA A*6801	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.597604	-0.224369	-4.821973	39591.670225
HLA A*3101	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.417241	-0.404745	-4.821986	26136.107529
HLA A*2602	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.597632	-0.224761	-4.822393	39594.240547
HLA A*0301	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.367552	-0.455159	-4.822710	23310.503268
HLA B*5301	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.566003	-0.257009	-4.823012	36813.172861
HLA B*4801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.419118	-0.404745	-4.823863	26249.325407
HLA A*6802	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.419677	-0.404745	-4.824422	26283.144588
HLA B*4501	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.601300	-0.224369	-4.825669	39930.023272
HLA B*4002	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.634850	-0.192252	-4.827102	43137.026889
HLA A*0211	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.422393	-0.404745	-4.827138	26448.030000
HLA A*6802	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.372991	-0.455159	-4.828149	23604.277282
HLA B*0702	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.423895	-0.404745	-4.828639	26539.616915
HLA B*4501	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.603992	-0.224761	-4.828753	40178.347731
HLA B*3901	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.424534	-0.404745	-4.829278	26578.698439
HLA B*1801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.506477	-0.322910	-4.829386	32097.905796
HLA B*1503	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.537182	-0.293904	-4.831086	34449.436118
HLA B*0803	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.510389	-0.322910	-4.833298	32388.332614
HLA B*4402	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.428711	-0.404745	-4.833456	26835.586664
HLA B*7301	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.609532	-0.224369	-4.833901	40694.166602
HLA A*3201	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.609631	-0.224761	-4.834392	40703.413992
HLA A*2601	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.379600	-0.455159	-4.834758	23966.234755
HLA A*2301	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.531705	-0.303590	-4.835295	34017.740829
HLA A*3002	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.610740	-0.224761	-4.835500	40807.481654
HLA A*6901	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.380932	-0.455159	-4.836090	24039.861819

HLA B*7301	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.622569	-0.214129	-4.836699	41934.305137
HLA A*3201	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.612819	-0.224369	-4.837188	41003.326205
HLA A*2402	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.535209	-0.303590	-4.838798	34293.242473
HLA A*3201	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.626512	-0.214129	-4.840641	42316.709186
HLA A*0202	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.537781	-0.303590	-4.841371	34496.992659
HLA A*2301	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.547774	-0.293904	-4.841677	35299.909827
HLA A*2402	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.585391	-0.257009	-4.842400	38493.836767
HLA B*1502	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.549073	-0.293904	-4.842977	35405.673588
HLA B*4403	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.624191	-0.219267	-4.843458	42091.131017
HLA B*4002	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.619113	-0.224761	-4.843874	41601.918474
HLA A*3301	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.619527	-0.224761	-4.844288	41641.548209
HLA B*1801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.440247	-0.404745	-4.844992	27557.959997
HLA B*7301	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.588279	-0.257009	-4.845288	38750.625526
HLA A*2602	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.632320	-0.214129	-4.846449	42886.421910
HLA B*1509	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.524119	-0.322910	-4.847029	33428.660993
HLA A*0250	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.590710	-0.257009	-4.847720	38968.207974
HLA B*4501	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.655996	-0.192252	-4.848247	45289.296451
HLA A*3301	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.634249	-0.214129	-4.848378	43077.326406
HLA A*0101	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.393290	-0.455159	-4.848449	24733.766593
HLA B*4403	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.624804	-0.224369	-4.849173	42150.604875
HLA B*1509	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.556276	-0.293904	-4.850180	35997.835018
HLA B*4002	1:381-389	9	ELLKFFNDD	0.665966	-0.885233	-4.631808	-0.219267	-4.851075	42835.873371
HLA A*3201	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.559526	-0.293904	-4.853429	36268.176450
HLA B*5401	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.559958	-0.293904	-4.853862	36304.296478
HLA A*0201	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.399204	-0.455159	-4.854362	25072.862089
HLA A*0206	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.531680	-0.322910	-4.854589	34015.716535
HLA B*1503	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.532995	-0.322910	-4.855905	34118.924696
HLA A*3002	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.552637	-0.303590	-4.856227	35697.436518
HLA A*3301	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.632200	-0.224369	-4.856569	42874.590992
HLA A*3201	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.553542	-0.303590	-4.857131	35771.864883
HLA A*0211	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.535404	-0.322910	-4.858313	34308.644310
HLA A*2603	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.636347	-0.224369	-4.860716	43285.937804
HLA B*3801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.566861	-0.293904	-4.860765	36885.936320
HLA B*4002	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.647279	-0.214129	-4.861408	44389.370357
HLA B*4403	1:47-55	9	DTDAQRDSE	0.781602	-0.973854	-4.669176	-0.192252	-4.861428	46684.873357
HLA A*3002	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.604838	-0.257009	-4.861847	40256.673725
HLA B*4601	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.406727	-0.455159	-4.861885	25510.969460
HLA A*3101	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.407331	-0.455159	-4.862489	25546.463089
HLA B*3801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.541376	-0.322910	-4.864286	34783.713742
HLA A*3002	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.542302	-0.322910	-4.865211	34857.934172
HLA A*6801	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.651156	-0.214129	-4.865285	44787.377679
HLA B*4501	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.651929	-0.214129	-4.866058	44867.163634
HLA B*4002	1:173-181	9	GPVTFAAGS	0.871089	-1.095458	-4.642465	-0.224369	-4.866834	43900.037380
HLA A*2301	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.544061	-0.322910	-4.866971	34999.465313
HLA A*6801	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.642568	-0.224761	-4.867329	43910.488374
HLA A*2603	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.644636	-0.224761	-4.869397	44120.031534
HLA B*3801	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.567650	-0.303590	-4.871240	36953.045700
HLA B*1501	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.417145	-0.455159	-4.872303	26130.311041
HLA B*5101	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.468361	-0.404745	-4.873106	29400.925589
HLA A*1101	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.470407	-0.404745	-4.875152	29539.790054
HLA A*2501	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.470508	-0.404745	-4.875253	29546.662554
HLA B*4403	1:80-88	9	GPYGPYRQS	0.893656	-1.118417	-4.651306	-0.224761	-4.876067	44802.887228
HLA B*4403	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.661963	-0.214129	-4.876093	45915.917413
HLA A*3201	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.619574	-0.257009	-4.876583	41646.053976
HLA B*1502	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.554575	-0.322910	-4.877485	35857.115909
HLA A*2603	1:251-259	9	LGEGTKKLS	0.918600	-1.132729	-4.663497	-0.214129	-4.877627	46078.409474
HLA B*7301	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.556309	-0.322910	-4.879219	36000.561542
HLA B*0802	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.476056	-0.404745	-4.880800	29926.475098
HLA A*0202	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.477251	-0.404745	-4.881996	30008.995207
HLA B*0801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.427482	-0.455159	-4.882641	26759.766119
HLA B*5701	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.429836	-0.455159	-4.884995	26905.216889
HLA A*0212	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.429966	-0.455159	-4.885124	26913.223563
HLA B*1517	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.481795	-0.404745	-4.886540	30324.619355
HLA A*2402	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.593398	-0.293904	-4.887302	39210.126665
HLA B*7301	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.584682	-0.303590	-4.888271	38430.997403

HLA B*1502	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.632599	-0.257009	-4.889609	42914.040083
HLA A*0203	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.435485	-0.455159	-4.890643	27257.414550
HLA B*3501	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.439321	-0.455159	-4.894480	27499.282864
HLA B*4001	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.439425	-0.455159	-4.894583	27505.829438
HLA A*0219	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.439491	-0.455159	-4.894649	27509.996251
HLA A*3301	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.638278	-0.257009	-4.895287	43478.855919
HLA B*4801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.440886	-0.455159	-4.896045	27598.541105
HLA A*2501	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.443043	-0.455159	-4.898201	27735.944048
HLA B*5301	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.604608	-0.293904	-4.898511	40235.336535
HLA B*5401	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.494107	-0.404745	-4.898851	31196.556548
HLA B*5301	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.595614	-0.303590	-4.899204	39410.669226
HLA B*4501	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.642585	-0.257009	-4.899594	43912.151262
HLA B*7301	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.606337	-0.293904	-4.900241	40395.860071
HLA A*2602	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.643891	-0.257009	-4.900900	44044.433396
HLA B*4501	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.598151	-0.303590	-4.901741	39641.607157
HLA A*2403	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.449887	-0.455159	-4.905046	28176.497209
HLA B*4002	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.603731	-0.303590	-4.907321	40154.227968
HLA A*2603	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.651736	-0.257009	-4.908745	44847.264485
HLA A*2602	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.616830	-0.293904	-4.910733	41383.732595
HLA A*3301	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.617647	-0.293904	-4.911551	41461.716709
HLA A*0250	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.590739	-0.322910	-4.913648	38970.737820
HLA B*0702	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.458949	-0.455159	-4.914107	28770.603111
HLA A*2902	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.459506	-0.455159	-4.914664	28807.514818
HLA A*0202	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.593330	-0.322910	-4.916240	39203.975596
HLA A*8001	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.468572	-0.455159	-4.923731	29415.244091
HLA A*0216	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.469103	-0.455159	-4.924262	29451.230191
HLA A*2402	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.601389	-0.322910	-4.924299	39938.232762
HLA A*0206	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.473100	-0.455159	-4.928258	29723.497745
HLA B*0803	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.523668	-0.404745	-4.928413	33393.956713
HLA B*1509	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.524906	-0.404745	-4.929651	33489.299116
HLA A*2301	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.525632	-0.404745	-4.930377	33545.328513
HLA A*6801	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.638652	-0.293904	-4.932555	43516.271320
HLA B*0802	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.478252	-0.455159	-4.933411	30078.234075
HLA A*0250	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.529824	-0.404745	-4.934568	33870.649957
HLA B*4002	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.643261	-0.293904	-4.937165	43980.621831
HLA A*6801	1:161-169	9	PDDDLAWND	0.934581	-1.191590	-4.682735	-0.257009	-4.939744	48165.387982
HLA B*4501	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.648127	-0.293904	-4.942031	44476.146173
HLA A*2602	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.620988	-0.322910	-4.943898	41781.905996
HLA B*4002	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.492666	-0.455159	-4.947825	31093.271946
HLA A*2603	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.655918	-0.293904	-4.949822	45281.211840
HLA B*2705	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.495314	-0.455159	-4.950473	31283.425004
HLA A*1101	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.496628	-0.455159	-4.951786	31378.173280
HLA B*1801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.496982	-0.455159	-4.952141	31403.816370
HLA B*3801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.547705	-0.404745	-4.952450	35294.372172
HLA A*3201	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.629949	-0.322910	-4.952859	42652.960787
HLA B*1517	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.498230	-0.455159	-4.953389	31494.158277
HLA B*5101	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.498237	-0.455159	-4.953396	31494.669421
HLA B*4403	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.499268	-0.455159	-4.954427	31569.556304
HLA B*4501	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.634775	-0.322910	-4.957685	43129.559806
HLA A*3301	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.638276	-0.322910	-4.961186	43478.620704
HLA B*3901	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.508565	-0.455159	-4.963724	32252.649002
HLA B*4002	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.642000	-0.322910	-4.964909	43853.038677
HLA B*4403	1:69-77	9	GLDWDEGPE	0.508978	-0.802882	-4.671772	-0.293904	-4.965676	46964.787966
HLA B*1509	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.510649	-0.455159	-4.965808	32407.787573
HLA B*0803	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.513704	-0.455159	-4.968862	32636.510217
HLA B*4403	1:6-14	9	TVRVRFCPS	0.673708	-0.977298	-4.671620	-0.303590	-4.975209	46948.276040
HLA A*2402	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.573641	-0.404745	-4.978386	37466.353451
HLA A*3002	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.575911	-0.404745	-4.980656	37662.663357
HLA B*4002	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.577065	-0.404745	-4.981809	37762.838002
HLA B*1503	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.527592	-0.455159	-4.982750	33697.021873
HLA B*5301	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.578399	-0.404745	-4.983144	37879.054758
HLA B*4403	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.662844	-0.322910	-4.985754	46009.161973
HLA B*4501	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.537358	-0.455159	-4.992517	34463.416527
HLA A*2603	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.671378	-0.322910	-4.994287	46922.122876
HLA B*1502	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.590168	-0.404745	-4.994912	38919.540429

HLA B*3801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.541164	-0.455159	-4.996323	34766.782021
HLA A*2602	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.592247	-0.404745	-4.996992	39106.324312
HLA A*2301	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.545060	-0.455159	-5.000218	35080.028765
HLA A*6801	1:75-83	9	GPEVGGPYG	0.627889	-0.950799	-4.678969	-0.322910	-5.001879	47749.501122
HLA A*0211	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.549146	-0.455159	-5.004304	35411.611850
HLA A*2603	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.600463	-0.404745	-5.005208	39853.195226
HLA A*3201	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.607676	-0.404745	-5.012421	40520.618488
HLA B*5401	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.557787	-0.455159	-5.012946	36123.273647
HLA B*4501	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.616801	-0.404745	-5.021546	41381.046105
HLA A*2602	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.576910	-0.455159	-5.032068	37749.357086
HLA A*3301	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.631638	-0.404745	-5.036383	42819.191533
HLA B*7301	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.584863	-0.455159	-5.040021	38447.009610
HLA A*0202	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.588751	-0.455159	-5.043909	38792.785398
HLA A*0250	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.594228	-0.455159	-5.049386	39285.077429
HLA A*6801	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.594242	-0.455159	-5.049400	39286.352617
HLA B*4403	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.645200	-0.404745	-5.049944	44177.353014
HLA A*2402	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.600616	-0.455159	-5.055774	39867.211780
HLA A*2603	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.601997	-0.455159	-5.057156	39994.231890
HLA B*5301	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.602589	-0.455159	-5.057748	40048.792892
HLA A*3002	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.603174	-0.455159	-5.058333	40102.777467
HLA B*1502	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.612434	-0.455159	-5.067592	40966.963293
HLA A*6801	1:213-221	9	LRGEDLLPS	0.530674	-0.935419	-4.670966	-0.404745	-5.075711	46877.721288
HLA A*3201	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.626784	-0.455159	-5.081943	42343.273251
HLA A*3301	1:46-54	9	EDTDAQRDS	0.755348	-1.210507	-4.627456	-0.455159	-5.082615	42408.838670