There are more than 10,000 predictions to display.

To enable speedy output, the format was set to 'text' only.

In order to see the results in an html table (which allows for sorting), limit the number of predictions generated on the previous page.

Predictions

```
Allele	Position	PepLength	Sequence	Proteasome	TAP	MHC	Processing
	Total

HLA B*1517	1:136-144	9	QAYRKPITY	1.611085	1.319091	-0.971174
	2.930176	1.959003	9.357799

HLA B*1517	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-0.718773
	2.636993	1.918220	5.233271

HLA B*1517	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-0.850156
	2.710432	1.860276	7.082009

HLA B*1517	1:83-91	9	SSTPREAPY	1.031192	1.298355	-0.699634
	2.329547	1.629912	5.007654

HLA B*3501	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-1.104422
	2.710432	1.606010	12.718105

HLA B*1517	1:20-28	9	VATAAPKTY	1.520765	1.290711	-1.310068
	2.811476	1.501408	20.420583

HLA A*0211	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.565704
	2.001898	1.436193	3.678784

HLA A*0250	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-0.550635
	1.925846	1.375212	3.553323

HLA A*0212	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.641550
	2.001898	1.360347	4.380769

HLA A*0219	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.684927
	2.001898	1.316971	4.840905

HLA A*0250	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.691909
	2.001898	1.309988	4.919367

HLA A*0202	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-0.622158
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							1.925846	1.303689	4.189457
HLA A*3002	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-1.454825	2.710432	1.255608	28.498671
HLA B*1503	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-1.497068	2.710432	1.213364	31.410030
HLA A*2902	1:52-60	9	INISLPSYY	1.208811	1.305102	-1.326688	2.513913	1.187225	21.217216
HLA B*3901	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.819453	2.001898	1.182444	6.598624
HLA A*0216	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.836868	2.001898	1.165030	6.868593
HLA A*3002	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-1.796651	2.896488	1.099837	62.611078
HLA B*3501	1:136-144	9	QAYRKPITY	1.611085	1.319091	-1.839271	2.930176	1.090906	69.067039
HLA A*3002	1:51-59	9	NINISLPSY	1.394333	1.278645	-1.615910	2.672978	1.057068	41.296191
HLA B*3501	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-1.863301	2.896488	1.033187	72.996388
HLA A*2403	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-1.179263	2.208753	1.029490	15.109946
HLA B*1517	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-0.742395	1.751039	1.008644	5.525798
HLA B*1503	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-0.994927	2.001898	1.006971	9.883870
HLA A*2602	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-1.653013	2.636993	0.983980	44.979339
HLA B*3501	1:20-28	9	VATAAPKTY	1.520765	1.290711	-1.845849	2.811476	0.965626	70.121209
HLA B*5801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-1.675178	2.636993	0.961815	47.334534

HLA B*3501	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-1.281231	2.240828	0.959597	19.108674
HLA A*2902	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-1.753139	2.710432	0.957294	56.642018
HLA B*1501	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-1.967369	2.896488	0.929119	92.761863
HLA B*1501	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-1.792347	2.710432	0.918085	61.993610
HLA B*1503	1:136-144	9	QAYRKPITY	1.611085	1.319091	-2.051702	2.930176	0.878475	112.642395
HLA B*1503	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-1.964644	2.823193	0.858549	92.181561
HLA A*0203	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.067817	1.925846	0.858029	11.690079
HLA B*1501	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-1.990136	2.823193	0.833057	97.754322
HLA A*0211	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.098365	1.925846	0.827481	12.541961
HLA A*0211	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-0.576559	1.338234	0.761675	3.771889
HLA A*0201	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.228738	1.925846	0.697108	16.933174
HLA B*5801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-2.045424	2.710432	0.665008	111.025836
HLA A*0203	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-0.677103	1.338234	0.661131	4.754477
HLA B*1502	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-2.239731	2.896488	0.656757	173.672542
HLA A*3002	1:52-60	9	INISLPSYY	1.208811	1.305102	-1.916917	2.513913	0.596997	82.587937
HLA A*0211	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.137437	1.732070	0.594633	13.722631

HLA A*0212	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.137757	1.732070	0.594313	13.732731
HLA B*1503	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-2.122877	2.697803	0.574926	132.701910
HLA A*0206	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-1.437246	2.001898	0.564652	27.368170
HLA A*6802	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-1.349920	1.867525	0.517604	22.383093
HLA A*0201	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-1.488371	2.001898	0.513527	30.787226
HLA A*0216	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.413915	1.925846	0.511931	25.936739
HLA A*0219	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.232963	1.732070	0.499108	17.098686
HLA B*1503	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-1.761353	2.240828	0.479475	57.723482
HLA B*1501	1:92-100	9	ELNITSATY	1.311755	1.126521	-1.965885	2.438276	0.472392	92.445247
HLA A*0250	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-0.874257	1.338234	0.463976	7.486132
HLA A*3002	1:92-100	9	ELNITSATY	1.311755	1.126521	-1.977345	2.438276	0.460931	94.917300
HLA A*0206	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.489245	1.925846	0.436602	30.849247
HLA B*5701	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-2.301993	2.710432	0.408440	200.443747
HLA B*5701	1:20-28	9	VATAAPKTY	1.520765	1.290711	-2.427972	2.811476	0.383504	267.899497
HLA B*4601	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-2.328593	2.710432	0.381839	213.104873
HLA A*3002	1:83-91	9	SSTPREAPY	1.031192	1.298355	-1.950745	2.329547	0.378802	89.278011

HLA B*1503	1:52-60	9	INISLPSYY	1.208811	1.305102	-2.135141	2.513913	0.378772	136.502777
HLA A*0212	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.598928	1.925846	0.326918	39.712563
HLA B*1517	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-2.302096	2.611929	0.309833	200.491465
HLA A*0211	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-0.717885	1.020870	0.302985	5.222580
HLA A*0250	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.446949	1.732070	0.285121	27.986535
HLA B*1501	1:51-59	9	NINISLPSY	1.394333	1.278645	-2.398857	2.672978	0.274121	250.528466
HLA A*0206	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.071534	1.338234	0.266699	11.790557
HLA A*0202	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.466835	1.732070	0.265235	29.297811
HLA A*3001	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-0.998451	1.254764	0.256313	9.964402
HLA A*3002	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-2.571286	2.823193	0.251907	372.636837
HLA B*5301	1:140-148	9	KPITYDTLW	1.293618	0.385080	-1.433491	1.678698	0.245207	27.132592
HLA A*3201	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-2.468557	2.710432	0.241875	294.141906
HLA A*2403	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-1.596879	1.838116	0.241236	39.525664
HLA A*3101	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-1.350268	1.590000	0.239732	22.401022
HLA B*0702	1:85-93	9	TPREAPYEL	1.651184	0.319388	-1.739921	1.970572	0.230651	54.944031
HLA A*3201	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-1.580597	1.793265	0.212667	38.071259

HLA B*1502	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.225926	2.438276	0.212351	168.238577
HLA A*0216	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.131799	1.338234	0.206435	13.545611
HLA A*3001	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-0.836553	1.037888	0.201335	6.863615
HLA B*1503	1:20-28	9	VATAAPKTY	1.520765	1.290711	-2.610621	2.811476	0.200855	407.963080
HLA A*0206	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-0.827747	1.020870	0.193123	6.725848
HLA B*1502	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-2.641427	2.823193	0.181766	437.952802
HLA A*0219	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-1.748322	1.925846	0.177524	56.017313
HLA A*2603	1:136-144	9	QAYRKPITY	1.611085	1.319091	-2.758916	2.930176	0.171261	574.004975
HLA A*2902	1:136-144	9	QAYRKPITY	1.611085	1.319091	-2.759841	2.930176	0.170335	575.229769
HLA B*3501	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.268945	2.438276	0.169332	185.756772
HLA A*2602	1:51-59	9	NINISLPSY	1.394333	1.278645	-2.514029	2.672978	0.158949	326.609517
HLA A*6801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-1.213283	1.368126	0.154843	16.341181
HLA A*2602	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-2.742164	2.896488	0.154325	552.285738
HLA A*3201	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.184418	1.338234	0.153816	15.290359
HLA B*5301	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-2.129569	2.240828	0.111259	134.762329
HLA A*2902	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-2.806338	2.896488	0.090151	640.232420

HLA A*0201	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.248211	1.338234	0.090023	17.709687
HLA A*1101	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-0.966649	1.037888	0.071240	9.260802
HLA B*1501	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-2.567320	2.636993	0.069673	369.249447
HLA A*0206	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-1.435573	1.478828	0.043255	27.262955
HLA A*3101	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-1.611169	1.653995	0.042826	40.847806
HLA B*5801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-2.909292	2.930176	0.020884	811.506672
HLA A*0202	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.320725	1.338234	0.017508	20.927888
HLA A*2501	1:51-59	9	NINISLPSY	1.394333	1.278645	-2.659368	2.672978	0.013610	456.423479
HLA B*0702	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-2.230352	2.240828	0.010476	169.962072
HLA A*0219	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-1.470280	1.478828	0.008549	29.531093
HLA B*1517	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.448412	2.438276	-0.010136	280.809902
HLA A*0202	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.038117	2.001898	-0.036220	109.173480
HLA A*0250	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.110498	1.020870	-0.089628	12.897282
HLA A*0202	1:199-207	9	FFFNPGELL	1.344812	0.501173	-1.943503	1.845985	-0.097519	87.801794
HLA A*2902	1:51-59	9	NINISLPSY	1.394333	1.278645	-2.777683	2.672978	-0.104705	599.353910
HLA A*2403	1:199-207	9	FFFNPGELL	1.344812	0.501173	-1.950989	1.845985	-0.105004	89.328255

HLA A*0206	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-1.903952	1.793265	-0.110688	80.158976
HLA B*5801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-2.936227	2.811476	-0.124751	863.428920
HLA A*0250	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-1.616324	1.478828	-0.137495	41.335530
HLA A*6901	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-2.007771	1.867525	-0.140247	101.805491
HLA B*1503	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-2.779112	2.636993	-0.142119	601.328558
HLA A*6802	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-2.074647	1.925846	-0.148801	118.753644
HLA B*1503	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.057991	2.896488	-0.161503	1142.854652
HLA A*3201	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.092622	2.930176	-0.162446	1237.720002
HLA B*1503	1:139-147	9	RKPITYDTL	1.549612	0.515162	-2.235892	2.064774	-0.171118	172.144084
HLA A*6901	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.912753	1.732070	-0.180683	81.800005
HLA B*1517	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-1.551464	1.368668	-0.182795	35.601117
HLA A*0101	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-2.803781	2.611929	-0.191853	636.475106
HLA A*2501	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.637335	2.438276	-0.199058	433.844910
HLA A*0206	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-2.858726	2.636993	-0.221734	722.314742
HLA A*0301	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.157863	2.930176	-0.227686	1438.344473
HLA A*0203	1:77-85	9	FLSAATSST	0.627583	-0.297236	-0.569073	0.330347	-0.238726	3.707434

HLA A*3201	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-1.972383	1.732070	-0.240313	93.838976
HLA A*3002	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.072266	2.811476	-0.260791	1181.045071
HLA A*8001	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.209035	2.930176	-0.278858	1618.209298
HLA A*0203	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.292924	2.001898	-0.291026	196.301447
HLA B*1517	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.192114	2.896488	-0.295625	1556.373047
HLA A*2501	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-2.600570	2.288348	-0.312222	398.629803
HLA B*3501	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-2.952551	2.633172	-0.319378	896.501071
HLA A*3201	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.017223	2.697803	-0.319420	1040.453647
HLA A*0202	1:77-85	9	FLSAATSST	0.627583	-0.297236	-0.650680	0.330347	-0.320333	4.473840
HLA B*3501	1:85-93	9	TPREAPYEL	1.651184	0.319388	-2.292989	1.970572	-0.322418	196.331184
HLA B*5801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-2.003439	1.678698	-0.324740	100.794945
HLA B*1502	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-2.954285	2.626012	-0.328272	900.087504
HLA A*0203	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.060813	1.732070	-0.328743	115.030545
HLA B*5701	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.269327	2.930176	-0.339151	1859.204562
HLA B*3501	1:83-91	9	SSTPREAPY	1.031192	1.298355	-2.673108	2.329547	-0.343561	471.094209
HLA B*1801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-3.172759	2.823193	-0.349566	1488.533606

HLA A*6802	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.084820	1.732070	-0.352750	121.568264
HLA A*3201	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-2.971826	2.611929	-0.359897	937.186421
HLA A*2301	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-2.139751	1.779223	-0.360528	137.959361
HLA A*3301	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-1.957055	1.590000	-0.367056	90.584777
HLA B*1502	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.083149	2.710432	-0.372717	1211.014340
HLA B*3901	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-2.308374	1.925846	-0.382527	203.410662
HLA B*0702	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-1.310482	0.927533	-0.382949	20.440036
HLA A*0250	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-1.190653	0.804086	-0.386567	15.511479
HLA B*1503	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-2.675316	2.288348	-0.386968	473.495964
HLA A*6802	1:96-104	9	TSATYQSAI	0.928477	0.250556	-1.568685	1.179033	-0.389653	37.041226
HLA A*0201	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.126918	1.732070	-0.394848	133.942465
HLA A*2602	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-2.262690	1.867525	-0.395166	183.100836
HLA A*8001	1:52-60	9	INISLPSYY	1.208811	1.305102	-2.910382	2.513913	-0.396469	813.546265
HLA A*0250	1:77-85	9	FLSAATSST	0.627583	-0.297236	-0.735751	0.330347	-0.405403	5.441901
HLA B*4001	1:87-95	9	REAPYELNI	1.162222	0.222672	-1.795317	1.384894	-0.410423	62.418981
HLA A*2902	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.048377	2.636993	-0.411384	1117.832952

HLA B*1501	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.346855	2.930176	-0.416679	2222.570177
HLA A*6901	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.451451	1.020870	-0.430581	28.278134
HLA A*3201	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.072600	2.636993	-0.435607	1181.952703
HLA A*0250	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-1.334733	0.895143	-0.439590	21.613895
HLA A*3002	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.069832	2.626012	-0.443820	1174.444247
HLA B*0702	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-1.537691	1.076055	-0.461636	34.489821
HLA B*1502	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-2.751938	2.288348	-0.463590	564.855922
HLA A*2902	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.905932	2.438276	-0.467656	805.252962
HLA A*2602	1:83-91	9	SSTPREAPY	1.031192	1.298355	-2.806234	2.329547	-0.476688	640.080040
HLA A*3101	1:79-87	9	SAATSSTPR	0.650358	0.717768	-1.845417	1.368126	-0.477291	70.051444
HLA A*2602	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.177425	2.697803	-0.479622	1504.612692
HLA A*0216	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-1.394048	0.895143	-0.498905	24.776966
HLA A*2403	1:147-155	9	LWQADTDPL	0.954861	0.515252	-1.969132	1.470113	-0.499019	93.139001
HLA B*5801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-1.867906	1.368668	-0.499238	73.774515
HLA A*6802	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-2.256018	1.751039	-0.504979	180.309160
HLA B*1501	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.517652	2.001898	-0.515754	329.345505

HLA B*1503	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-2.442778	1.925846	-0.516932	277.190507
HLA B*1501	1:83-91	9	SSTPREAPY	1.031192	1.298355	-2.847012	2.329547	-0.517465	703.091660
HLA B*1517	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.147163	2.626012	-0.521151	1403.341454
HLA B*5301	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.161608	2.633172	-0.528436	1450.801474
HLA B*3501	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.156190	2.626012	-0.530178	1432.814855
HLA A*0211	1:199-207	9	FFFNPGELL	1.344812	0.501173	-2.386908	1.845985	-0.540923	243.729220
HLA A*6801	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.982573	2.438276	-0.544296	960.666247
HLA B*5701	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-1.917612	1.368668	-0.548944	82.720294
HLA B*3501	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.227332	2.672978	-0.554355	1687.844689
HLA A*0211	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-1.800767	1.245899	-0.554869	63.207335
HLA B*1503	1:92-100	9	ELNITSATY	1.311755	1.126521	-2.996876	2.438276	-0.558600	992.832983
HLA B*1502	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.371469	2.811476	-0.559993	2352.169896
HLA A*2601	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.235889	2.672978	-0.562911	1721.429756
HLA B*1502	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.494328	2.930176	-0.564152	3121.245700
HLA A*1101	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.497373	2.930176	-0.567196	3143.206325
HLA B*1503	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-2.365302	1.793265	-0.572037	231.900527

HLA A*2602	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-2.860935	2.288348	-0.572587	725.997281
HLA A*2403	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-2.352276	1.779223	-0.573053	225.048535
HLA A*0203	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.598341	1.020870	-0.577471	39.658890
HLA B*1502	1:199-207	9	FFFNPGELL	1.344812	0.501173	-2.424932	1.845985	-0.578947	266.030643
HLA A*2602	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-3.402416	2.823193	-0.579223	2525.899715
HLA A*2601	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.036211	2.438276	-0.597935	1086.954274
HLA B*5301	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.528236	2.930176	-0.598059	3374.704298
HLA B*1503	1:83-91	9	SSTPREAPY	1.031192	1.298355	-2.929549	2.329547	-0.600003	850.255313
HLA A*0212	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-1.942380	1.338234	-0.604147	87.575039
HLA A*0201	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.628968	1.020870	-0.608099	42.556748
HLA A*2602	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.553948	2.930176	-0.623772	3580.539660
HLA A*3002	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.562693	2.930176	-0.632517	3653.366749
HLA A*6801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.570113	2.930176	-0.639936	3716.318654
HLA A*2602	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.155711	2.513913	-0.641798	1431.234448
HLA B*1502	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.322411	2.672978	-0.649434	2100.929313
HLA B*1501	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.163690	2.513913	-0.649776	1457.772092

HLA B*1517	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.330137	2.672978	-0.657159	2138.634395
HLA B*3501	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-3.280717	2.611929	-0.668789	1908.611251
HLA A*2902	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.480311	2.811476	-0.668835	3022.114604
HLA B*1502	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.367193	2.697803	-0.669390	2329.124076
HLA B*3501	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-2.958805	2.288348	-0.670457	909.505106
HLA A*0216	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.694077	1.020870	-0.673208	49.439875
HLA A*2902	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.006053	2.329547	-0.676507	1014.035793
HLA A*0211	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.318427	2.636993	-0.681434	2081.741087
HLA B*1502	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.687308	2.001898	-0.685410	486.752345
HLA B*3501	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.384165	2.697803	-0.686363	2421.950732
HLA B*3901	1:85-93	9	TPREAPYEL	1.651184	0.319388	-2.664222	1.970572	-0.693650	461.553462
HLA A*2902	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.328896	2.626012	-0.702884	2132.534270
HLA A*1101	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.417147	2.710432	-0.706715	2613.047923
HLA A*0216	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.439597	1.732070	-0.707527	275.167507
HLA A*3101	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-1.748529	1.037888	-0.710641	56.043988
HLA A*6801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-1.749530	1.037888	-0.711642	56.173296

HLA B*5301	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.524232	2.811476	-0.712756	3343.737703
HLA B*1501	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.012721	2.288348	-0.724373	1029.724684
HLA B*1503	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.401246	2.672978	-0.728268	2519.103784
HLA B*1501	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.428091	2.697803	-0.730289	2679.731466
HLA B*1517	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-2.886018	2.152457	-0.733561	769.162489
HLA A*0212	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-1.743698	0.999064	-0.744635	55.424079
HLA A*3001	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.679500	2.930176	-0.749324	4780.796613
HLA A*1101	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.648445	2.896488	-0.751956	4450.868623
HLA B*1503	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.378216	2.626012	-0.752204	2389.001422
HLA A*0301	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-1.790646	1.037888	-0.752758	61.751271
HLA B*1503	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-3.137747	2.377639	-0.760107	1373.240548
HLA A*1101	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.090231	2.329547	-0.760684	1230.922283
HLA A*2902	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.416297	2.633172	-0.783125	2607.935591
HLA B*0702	1:24-32	9	APKTYCEEL	1.537287	0.413098	-2.747192	1.950385	-0.796806	558.716795
HLA B*5701	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.129547	2.329547	-0.800000	1347.556290
HLA A*8001	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.629367	2.811476	-0.817891	4259.581745

HLA B*0801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.822746	2.001898	-0.820849	664.884893
HLA B*4801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.845889	2.001898	-0.843991	701.275865
HLA A*3002	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.482247	2.636993	-0.845254	3035.616503
HLA A*0250	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-1.830023	0.977336	-0.852687	67.611920
HLA A*0101	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.184661	2.329547	-0.855115	1529.893272
HLA A*2603	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.495766	2.636993	-0.858773	3131.596810
HLA B*1517	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-2.192582	1.328019	-0.864562	155.805109
HLA A*2403	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.155363	2.288348	-0.867015	1430.088970
HLA A*0206	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.601829	1.732070	-0.869759	399.787388
HLA B*4002	1:87-95	9	REAPYELNI	1.162222	0.222672	-2.264640	1.384894	-0.879746	183.924845
HLA A*6901	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-1.646077	0.754093	-0.891985	44.266724
HLA A*2601	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.789010	2.896488	-0.892521	6151.907036
HLA B*4801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-2.695743	1.793265	-0.902478	496.298204
HLA B*0702	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-2.772853	1.867525	-0.905328	592.724394
HLA A*8001	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.630053	2.710432	-0.919621	4266.315871
HLA B*1801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.163032	2.240828	-0.922204	1455.565576

HLA B*3501	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-1.850403	0.927533	-0.922870	70.860253
HLA A*0216	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-2.172451	1.245899	-0.926553	148.748059
HLA A*0206	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.638069	2.710432	-0.927637	4345.797138
HLA B*1517	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.933797	2.001898	-0.931900	858.612532
HLA A*6801	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.446601	2.513913	-0.932687	2796.407890
HLA A*6801	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.608663	2.672978	-0.935685	4061.283393
HLA A*3001	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.650677	2.710432	-0.940244	4473.802275
HLA B*0802	1:136-144	9	QAYRKPITY	1.611085	1.319091	-3.871129	2.930176	-0.940953	7432.398103
HLA A*3101	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.651847	2.710432	-0.941414	4485.871508
HLA A*2501	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.844091	2.896488	-0.947603	6983.788691
HLA A*0202	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-1.969545	1.020870	-0.948675	93.227724
HLA B*4801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-3.013858	2.064774	-0.949084	1032.424434
HLA B*1501	1:20-28	9	VATAAPKTY	1.520765	1.290711	-3.763494	2.811476	-0.952019	5800.886350
HLA B*3901	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-2.825326	1.867525	-0.957802	668.846101
HLA B*1501	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-3.585399	2.626012	-0.959386	3849.450104
HLA A*6901	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-2.963152	2.001898	-0.961254	918.653404

HLA B*5301	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.675464	2.710432	-0.965031	4736.568832
HLA A*8001	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-3.790922	2.823193	-0.967729	6179.057617
HLA B*5701	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.606690	2.636993	-0.969697	4042.869546
HLA A*0101	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.873281	2.896488	-0.976793	7469.320451
HLA A*8001	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.621228	2.633172	-0.988056	4180.501090
HLA A*2602	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-2.739185	1.751039	-0.988146	548.510167
HLA B*1503	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-2.330309	1.338234	-0.992075	213.948135
HLA B*1801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.705960	2.710432	-0.995528	5081.128383
HLA A*0203	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-2.475558	1.478828	-0.996730	298.922336
HLA B*1517	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.697897	2.697803	-1.000094	4987.658793
HLA A*2902	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-3.827151	2.823193	-1.003958	6716.628123
HLA B*3501	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-2.872443	1.867525	-1.004918	745.491630
HLA B*0702	1:177-185	9	APNAGLDPV	0.672482	0.029184	-1.708264	0.701666	-1.006598	51.081490
HLA A*2403	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.012754	2.001898	-1.010856	1029.802676
HLA B*1502	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.534838	2.513913	-1.020924	3426.397760
HLA A*1101	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.658449	2.636993	-1.021456	4554.585744

HLA B*1517	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-2.043385	1.020870	-1.022515	110.505705
HLA A*0211	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.028865	0.999064	-1.029801	106.872232
HLA A*8001	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.704137	2.672978	-1.031159	5059.842142
HLA A*3001	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-2.103715	1.071973	-1.031742	126.973992
HLA B*0801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-2.997619	1.950385	-1.047233	994.531708
HLA B*2705	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-2.843676	1.793265	-1.050411	697.711173
HLA B*1503	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.267123	2.208753	-1.058370	1849.793970
HLA B*3901	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.301976	2.240828	-1.061148	2004.359505
HLA A*2301	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-3.439792	2.377639	-1.062153	2752.908085
HLA A*6801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-2.655003	1.590000	-1.065003	451.858685
HLA A*8001	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.703113	2.636993	-1.066120	5047.921497
HLA A*6901	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-2.229633	1.161468	-1.068165	169.680945
HLA B*3501	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-3.892866	2.823193	-1.069674	7813.873913
HLA A*6801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.966184	2.896488	-1.069696	9250.909408
HLA A*1101	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.743284	2.672978	-1.070306	5537.121929
HLA B*3501	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.710377	2.636993	-1.073384	5133.070156

HLA A*2603	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.511714	2.438276	-1.073438	3248.733944
HLA A*0101	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.715635	2.636993	-1.078642	5195.595685
HLA B*1502	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.323177	2.240828	-1.082349	2104.637831
HLA A*0202	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-2.424401	1.339576	-1.084824	265.705584
HLA A*2403	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-3.466021	2.377639	-1.088382	2924.296213
HLA A*0101	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.027323	2.930176	-1.097146	10649.340830
HLA A*2603	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.730968	2.633172	-1.097796	5382.302300
HLA A*2603	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-3.994782	2.896488	-1.098294	9880.578194
HLA B*0801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-3.251363	2.152457	-1.098906	1783.869229
HLA A*0211	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-1.905089	0.804086	-1.101004	80.369138
HLA A*0206	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-2.109170	1.002409	-1.106762	128.579069
HLA A*2403	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-3.814074	2.697803	-1.116271	6517.395404
HLA B*1517	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.405353	2.288348	-1.117005	2543.038646
HLA A*2301	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.411269	2.288348	-1.122921	2577.917195
HLA B*5801	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.638873	2.513913	-1.124960	4353.845097
HLA B*0801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.060784	2.930176	-1.130608	11502.284151

HLA A*2602	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.572744	2.438276	-1.134468	3738.904466
HLA B*5801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.428279	2.288348	-1.139931	2680.891481
HLA A*0216	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-2.619643	1.478828	-1.140815	416.526737
HLA A*3301	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-2.796423	1.653995	-1.142428	625.781666
HLA B*5801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-3.755638	2.611929	-1.143709	5696.887970
HLA A*8001	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.046184	2.896488	-1.149696	11122.038456
HLA B*4601	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.080290	2.930176	-1.150113	12030.661755
HLA B*1517	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.669078	2.513913	-1.155165	4667.431497
HLA B*1503	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-2.891680	1.732070	-1.159610	779.256359
HLA B*1502	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.492552	2.329547	-1.163005	3108.506261
HLA A*3001	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.065417	2.896488	-1.168929	11625.650872
HLA A*2603	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.683565	2.513913	-1.169652	4825.750642
HLA A*3201	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.173689	2.001898	-1.171791	1491.725933
HLA B*2705	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-2.294756	1.122935	-1.171821	197.131533
HLA A*0101	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.883718	2.710432	-1.173285	7650.987712
HLA A*2601	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.811588	2.636993	-1.174595	6480.198584

HLA A*0301	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.852441	2.672978	-1.179463	7119.363376
HLA A*2403	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.820850	2.636993	-1.183857	6619.877985
HLA A*2501	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.009551	2.823193	-1.186358	10222.361196
HLA A*3201	1:48-56	9	PAYNINISL	1.435478	0.251657	-2.875069	1.687135	-1.187934	750.014218
HLA B*4403	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.011290	2.823193	-1.188097	10263.366582
HLA A*0211	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.905234	2.710432	-1.194802	8039.593458
HLA B*5301	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.166443	1.970572	-1.195872	1467.044299
HLA A*0206	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.021783	2.823193	-1.198590	10514.355120
HLA A*2601	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.909661	2.710432	-1.199228	8121.953858
HLA B*4402	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.910906	2.710432	-1.200473	8145.274876
HLA A*1101	1:79-87	9	SAATSSTPR	0.650358	0.717768	-2.572150	1.368126	-1.204024	373.379436
HLA B*1801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-3.816823	2.611929	-1.204894	6558.778547
HLA B*1503	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-3.824374	2.611929	-1.212446	6673.815746
HLA A*0202	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.849476	2.636993	-1.212483	7070.923034
HLA A*8001	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.653863	2.438276	-1.215586	4506.741909
HLA B*1509	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.424849	2.208753	-1.216096	2659.800030

HLA A*6802	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-2.707406	1.486927	-1.220479	509.806710
HLA A*0201	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-2.705089	1.478828	-1.226261	507.094564
HLA A*2402	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.437621	2.208753	-1.228868	2739.181357
HLA A*2601	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.053383	2.823193	-1.230190	11307.932682
HLA A*2603	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-2.981435	1.751039	-1.230397	958.154142
HLA A*6801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.870076	2.636993	-1.233084	7414.406529
HLA B*3501	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-2.721540	1.486927	-1.234613	526.671781
HLA A*6802	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-2.401498	1.161468	-1.240030	252.056500
HLA B*5401	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.481833	2.240828	-1.241005	3032.727546
HLA B*1503	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.874634	2.633172	-1.241462	7492.631873
HLA A*0219	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-2.587168	1.339576	-1.247592	386.516736
HLA B*1801	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.921305	2.672978	-1.248327	8342.660403
HLA A*2402	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-3.628643	2.377639	-1.251004	4252.490144
HLA B*5101	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.181731	2.930176	-1.251554	15196.055852
HLA A*3101	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.889145	2.636993	-1.252152	7747.200839
HLA A*0211	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-2.147876	0.895143	-1.252733	140.564514

HLA B*0801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.498768	2.240828	-1.257941	3153.323183
HLA A*8001	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.588218	2.329547	-1.258672	3874.521514
HLA B*2705	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.084782	2.823193	-1.261589	12155.749226
HLA A*3001	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.899177	2.636993	-1.262184	7928.245976
HLA A*6901	1:149-157	9	QADTDPLPV	0.679726	0.062986	-2.005276	0.742712	-1.262564	101.222265
HLA A*0203	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.270133	0.999064	-1.271070	186.265960
HLA B*1801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.203981	2.930176	-1.273804	15994.862244
HLA A*1101	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.098973	2.823193	-1.275780	12559.507841
HLA A*3001	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.088701	2.811476	-1.277225	12265.935396
HLA A*2402	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.914594	2.636993	-1.277602	8214.751613
HLA B*1801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.175392	2.896488	-1.278904	14975.866866
HLA A*6801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-3.992217	2.710432	-1.281784	9822.379777
HLA B*1509	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.212711	2.930176	-1.282535	16319.663150
HLA A*3101	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.215413	2.930176	-1.285237	16421.510340
HLA A*0212	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-2.308280	1.020870	-1.287410	203.366650
HLA B*4402	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.110842	2.823193	-1.287649	12907.502553

HLA A*3201	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.187088	2.896488	-1.290599	15384.653060
HLA A*6901	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.217009	1.925846	-1.291162	1648.195957
HLA B*0702	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-2.017775	0.723137	-1.294639	104.177831
HLA B*1503	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.046192	1.751039	-1.295153	1112.223038
HLA A*2402	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.713563	2.415459	-1.298104	5170.863836
HLA B*1509	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.126711	2.823193	-1.303518	13387.843944
HLA A*3201	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.742340	2.438276	-1.304063	5525.093017
HLA B*5801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.633667	2.329547	-1.304120	4301.961453
HLA B*3501	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.820516	2.513913	-1.306603	6614.794519
HLA A*2603	1:51-59	9	NINISLPSY	1.394333	1.278645	-3.980577	2.672978	-1.307599	9562.630460
HLA A*0250	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-2.383355	1.075733	-1.307622	241.743707
HLA A*0250	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.518852	2.208753	-1.310099	3302.568860
HLA A*0301	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.024611	2.710432	-1.314179	10583.063966
HLA A*2603	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-3.929984	2.611929	-1.318055	8511.058255
HLA A*2902	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.164108	1.845985	-1.318123	1459.176545
HLA A*0301	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.142631	2.823193	-1.319438	13887.713601

HLA B*4002	1:91-99	9	YELNITSAT	0.787532	-0.429583	-1.678167	0.357949	-1.320217	47.661384
HLA B*1503	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.168558	1.845985	-1.322573	1474.204609
HLA A*2902	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.020472	2.697803	-1.322669	10482.663104
HLA B*1801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.963008	2.636993	-1.326015	9183.493529
HLA A*2501	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.256388	2.930176	-1.326212	18046.297664
HLA A*3002	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-3.960071	2.633172	-1.326899	9121.600933
HLA B*1503	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-2.530893	1.203934	-1.326960	339.541950
HLA A*2602	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.140215	2.811476	-1.328740	13810.693310
HLA B*4601	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.140568	2.811476	-1.329092	13821.905006
HLA B*3801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.261595	2.930176	-1.331418	18263.944355
HLA B*1801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.143787	2.811476	-1.332311	13924.727286
HLA B*5401	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-2.287806	0.954583	-1.333223	194.002051
HLA B*5301	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-2.824494	1.486927	-1.337568	667.566419
HLA A*2902	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.627633	2.288348	-1.339285	4242.609276
HLA A*6801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.670121	2.329547	-1.340575	4678.656100
HLA A*0301	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.240752	2.896488	-1.344264	17408.136919

HLA A*0206	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.042843	2.697803	-1.345041	11036.806404
HLA A*0206	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.635001	2.288348	-1.346653	4315.200924
HLA A*0203	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-3.986160	2.636993	-1.349167	9686.340901
HLA A*2601	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.279368	2.930176	-1.349192	19026.917248
HLA A*2301	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.198142	1.845985	-1.352158	1578.128924
HLA A*2301	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.561237	2.208753	-1.352484	3641.133405
HLA B*5801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.250982	2.896488	-1.354494	17823.046967
HLA B*3501	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.356874	2.001898	-1.354976	2274.435821
HLA A*0206	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.777023	2.415459	-1.361564	5984.428624
HLA A*6901	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.292883	2.930176	-1.362706	19628.299093
HLA A*2301	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.000102	2.636993	-1.363109	10002.339551
HLA A*0212	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-2.843770	1.478828	-1.364941	697.862171
HLA B*4601	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.003142	2.636993	-1.366149	10072.605552
HLA A*2403	1:139-147	9	RKPITYDTL	1.549612	0.515162	-3.431272	2.064774	-1.366498	2699.432539
HLA B*5801	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.118556	1.751039	-1.367517	1313.880977
HLA B*4501	1:87-95	9	REAPYELNI	1.162222	0.222672	-2.754278	1.384894	-1.369384	567.907721

HLA B*1503	1:24-32	9	APKTYCEEL	1.537287	0.413098	-3.322411	1.950385	-1.372026	2100.929313
HLA A*3001	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.701717	2.329547	-1.372170	5031.726167
HLA A*6801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.196819	2.823193	-1.373626	15733.280075
HLA A*0101	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.814713	2.438276	-1.376437	6526.992745
HLA B*4402	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.307121	2.930176	-1.376944	20282.456172
HLA A*0301	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.816471	2.438276	-1.378194	6553.458366
HLA B*0801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.276237	2.896488	-1.379748	18890.200426
HLA B*4601	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.276448	2.896488	-1.379960	18899.400116
HLA A*2602	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.090811	2.710432	-1.380378	12325.669276
HLA B*0801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-2.641615	1.254764	-1.386851	438.142385
HLA B*5401	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-2.246108	0.856017	-1.390090	176.241290
HLA B*3801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.287336	2.896488	-1.390847	19379.186086
HLA A*6801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.204131	2.811476	-1.392655	16000.401151
HLA A*2603	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.260319	1.867525	-1.392795	1821.039017
HLA A*0206	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.240161	1.845985	-1.394176	1738.443856
HLA A*6901	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.031467	2.636993	-1.394474	10751.454425

HLA B*2705	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.327143	2.930176	-1.396966	21239.429996
HLA B*4402	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-3.774654	2.377639	-1.397015	5951.883346
HLA A*2902	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.013475	2.611929	-1.401546	10315.133716
HLA B*1517	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.269299	1.867525	-1.401774	1859.083869
HLA A*3101	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.226357	2.823193	-1.403164	16840.578234
HLA B*1517	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.036486	2.633172	-1.403313	10876.413701
HLA A*8001	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.029480	2.626012	-1.403467	10702.359964
HLA A*0301	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.215028	2.811476	-1.403552	16406.947279
HLA A*2301	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.819976	2.415459	-1.404517	6606.569018
HLA A*3001	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.078800	2.672978	-1.405822	11989.468836
HLA A*2402	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.022036	2.611929	-1.410108	10520.500117
HLA B*4601	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.235750	2.823193	-1.412557	17208.786251
HLA A*3101	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.312494	2.896488	-1.416005	20534.957974
HLA B*1503	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-2.745138	1.328019	-1.417119	556.081282
HLA A*2602	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.030020	2.611929	-1.418091	10715.684926
HLA A*2501	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.748190	2.329547	-1.418643	5600.023011

HLA A*3001	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.245938	2.823193	-1.422745	17617.229310
HLA A*6801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.714869	2.288348	-1.426521	5186.440683
HLA B*1501	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.060009	2.633172	-1.426836	11481.767863
HLA B*5401	1:177-185	9	APNAGLDPV	0.672482	0.029184	-2.130142	0.701666	-1.428476	134.940334
HLA A*0203	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-2.674668	1.245899	-1.428769	472.789501
HLA A*0202	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.222643	1.793265	-1.429378	1669.717156
HLA B*0702	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.326184	2.896488	-1.429696	21192.601288
HLA A*0219	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-2.768055	1.338234	-1.429821	586.212606
HLA A*0203	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-2.505881	1.075733	-1.430148	320.538958
HLA B*4801	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.360663	2.930176	-1.430487	22943.673822
HLA A*3001	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-2.211025	0.779687	-1.431338	162.564290
HLA A*1101	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.243959	2.811476	-1.432484	17537.163093
HLA A*0211	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-2.912285	1.478828	-1.433457	817.119056
HLA A*0202	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.213574	1.779223	-1.434351	1635.211367
HLA A*2301	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.132838	2.697803	-1.435035	13578.071717
HLA A*0219	1:77-85	9	FLSAATSST	0.627583	-0.297236	-1.765431	0.330347	-1.435084	58.268149

HLA A*2603	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.246845	2.811476	-1.435369	17654.056349
HLA A*2902	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.858127	2.415459	-1.442668	7213.182391
HLA A*0101	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.254283	2.811476	-1.442807	17959.034220
HLA A*6801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-2.977535	1.534232	-1.443303	949.588040
HLA A*3002	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.141198	2.697803	-1.443395	13841.959234
HLA A*2501	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.056997	2.611929	-1.445068	11402.411820
HLA A*1101	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.959756	2.513913	-1.445843	9114.990851
HLA B*5801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.269266	2.823193	-1.446073	18589.411614
HLA A*0216	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.084453	2.636993	-1.447460	12146.546136
HLA A*2402	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.227107	1.779223	-1.447884	1686.968335
HLA A*6802	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-2.786625	1.338234	-1.448392	611.822554
HLA A*0101	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.121843	2.672978	-1.448865	13238.613660
HLA A*2402	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.379753	2.930176	-1.449576	23974.663791
HLA A*3201	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.375702	1.925846	-1.449856	2375.212441
HLA B*0803	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.380554	2.930176	-1.450377	24018.932404
HLA A*2603	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.161859	2.710432	-1.451427	14516.400343

HLA A*3301	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.381674	2.930176	-1.451498	24080.993711
HLA B*4402	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.348554	2.896488	-1.452065	22312.781583
HLA B*4601	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.078222	2.626012	-1.452210	11973.523471
HLA A*0203	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.383312	2.930176	-1.453136	24171.967148
HLA B*4402	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.265375	2.811476	-1.453899	18423.616999
HLA B*4001	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.350915	2.896488	-1.454427	22434.425191
HLA A*0212	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.384844	2.930176	-1.454667	24257.378208
HLA B*2705	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.353499	2.896488	-1.457011	22568.327743
HLA B*5301	1:52-60	9	INISLPSYY	1.208811	1.305102	-3.971085	2.513913	-1.457172	9355.897469
HLA A*0201	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.388338	2.930176	-1.458161	24453.303818
HLA B*1801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-2.992657	1.534232	-1.458425	983.233170
HLA B*1517	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.282413	2.823193	-1.459221	19160.787830
HLA A*6802	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.389400	2.930176	-1.459223	24513.171913
HLA B*0702	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.389735	2.930176	-1.459559	24532.142986
HLA A*2501	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.171031	2.710432	-1.460599	14826.250256
HLA A*6901	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.357301	2.896488	-1.460812	22766.739948

HLA B*4801	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.358177	2.896488	-1.461689	22812.727077
HLA A*6901	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.075276	2.611929	-1.463347	11892.569981
HLA B*5701	1:140-148	9	KPITYDTLW	1.293618	0.385080	-3.143771	1.678698	-1.465072	1392.421428
HLA A*0101	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.289133	2.823193	-1.465940	19459.554300
HLA A*3101	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.277872	2.811476	-1.466396	18961.461448
HLA B*0802	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.363924	2.896488	-1.467436	23116.604624
HLA B*3901	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.291116	2.823193	-1.467923	19548.608737
HLA B*5701	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.291219	2.823193	-1.468026	19553.262547
HLA A*0206	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-2.068910	0.600517	-1.468392	117.195113
HLA B*4001	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.399291	2.930176	-1.469114	25077.881323
HLA A*2501	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.106200	2.636993	-1.469207	12770.256994
HLA A*0219	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.107332	2.636993	-1.470339	12803.599742
HLA A*0250	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.316744	1.845985	-1.470760	2073.693101
HLA A*0212	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.368602	2.896488	-1.472113	23366.941416
HLA A*0211	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.403165	2.930176	-1.472989	25302.599630
HLA B*5101	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.284542	2.811476	-1.473066	19254.932270

HLA A*0219	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.403428	2.930176	-1.473252	25317.935313
HLA B*5701	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.085740	2.611929	-1.473812	12182.609451
HLA A*2402	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.173475	2.697803	-1.475672	14909.902065
HLA B*0702	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.173959	2.697803	-1.476156	14926.527476
HLA A*6802	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.115198	2.636993	-1.478205	13037.615379
HLA B*0803	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.377004	2.896488	-1.480515	23823.393713
HLA A*6801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.115809	2.633172	-1.482637	13055.966616
HLA A*2403	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.413270	2.930176	-1.483094	25898.241635
HLA B*1509	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.380340	2.896488	-1.483851	24007.110796
HLA B*5101	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-2.238895	0.754093	-1.484802	173.338384
HLA B*4403	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.196410	2.710432	-1.485978	15718.476981
HLA A*2601	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.185086	2.697803	-1.487283	15313.904897
HLA B*3901	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.418037	2.930176	-1.487861	26184.083886
HLA B*5301	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.125752	2.636993	-1.488759	13358.326417
HLA B*1801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.904257	2.415459	-1.488798	8021.520585
HLA B*1502	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.126894	2.636993	-1.489901	13393.494422

HLA B*1501	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.416701	1.925846	-1.490855	2610.363406
HLA A*3201	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-2.859544	1.368668	-1.490876	723.675882
HLA B*1501	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-2.268611	0.776623	-1.491988	185.614128
HLA B*2705	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.202449	2.710432	-1.492016	15938.543786
HLA A*6901	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.165021	2.672978	-1.492043	14622.490362
HLA A*0201	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.389580	2.896488	-1.493092	24523.385282
HLA B*5801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.908754	2.415459	-1.493295	8105.011150
HLA B*1503	1:96-104	9	TSATYQSAI	0.928477	0.250556	-2.673408	1.179033	-1.494376	471.420538
HLA B*5701	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.392090	2.896488	-1.495601	24665.485672
HLA B*4601	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.194568	2.697803	-1.496766	15651.950551
HLA A*0212	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.210667	2.710432	-1.500235	16243.033440
HLA A*0216	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.430673	2.930176	-1.500496	26957.084128
HLA A*6901	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.252843	1.751039	-1.501804	1789.959438
HLA B*4403	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.040765	1.534232	-1.506533	1098.410249
HLA B*3501	1:140-148	9	KPITYDTLW	1.293618	0.385080	-3.187274	1.678698	-1.508575	1539.124538
HLA A*3001	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-2.319219	0.809025	-1.510194	208.554198

HLA B*4601	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.517936	2.001898	-1.516038	3295.608258
HLA A*0202	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-3.932380	2.415459	-1.516921	8558.152831
HLA A*0203	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.340237	2.823193	-1.517044	21889.535068
HLA A*2403	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.413750	2.896488	-1.517261	25926.839162
HLA A*3001	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.217467	2.697803	-1.519664	16499.339085
HLA A*0219	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.420274	2.896488	-1.523786	26319.285393
HLA B*3901	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.137091	2.611929	-1.525162	13711.679900
HLA A*0203	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.421928	2.896488	-1.525440	26419.715147
HLA B*1801	1:92-100	9	ELNITSATY	1.311755	1.126521	-3.965484	2.438276	-1.527208	9236.007598
HLA A*0301	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.165660	2.636993	-1.528668	14644.023046
HLA B*3901	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.425708	2.896488	-1.529220	26650.689667
HLA A*0250	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-2.209662	0.680076	-1.529586	162.055006
HLA A*0216	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.428260	2.896488	-1.531772	26807.727046
HLA A*3201	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.343331	2.811476	-1.531855	22046.051066
HLA A*6801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-3.186639	1.653995	-1.532645	1536.878026
HLA A*2602	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.167568	2.633172	-1.534396	14708.493250

HLA A*6901	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.358210	2.823193	-1.535017	22814.454943
HLA A*0101	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.168325	2.633172	-1.535152	14734.137543
HLA A*2403	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.359357	2.823193	-1.536164	22874.765270
HLA A*6802	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.433246	2.896488	-1.536757	27117.247196
HLA B*5801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.234937	2.697803	-1.537135	17176.604601
HLA A*2301	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.467515	2.930176	-1.537339	29343.721242
HLA B*0801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.360719	2.823193	-1.537526	22946.652961
HLA A*0206	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.469444	2.930176	-1.539268	29474.341799
HLA B*5301	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.237174	2.697803	-1.539371	17265.295992
HLA B*4403	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.472809	2.930176	-1.542632	29703.565128
HLA A*0216	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.253078	2.710432	-1.542645	17909.262092
HLA B*1503	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.230128	1.687135	-1.542993	1698.745693
HLA A*0206	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.439519	2.896488	-1.543030	27511.782222
HLA A*0201	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.182854	2.636993	-1.545861	15235.402595
HLA A*3001	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-2.500923	0.954978	-1.545945	316.900852
HLA A*3101	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.219064	2.672978	-1.546086	16560.147389

HLA A*1101	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.244591	2.697803	-1.546789	17562.702807
HLA A*0202	1:147-155	9	LWQADTDPL	0.954861	0.515252	-3.018938	1.470113	-1.548825	1044.570750
HLA A*2601	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.361210	2.811476	-1.549735	22972.612654
HLA A*0212	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.374555	2.823193	-1.551363	23689.476561
HLA B*4801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.374901	2.823193	-1.551708	23708.323198
HLA A*0201	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.375115	2.823193	-1.551922	23719.997677
HLA B*0802	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.375507	2.823193	-1.552314	23741.437227
HLA B*2705	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.367258	2.811476	-1.555782	23294.745192
HLA A*0201	1:77-85	9	FLSAATSST	0.627583	-0.297236	-1.887501	0.330347	-1.557154	77.179341
HLA A*0211	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.454165	2.896488	-1.557677	28455.447151
HLA B*0802	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.370425	2.811476	-1.558949	23465.243760
HLA A*0250	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.196467	2.636993	-1.559474	15720.517958
HLA A*6901	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.371012	2.811476	-1.559537	23497.001323
HLA A*2403	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.171887	2.611929	-1.559958	14855.474868
HLA A*6901	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.270577	2.710432	-1.560144	18645.612593
HLA B*4001	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.383512	2.823193	-1.560319	24183.084955

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HLA B*0801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.372152
	2.811476	-1.560676	23558.733618

HLA B*1501	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-2.899612
	1.338234	-1.561379	793.619292

HLA A*0203	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.235414
	2.672978	-1.562436	17195.478439

HLA A*2501	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.374330
	2.811476	-1.562854	23677.176641

HLA B*5801	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.236995
	2.672978	-1.564018	17258.198798

HLA A*3201	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.852615
	2.288348	-1.564267	7122.214054

HLA A*2402	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.389982
	2.823193	-1.566789	24546.082143

HLA B*1801	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.081887
	2.513913	-1.567974	12075.000752

HLA B*0702	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.858338
	2.288348	-1.569990	7216.695273

HLA B*5801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.196519
	2.626012	-1.570506	15722.389088

HLA B*1509	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.382306
	2.811476	-1.570831	24116.063334

HLA B*2705	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.269576
	2.697803	-1.571773	18602.691153

HLA B*3501	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-2.407202
	0.835252	-1.571950	255.389155

HLA B*4801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.384990
	2.811476	-1.573514	24265.515816

HLA B*3501	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-2.529977
	0.954583	-1.575394	338.826320

HLA A*0219	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.286875
	2.710432	-1.576443	19358.648483
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HLA B*5301	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.474004	2.896488	-1.577516	29785.470580
HLA A*0202	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.786806	2.208753	-1.578053	6120.768404
HLA A*0202	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.401878	2.823193	-1.578685	25227.698139
HLA B*4601	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.193248	2.611929	-1.581320	15604.435291
HLA B*3801	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.394258	2.811476	-1.582782	24788.956533
HLA B*5101	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.480376	2.896488	-1.583888	30225.693159
HLA A*0250	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.480823	2.896488	-1.584334	30256.777485
HLA B*0702	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.396342	2.811476	-1.584866	24908.193973
HLA A*0201	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.396756	2.811476	-1.585280	24931.921368
HLA B*4001	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.399636	2.811476	-1.588160	25097.832533
HLA B*3801	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.411924	2.823193	-1.588731	25818.084845
HLA B*0702	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.412215	2.823193	-1.589023	25835.410105
HLA A*0206	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.263246	2.672978	-1.590268	18333.537164
HLA B*5401	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.521701	2.930176	-1.591525	33243.088128
HLA B*4403	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.229414	2.636993	-1.592421	16959.524797
HLA A*0301	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.220009	2.626012	-1.593996	16596.201181

HLA B*4402	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.267024	2.672978	-1.594046	18493.718175
HLA A*2403	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.010843	2.415459	-1.595385	10252.822504
HLA B*1517	1:96-104	9	TSATYQSAI	0.928477	0.250556	-2.774450	1.179033	-1.595418	594.908880
HLA A*6802	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.420326	2.823193	-1.597133	26322.418037
HLA B*4001	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.295406	2.697803	-1.597603	19742.675803
HLA B*1502	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.231549	2.633172	-1.598377	17043.130173
HLA B*4601	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.271502	2.672978	-1.598524	18685.398033
HLA A*0206	1:77-85	9	FLSAATSST	0.627583	-0.297236	-1.928951	0.330347	-1.598603	84.908405
HLA A*2403	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.410277	2.811476	-1.598801	25720.359509
HLA A*2603	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.422537	2.823193	-1.599344	26456.759376
HLA A*3001	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-2.927792	1.328019	-1.599773	846.821624
HLA A*0250	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.038173	2.438276	-1.599896	10918.743116
HLA B*0803	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.424966	2.823193	-1.601773	26605.168568
HLA B*3501	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.529443	1.925846	-1.603597	3384.101340
HLA A*0212	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.240741	2.636993	-1.603748	17407.666045
HLA A*0202	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.534236	2.930176	-1.604059	34216.522048

HLA B*5101	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.427541	2.823193	-1.604348	26763.385548
HLA A*0250	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.535256	2.930176	-1.605079	34296.953127
HLA B*4403	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.121490	2.513913	-1.607577	13227.875102
HLA A*2902	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-3.339675	1.732070	-1.607605	2186.127344
HLA A*3101	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.305619	2.697803	-1.607817	20212.462412
HLA A*3301	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.245108	2.636993	-1.608115	17583.617952
HLA A*2603	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.937723	2.329547	-1.608176	8664.086245
HLA A*3201	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.431582	2.823193	-1.608389	27013.581332
HLA A*3301	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.505777	2.896488	-1.609288	32046.200944
HLA B*0801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.580578	1.970572	-1.610006	3806.953319
HLA A*0212	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.422128	2.811476	-1.610652	26431.866798
HLA A*0219	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.435642	2.823193	-1.612449	27267.296134
HLA B*1509	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.322930	2.710432	-1.612498	21034.404958
HLA B*4402	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.250106	2.636993	-1.613113	17787.118305
HLA B*0702	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.324037	2.710432	-1.613604	21088.070179
HLA B*1503	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-2.736581	1.122935	-1.613646	545.232145

HLA A*0301	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.311970	2.697803	-1.614167	20510.199430
HLA A*0219	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-2.635671	1.020870	-1.614801	432.186375
HLA B*4402	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.130893	2.513913	-1.616979	13517.386281
HLA A*0216	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.463512	1.845985	-1.617527	2907.449043
HLA A*0211	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.827424	2.208753	-1.618671	6720.844447
HLA A*0219	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.430471	2.811476	-1.618995	26944.545250
HLA B*4601	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.133021	2.513913	-1.619108	13583.802483
HLA A*2301	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.443005	2.823193	-1.619813	27733.543377
HLA B*4601	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.949531	2.329547	-1.619985	8902.895553
HLA B*0801	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.293162	2.672978	-1.620184	19640.939405
HLA A*6802	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.433375	2.811476	-1.621899	27125.316968
HLA A*0203	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.433434	2.811476	-1.621958	27128.985840
HLA A*3001	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.250359	2.626012	-1.624347	17797.513786
HLA B*4402	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.322345	2.697803	-1.624543	21006.089377
HLA B*3501	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.042063	2.415459	-1.626604	11017.001173
HLA A*0216	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.449922	2.823193	-1.626729	28178.783777

HLA A*3101	1:83-91	9	SSTPREAPY	1.031192	1.298355	-3.956725	2.329547	-1.627179	9051.600993
HLA A*2403	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.337652	2.710432	-1.627220	21759.659933
HLA A*0203	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.325341	2.697803	-1.627538	21151.482016
HLA B*7301	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.558048	2.930176	-1.627871	36144.972104
HLA B*4801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.338627	2.710432	-1.628195	21808.567514
HLA A*0219	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-2.523464	0.895143	-1.628322	333.783117
HLA B*5301	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.451588	2.823193	-1.628395	28287.074189
HLA B*3801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.339048	2.710432	-1.628615	21829.696508
HLA A*0216	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.440409	2.811476	-1.628933	27568.248817
HLA A*2301	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.525425	2.896488	-1.628937	33529.362382
HLA A*2402	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.441300	2.811476	-1.629824	27624.831308
HLA A*0201	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.340394	2.710432	-1.629962	21897.470644
HLA A*0211	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.068476	2.438276	-1.630200	11707.827258
HLA B*3901	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.839552	2.208753	-1.630799	6911.174926
HLA B*3901	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.443442	2.811476	-1.631967	27761.464006
HLA A*6802	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-2.654096	1.020870	-1.633226	450.916090

HLA B*1501	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.385547	1.751039	-1.634508	2429.667260
HLA B*3901	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.346545	2.710432	-1.636113	22209.813133
HLA B*4402	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.270370	2.633172	-1.637198	18636.738084
HLA B*5301	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.312759	2.672978	-1.639781	20547.515191
HLA A*2301	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.642129	2.001898	-1.640232	4386.613387
HLA B*0803	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.451771	2.811476	-1.640295	28299.013043
HLA A*0301	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.273579	2.633172	-1.640407	18774.972013
HLA B*5701	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.154876	2.513913	-1.640963	14284.869181
HLA A*8001	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.339102	2.697803	-1.641299	21832.412891
HLA B*1801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.275250	2.633172	-1.642077	18847.327717
HLA A*0101	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.340255	2.697803	-1.642453	21890.482449
HLA A*2301	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.254403	2.611929	-1.642474	17963.989879
HLA A*3001	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.275680	2.633172	-1.642507	18865.995994
HLA A*3001	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-2.981590	1.338234	-1.643357	958.496314
HLA A*0203	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.353955	2.710432	-1.643523	22592.026054
HLA B*0801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.342551	2.697803	-1.644748	22006.490062

HLA B*5801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.647143	2.001898	-1.645246	4437.548990
HLA B*7301	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.468481	2.823193	-1.645288	29409.038551
HLA B*5801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.281126	2.633172	-1.647954	19104.067508
HLA B*5401	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-2.725826	1.076055	-1.649771	531.894513
HLA B*1509	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.347788	2.697803	-1.649985	22273.464909
HLA A*2402	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-3.488276	1.838116	-1.650160	3078.050096
HLA B*5701	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.348652	2.697803	-1.650850	22317.851965
HLA A*1101	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.277080	2.626012	-1.651068	18926.923682
HLA A*0201	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-2.897737	1.245899	-1.651839	790.200550
HLA B*1503	1:87-95	9	REAPYELNI	1.162222	0.222672	-3.037546	1.384894	-1.652652	1090.299422
HLA B*1509	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.264609	2.611929	-1.652680	18391.153303
HLA A*0212	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.327648	2.672978	-1.654670	21264.148505
HLA A*2902	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.434355	1.779223	-1.655132	2718.660661
HLA A*2403	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-3.899421	2.240828	-1.658594	7932.707888
HLA B*5101	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.629193	1.970572	-1.658621	4257.876840
HLA B*3901	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.074557	2.415459	-1.659098	11872.898997

HLA A*2402	1:139-147	9	RKPITYDTL	1.549612	0.515162	-3.724949	2.064774	-1.660174	5308.217458
HLA A*2301	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.473001	2.811476	-1.661525	29716.744877
HLA B*1501	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.274244	2.611929	-1.662316	18803.738485
HLA A*0202	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.558837	2.896488	-1.662349	36210.733392
HLA A*0206	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.473868	2.811476	-1.662392	29776.126152
HLA B*4403	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.474134	2.811476	-1.662658	29794.334383
HLA B*0802	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.373597	2.710432	-1.663165	23637.245988
HLA B*1801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.361812	2.697803	-1.664009	23004.450193
HLA B*4501	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.487458	2.823193	-1.664265	30722.575277
HLA A*0216	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.363052	2.697803	-1.665250	23070.254536
HLA A*2402	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.562425	2.896488	-1.665937	36511.105630
HLA B*5401	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.562972	2.896488	-1.666484	36557.157049
HLA A*0211	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.339539	2.672978	-1.666561	21854.392581
HLA B*3801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.278579	2.611929	-1.666650	18992.363002
HLA A*3201	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.877299	2.208753	-1.668546	7538.739063
HLA B*0803	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.379283	2.710432	-1.668850	23948.737764

HLA A*0250	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.379478	2.710432	-1.669045	23959.493660
HLA A*0202	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.957759	2.288348	-1.669411	9073.172647
HLA A*6802	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.380227	2.710432	-1.669795	24000.877567
HLA A*6802	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.281732	2.611929	-1.669803	19130.750654
HLA A*0211	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.481426	2.811476	-1.669951	30298.873996
HLA B*3801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.368311	2.697803	-1.670508	23351.271515
HLA A*6802	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-3.150406	1.478828	-1.671577	1413.857512
HLA A*0211	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.451534	1.779223	-1.672311	2828.358376
HLA B*1517	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.598382	1.925846	-1.672536	3966.267021
HLA A*0211	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.496012	2.823193	-1.672819	31333.729645
HLA A*0212	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.370876	2.697803	-1.673073	23489.629742
HLA B*5101	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.383913	2.710432	-1.673481	24205.466861
HLA B*4403	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.090359	2.415459	-1.674901	12312.873266
HLA A*2501	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.373176	2.697803	-1.675374	23614.367464
HLA A*2601	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.005083	2.329547	-1.675536	10117.716395
HLA B*2705	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.678203	2.001898	-1.676306	4766.541212

HLA A*2301	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.602691	1.925846	-1.676845	4005.815147
HLA B*4501	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.609236	2.930176	-1.679060	40666.437037
HLA A*0206	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.430366	1.751039	-1.679327	2693.801419
HLA B*5701	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.353387	2.672978	-1.680409	22562.468081
HLA A*3001	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.292528	2.611929	-1.680599	19612.271415
HLA A*3301	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.391032	2.710432	-1.680600	24605.511809
HLA A*6901	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.316187	2.633172	-1.683015	20710.339050
HLA B*4601	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.316319	2.633172	-1.683146	20716.614276
HLA B*4801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.381623	2.697803	-1.683820	24078.127821
HLA A*0201	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.381806	2.697803	-1.684003	24088.290245
HLA A*0211	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-2.549027	0.864656	-1.684371	354.019157
HLA A*6901	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.122679	2.438276	-1.684402	13264.134745
HLA A*0216	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.357663	2.672978	-1.684685	22785.715344
HLA B*4801	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.357794	2.672978	-1.684816	22792.619409
HLA A*0250	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.357865	2.672978	-1.684887	22796.318875
HLA B*4601	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.172547	1.486927	-1.685621	1487.809030

HLA A*0301	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.199587	2.513913	-1.685674	15833.866069
HLA B*1503	1:219-227	9	PRSAIDSML	1.524069	0.315829	-3.526046	1.839898	-1.686148	3357.731807
HLA B*3901	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.384078	2.697803	-1.686275	24214.635020
HLA B*5401	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.498366	2.811476	-1.686890	31504.041862
HLA A*6901	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.384938	2.697803	-1.687135	24262.627965
HLA A*3001	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.201678	2.513913	-1.687765	15910.286816
HLA A*2301	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.399784	2.710432	-1.689352	25106.387910
HLA B*4501	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.586735	2.896488	-1.690247	38613.138766
HLA B*0803	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.328386	2.636993	-1.691393	21300.300722
HLA B*5701	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.317590	2.626012	-1.691578	20777.335442
HLA A*2402	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.980239	2.288348	-1.691891	9555.183842
HLA A*3001	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-2.540352	0.847335	-1.693017	347.018369
HLA A*0219	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.366572	2.672978	-1.693594	23257.975821
HLA B*0802	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.391455	2.697803	-1.693653	24629.483835
HLA B*3801	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.367838	2.672978	-1.694860	23325.893429
HLA B*3801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.332695	2.636993	-1.695702	21512.688583

HLA A*0250	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.393619	2.697803	-1.695816	24752.506660
HLA B*4001	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.406349	2.710432	-1.695916	25488.759280
HLA A*2603	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.322030	2.626012	-1.696018	20990.867053
HLA B*4402	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.322298	2.626012	-1.696286	21003.816688
HLA B*7301	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.593372	2.896488	-1.696884	39207.793387
HLA B*1509	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.370637	2.672978	-1.697659	23476.671535
HLA A*0250	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-2.943609	1.245899	-1.697710	878.230817
HLA B*4001	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.371099	2.672978	-1.698121	23501.705092
HLA B*5701	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.331508	2.633172	-1.698336	21453.996257
HLA B*5401	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.521748	2.823193	-1.698556	33246.685151
HLA A*2402	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.038180	1.339576	-1.698604	1091.893154
HLA B*1509	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.332265	2.633172	-1.699092	21491.401352
HLA A*2603	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.397155	2.697803	-1.699352	24954.861333
HLA A*2601	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.988664	2.288348	-1.700316	9742.362848
HLA A*3001	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.493590	1.793265	-1.700326	3115.948125
HLA A*1101	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.333602	2.633172	-1.700429	21557.658687

HLA A*6801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.312468	2.611929	-1.700539	20533.736000
HLA B*3901	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-3.673805	1.973182	-1.700623	4718.512571
HLA B*0801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-3.989054	2.288348	-1.700706	9751.115824
HLA B*5301	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.326835	2.626012	-1.700823	21224.383041
HLA A*0219	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.398666	2.697803	-1.700863	25041.819440
HLA B*4403	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.597498	2.896488	-1.701010	39582.033003
HLA A*0202	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.415016	2.710432	-1.704584	26002.550347
HLA B*4002	1:136-144	9	QAYRKPITY	1.611085	1.319091	-4.634791	2.930176	-1.704615	43131.193120
HLA B*4403	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.402789	2.697803	-1.704987	25280.707625
HLA A*2601	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.317801	2.611929	-1.705873	20787.454183
HLA B*0801	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.416827	2.710432	-1.706395	26111.234126
HLA A*6802	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.405266	2.697803	-1.707463	25425.270564
HLA A*8001	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.319535	2.611929	-1.707607	20870.613953
HLA A*0201	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.381174	2.672978	-1.708196	24053.261010
HLA B*4001	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.346674	2.636993	-1.709681	22216.422510
HLA B*4002	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.533369	2.823193	-1.710176	34148.285478

HLA A*0211	1:77-85	9	FLSAATSST	0.627583	-0.297236	-2.040904
0.330347	-1.710556	109.876203

HLA B*2705	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.386185
2.672978	-1.713207	24332.426236

HLA B*0802	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.325376
2.611929	-1.713448	21153.198493

HLA A*3001	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.922879
2.208753	-1.714126	8372.954294

HLA B*0803	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.413259
2.697803	-1.715456	25897.541111

HLA A*6802	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.389714
2.672978	-1.716736	24530.948570

HLA A*0301	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.046429
2.329547	-1.716882	11128.297792

HLA A*0202	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.416179
2.697803	-1.718376	26072.275767

HLA B*1503	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-3.692300
1.973182	-1.719118	4923.798394

HLA B*2705	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.356655
2.636993	-1.719662	22732.894607

HLA B*0802	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.357496
2.636993	-1.720503	22776.964983

HLA A*0202	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.394084
2.672978	-1.721106	24779.034712

HLA A*2403	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.394660
2.672978	-1.721682	24811.899185

HLA B*4001	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.349120
2.626012	-1.723108	22341.891587

HLA B*4801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.650799
1.925846	-1.724953	4475.060997

HLA A*8001	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.140883
2.415459	-1.725424	13831.928485

HLA A*3101	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.351758	2.626012	-1.725746	22478.038552
HLA A*0201	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.520036	1.793265	-1.726771	3311.585879
HLA A*2601	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.359986	2.633172	-1.726814	22907.954309
HLA B*0702	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.400036	2.672978	-1.727058	25120.925154
HLA A*2601	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.355074	2.626012	-1.729061	22650.277914
HLA B*0802	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.402171	2.672978	-1.729193	25244.763789
HLA A*0211	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.427259	2.697803	-1.729456	26746.016752
HLA B*4002	1:42-50	9	QIQMSDPAY	1.582564	1.313924	-4.627008	2.896488	-1.730519	42365.040723
HLA A*3101	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.366497	2.633172	-1.733324	23253.949831
HLA A*0101	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.359382	2.626012	-1.733370	22876.126560
HLA A*0202	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.249053	2.513913	-1.735140	17744.061104
HLA B*1503	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-3.889215	2.152457	-1.736759	7748.458286
HLA B*5301	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-2.490952	0.754093	-1.736859	309.707836
HLA A*3201	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.409875	2.672978	-1.736897	25696.576837
HLA B*5101	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.374219	2.636993	-1.737227	23671.157134
HLA B*4801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.363555	2.626012	-1.737543	23096.978812

HLA A*6801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.154054	2.415459	-1.738595	14257.846927
HLA A*3101	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.351620	2.611929	-1.739691	22470.865079
HLA B*5701	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-3.892617	2.152457	-1.740161	7809.394346
HLA B*0801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.377311	2.636993	-1.740319	23840.283229
HLA B*2705	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.366527	2.626012	-1.740515	23255.585305
HLA A*3101	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.255462	2.513913	-1.741549	18007.873012
HLA A*0301	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.354369	2.611929	-1.742440	22613.547081
HLA A*0219	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.741619	0.999064	-1.742555	551.593002
HLA B*0803	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.416900	2.672978	-1.743922	26115.613519
HLA A*0250	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.555633	2.811476	-1.744157	35944.514609
HLA B*5101	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.443088	2.697803	-1.745285	27738.795113
HLA A*0202	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.557052	2.811476	-1.745576	36062.158036
HLA A*0206	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.085626	1.339576	-1.746049	1217.939296
HLA A*2403	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-3.336344	1.590000	-1.746344	2169.421234
HLA A*3301	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.572051	2.823193	-1.748858	37329.384099
HLA B*4801	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.386131	2.636993	-1.749139	24329.398803

HLA A*2501	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.263737	2.513913	-1.749824	18354.278010
HLA A*3301	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.562204	2.811476	-1.750728	36492.543373
HLA A*6802	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.384412	2.633172	-1.751239	24233.243952
HLA A*6901	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.377544	2.626012	-1.751532	23853.055004
HLA B*2705	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.363750	2.611929	-1.751822	23107.352164
HLA A*0211	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.545674	1.793265	-1.752409	3512.963216
HLA B*0802	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.386009	2.633172	-1.752837	24322.555559
HLA B*4402	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.365555	2.611929	-1.753626	23203.558192
HLA B*4801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.366551	2.611929	-1.754622	23256.843441
HLA A*2501	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.387915	2.633172	-1.754742	24429.503269
HLA A*0212	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.388558	2.633172	-1.755386	24465.742209
HLA A*0101	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.269884	2.513913	-1.755970	18615.879469
HLA B*0801	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.368059	2.611929	-1.756131	23337.758353
HLA B*0702	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.393145	2.636993	-1.756152	24725.471954
HLA A*3201	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.383122	2.626012	-1.757109	24161.377287
HLA A*0201	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.390753	2.633172	-1.757580	24589.676449

HLA A*0212	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.369683	2.611929	-1.757754	23425.163609
HLA A*2601	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.625453	1.867525	-1.757928	4221.363154
HLA B*4801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.391166	2.633172	-1.757994	24613.100425
HLA B*0801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.394836	2.633172	-1.761664	24821.968450
HLA A*3002	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.050324	2.288348	-1.761976	11228.563127
HLA A*3301	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.373907	2.611929	-1.761978	23654.131501
HLA A*0250	1:109-117	9	TQAVVLKVY	1.536032	1.287161	-4.585224	2.823193	-1.762032	38479.054042
HLA A*3001	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.200513	2.438276	-1.762236	15867.651890
HLA A*0216	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.374172	2.611929	-1.762244	23668.596105
HLA B*1509	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.276617	2.513913	-1.762704	18906.763093
HLA A*2601	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.277066	2.513913	-1.763153	18926.309337
HLA A*0219	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.376181	2.611929	-1.764253	23778.327720
HLA A*0219	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.398739	2.633172	-1.765566	25046.019470
HLA B*3901	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.439413	2.672978	-1.766435	27505.085431
HLA B*3901	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.403926	2.636993	-1.766934	25346.989022
HLA A*0201	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.379419	2.611929	-1.767490	23956.253424

HLA B*5101	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.440872	2.672978	-1.767894	27597.645290
HLA A*0201	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.394373	2.626012	-1.768361	24795.528574
HLA B*4001	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.562858	1.793265	-1.769593	3654.750512
HLA A*3002	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.381693	2.611929	-1.769765	24082.035938
HLA A*0202	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-2.574406	0.804086	-1.770320	375.323623
HLA B*0702	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.383866	2.611929	-1.771938	24202.848025
HLA A*3301	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.445808	2.672978	-1.772830	27913.114456
HLA A*0202	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.212232	2.438276	-1.773955	16301.662421
HLA A*0216	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-2.751585	0.977336	-1.774249	564.397737
HLA B*4001	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.386667	2.611929	-1.774739	24359.426530
HLA B*0702	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.401041	2.626012	-1.775029	25179.158354
HLA A*3101	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.215272	2.438276	-1.776996	16416.180892
HLA B*1509	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.415293	2.636993	-1.778300	26019.154814
HLA A*0202	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.390734	2.611929	-1.778806	24588.612253
HLA A*6802	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.194916	2.415459	-1.779457	15664.487516
HLA B*1509	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.405726	2.626012	-1.779714	25452.244250

HLA B*4001	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.414335	2.633172	-1.781162	25961.787766
HLA B*4002	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.420570	2.636993	-1.783577	26337.231946
HLA B*4002	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.161234	2.377639	-1.783595	14495.525823
HLA A*0101	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.201396	2.415459	-1.785937	15899.961421
HLA B*0802	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.412119	2.626012	-1.786107	25829.680306
HLA A*2403	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.421611	2.633172	-1.788439	26400.426948
HLA A*0216	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-3.997841	2.208753	-1.789088	9950.419463
HLA B*3501	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-2.543407	0.754093	-1.789314	349.467502
HLA A*6801	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.487241	2.697803	-1.789439	30707.288155
HLA B*5101	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.423380	2.633172	-1.790208	26508.192306
HLA B*4002	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.500770	2.710432	-1.790337	31678.878558
HLA B*0702	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.424851	2.633172	-1.791679	26598.116884
HLA B*0803	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.404164	2.611929	-1.792235	25360.842371
HLA A*0212	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.419257	2.626012	-1.793244	26257.705095
HLA A*0203	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.427113	2.633172	-1.793941	26737.047292
HLA A*3002	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.002822	2.208753	-1.794069	10065.197410

HLA B*3801	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.308126	2.513913	-1.794213	20329.473243
HLA B*0803	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.232555	2.438276	-1.794278	17082.638113
HLA A*0203	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.420530	2.626012	-1.794518	26334.809871
HLA A*2403	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.420890	2.626012	-1.794877	26356.616561
HLA A*0216	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-2.812897	1.017829	-1.795068	649.976154
HLA A*0216	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.422499	2.626012	-1.796487	26454.469425
HLA B*3801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.423176	2.626012	-1.797163	26495.718886
HLA A*3201	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.431105	2.633172	-1.797933	26983.931098
HLA A*2402	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.509132	2.710432	-1.798699	32294.726891
HLA A*3101	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.137079	1.338234	-1.798846	1371.132309
HLA B*5801	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.238020	2.438276	-1.799743	17298.953958
HLA B*5401	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.512158	2.710432	-1.801725	32520.540333
HLA A*0219	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.240987	2.438276	-1.802711	17417.557076
HLA A*0202	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-3.281864	1.478828	-1.803036	1913.656692
HLA B*0801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.429559	2.626012	-1.803547	26888.046969
HLA A*0211	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.219153	2.415459	-1.803695	16563.552105

HLA A*0211	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.415667	2.611929	-1.803738	26041.545401
HLA A*3301	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.242390	2.438276	-1.804113	17473.901565
HLA A*6802	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.430147	2.626012	-1.804134	26924.436910
HLA A*6802	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-2.657164	0.852998	-1.804166	454.113236
HLA B*1503	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.220267	2.415459	-1.804808	16606.080317
HLA B*2705	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.438718	2.633172	-1.805545	27461.076036
HLA A*0250	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.805196	0.999064	-1.806132	638.551328
HLA B*1502	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.419109	2.611929	-1.807180	26248.757389
HLA B*7301	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.618752	2.811476	-1.807276	41567.273396
HLA B*1801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.434373	2.626012	-1.808361	27187.755326
HLA A*0216	1:77-85	9	FLSAATSST	0.627583	-0.297236	-2.139122	0.330347	-1.808774	137.759486
HLA A*0216	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.442975	2.633172	-1.809802	27731.592986
HLA A*1101	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.248301	2.438276	-1.810025	17713.369789
HLA A*6901	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.225680	2.415459	-1.810221	16814.360233
HLA B*5301	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.422255	2.611929	-1.810326	26439.589574
HLA A*1101	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.229583	2.415459	-1.814124	16966.132022

HLA B*5101	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.055009	2.240828	-1.814181	11350.344887
HLA B*5101	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.192999	2.377639	-1.815360	15595.489520
HLA A*6801	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.441979	2.626012	-1.815966	27668.055351
HLA A*0211	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.155556	1.339576	-1.815979	1430.723513
HLA B*3901	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.450049	2.633172	-1.816877	28187.016961
HLA A*0216	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.816445	0.999064	-1.817381	655.307512
HLA B*3801	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.255789	2.438276	-1.817513	18021.419568
HLA A*0216	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.257135	2.438276	-1.818859	18077.370237
HLA A*3201	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.234860	2.415459	-1.819401	17173.538398
HLA B*3901	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.445684	2.626012	-1.819671	27905.112240
HLA A*2501	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.446020	2.626012	-1.820007	27926.708382
HLA A*3002	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.237585	2.415459	-1.822126	17281.649316
HLA B*4402	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.356869	1.534232	-1.822637	2274.411212
HLA B*3801	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.455892	2.633172	-1.822720	28568.818899
HLA B*5301	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.263084	2.438276	-1.824808	18326.694856
HLA A*0211	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-2.802320	0.977336	-1.824984	634.336998

HLA A*6802	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.263883	2.438276	-1.825606	18360.435308
HLA A*0202	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.512889	1.687135	-1.825754	3257.533485
HLA A*0206	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-2.721305	0.895143	-1.826162	526.386934
HLA B*4002	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.638743	2.811476	-1.827268	43525.453598
HLA B*4402	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.266176	2.438276	-1.827900	18457.635744
HLA A*0203	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.440863	2.611929	-1.828934	27597.048095
HLA B*1503	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.197311	1.368126	-1.829185	1575.109541
HLA A*6901	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.343505	2.513913	-1.829591	22054.878568
HLA B*5101	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.456167	2.626012	-1.830155	28586.907457
HLA B*3801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.246257	2.415459	-1.830798	17630.195866
HLA B*1509	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.271237	2.438276	-1.832960	18673.978814
HLA B*4002	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.531557	2.697803	-1.833755	34006.148775
HLA B*0801	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.272087	2.438276	-1.833811	18710.585391
HLA B*1501	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-3.162454	1.328019	-1.834434	1453.629750
HLA B*4501	1:20-28	9	VATAAPKTY	1.520765	1.290711	-4.646210	2.811476	-1.834734	44280.240309
HLA A*0202	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.585854	1.751039	-1.834816	3853.492294

HLA B*5101	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.447434	2.611929	-1.835506	28017.807043
HLA A*0212	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.274282	2.438276	-1.836005	18805.366173
HLA A*0219	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.463491	2.626012	-1.837478	29073.045000
HLA B*5101	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.355398	2.513913	-1.841484	22667.194126
HLA A*1101	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.455063	2.611929	-1.843134	28514.313347
HLA A*0203	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.281807	2.438276	-1.843531	19134.062789
HLA A*0206	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.455556	2.611929	-1.843628	28546.726203
HLA B*7301	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.554932	2.710432	-1.844500	35886.613454
HLA A*6802	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.691351	1.845985	-1.845366	4913.048716
HLA B*4001	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.262368	2.415459	-1.846909	18296.480446
HLA B*2705	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-3.820615	1.973182	-1.847433	6616.297673
HLA A*2301	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.520574	2.672978	-1.847596	33156.876230
HLA B*5401	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.546300	2.697803	-1.848498	35180.375361
HLA B*2705	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.362911	2.513913	-1.848998	23062.767300
HLA B*0803	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.482211	2.633172	-1.849039	30353.670613
HLA B*1509	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.264964	2.415459	-1.849505	18406.183051

HLA A*0203	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.364276	2.513913	-1.850363	23135.370977
HLA B*0803	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.477320	2.626012	-1.851307	30013.703592
HLA B*1509	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.853278	2.001898	-1.851380	7133.087916
HLA B*4501	1:130-138	9	KAFDWDQAY	1.345340	1.365092	-4.562105	2.710432	-1.851673	36484.252649
HLA B*1501	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.271035	2.415459	-1.855576	18665.292757
HLA A*6802	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.858874	2.001898	-1.856976	7225.602232
HLA B*1501	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.234916	2.377639	-1.857277	17175.768309
HLA B*3501	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.235360	2.377639	-1.857721	17193.338982
HLA A*3001	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.275301	2.415459	-1.859843	18849.571014
HLA A*0206	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.106127	1.245899	-1.860229	1276.812863
HLA A*2301	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.494405	2.633172	-1.861233	31217.997692
HLA B*5301	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.276897	2.415459	-1.861438	18918.938747
HLA B*4002	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-2.715140	0.853458	-1.861682	518.967369
HLA B*0802	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.376033	2.513913	-1.862120	23770.224900
HLA B*1801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.240184	2.377639	-1.862545	17385.361217
HLA A*2301	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.377234	2.513913	-1.863321	23836.027490

HLA B*4801	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.378594	2.513913	-1.864681	23910.806750
HLA A*6802	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.379123	2.513913	-1.865210	23939.929303
HLA B*4402	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.281805	2.415459	-1.866346	19133.959276
HLA B*0801	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.381263	2.513913	-1.867350	24058.206286
HLA B*4403	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.540408	2.672978	-1.867430	34706.271552
HLA B*1517	1:140-148	9	KPITYDTLW	1.293618	0.385080	-3.547873	1.678698	-1.869174	3530.796768
HLA B*2705	1:219-227	9	PRSAIDSML	1.524069	0.315829	-3.709447	1.839898	-1.869549	5122.085268
HLA A*0201	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.384604	2.513913	-1.870691	24243.996468
HLA B*1509	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.112365	2.240828	-1.871537	12952.830604
HLA B*1509	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.161347	2.288348	-1.872999	14499.290433
HLA A*2402	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.387818	2.513913	-1.873905	24424.085273
HLA A*6901	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.845036	1.970572	-1.874464	6998.993391
HLA B*1801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.845491	1.970572	-1.874920	7006.342820
HLA B*5401	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.548356	2.672978	-1.875378	35347.301824
HLA A*2602	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.501432	2.626012	-1.875420	31727.244383
HLA A*0212	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.389489	2.513913	-1.875576	24518.211745

HLA B*2705	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.314237	2.438276	-1.875961	20617.553789
HLA A*0206	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.504839	2.626012	-1.878827	31977.102355
HLA B*0702	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.392827	2.513913	-1.878914	24707.420668
HLA B*1502	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.295028	2.415459	-1.879569	19725.487574
HLA B*5701	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.295117	2.415459	-1.879658	19729.543073
HLA A*2402	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.553264	2.672978	-1.880286	35749.036595
HLA B*5401	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.368057	1.486927	-1.881131	2333.765606
HLA A*2602	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.807228	1.925846	-1.881381	6415.458068
HLA B*0802	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.170326	2.288348	-1.881979	14802.207261
HLA B*7301	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.555099	2.672978	-1.882121	35900.400227
HLA B*4001	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.397585	2.513913	-1.883672	24979.579121
HLA A*3001	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-3.475701	1.590000	-1.885702	2990.206905
HLA B*5701	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.175500	2.288348	-1.887152	14979.594148
HLA A*6801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.813764	1.925846	-1.887918	6512.742959
HLA B*2705	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.303690	2.415459	-1.888231	20122.887448
HLA B*4601	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.326915	2.438276	-1.888638	21228.287333

HLA A*2601	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.305246	2.415459	-1.889787	20195.083685
HLA A*0202	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.523090	2.633172	-1.889918	33349.544501
HLA B*0803	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.404683	2.513913	-1.890770	25391.181559
HLA A*2301	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.516925	2.626012	-1.890913	32879.473754
HLA A*3301	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.524805	2.633172	-1.891633	33481.509566
HLA A*2402	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.524911	2.633172	-1.891738	33489.661465
HLA B*4501	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.590135	2.697803	-1.892332	38916.592835
HLA A*0211	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.518887	2.626012	-1.892874	33028.334770
HLA A*3001	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.818844	1.925846	-1.892997	6589.364390
HLA A*0201	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-2.893193	0.999064	-1.894130	781.975999
HLA A*0211	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.528054	2.633172	-1.894882	33732.953556
HLA B*4403	1:87-95	9	REAPYELNI	1.162222	0.222672	-3.279853	1.384894	-1.894959	1904.815293
HLA B*0802	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.333353	2.438276	-1.895076	21545.300029
HLA A*3001	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.272809	2.377639	-1.895169	18741.686424
HLA A*0219	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.412577	2.513913	-1.898664	25856.943146
HLA B*1502	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.108248	2.208753	-1.899495	12830.642021

HLA A*0250	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-3.185413	1.285203	-1.900210	1532.544063
HLA A*0216	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.693982	1.793265	-1.900718	4942.907618
HLA A*3301	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.598736	2.697803	-1.900934	39695.042857
HLA B*4403	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.535624	2.633172	-1.902452	34326.095708
HLA A*0206	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.535650	2.633172	-1.902478	34328.138472
HLA A*3101	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.321828	2.415459	-1.906369	20981.103314
HLA B*5401	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.541066	2.633172	-1.907893	34758.883372
HLA A*0203	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.247590	1.339576	-1.908013	1768.437604
HLA B*5701	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.346317	2.438276	-1.908041	22198.161385
HLA B*1503	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-2.684738	0.776623	-1.908115	483.880049
HLA B*0803	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.149595	2.240828	-1.908767	14112.196833
HLA A*0203	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.197947	2.288348	-1.909599	15774.188511
HLA A*2301	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-3.501057	1.590000	-1.911057	3169.982628
HLA B*5401	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-1.695619	-0.215742	-1.911360	49.615643
HLA A*3201	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.240968	2.329547	-1.911422	17416.803275
HLA A*3001	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.063946	2.152457	-1.911490	11586.346144

HLA A*0206	1:139-147	9	RKPITYDTL	1.549612	0.515162	-3.978355	2.064774	-1.913581	9513.816275
HLA B*7301	1:191-199	9	AVTNDGVIF	1.536436	1.161367	-4.612180	2.697803	-1.914377	40943.034597
HLA B*0803	1:24-32	9	APKTYCEEL	1.537287	0.413098	-3.867093	1.950385	-1.916707	7363.640007
HLA B*5401	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.554009	2.636993	-1.917016	35810.396463
HLA A*0206	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.125808	2.208753	-1.917055	13360.060939
HLA A*0211	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-2.935714	1.017829	-1.917885	862.411230
HLA A*2403	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.431801	2.513913	-1.917887	27027.175816
HLA B*1517	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.335303	2.415459	-1.919844	21642.260431
HLA A*2602	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.161544	2.240828	-1.920716	14505.880853
HLA B*0802	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.336360	2.415459	-1.920901	21695.011618
HLA B*4403	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.535230	2.611929	-1.923301	34294.912218
HLA A*0206	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.363252	2.438276	-1.924976	23080.865615
HLA B*4801	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.363261	2.438276	-1.924985	23081.365080
HLA B*3901	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.439298	2.513913	-1.925385	27497.795223
HLA A*0203	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.719023	1.793265	-1.925759	5236.285344
HLA B*5401	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.552475	2.626012	-1.926463	35684.113782

HLA A*0212	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.343230
	2.415459	-1.927771	22040.923194

HLA A*0216	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.442207
	2.513913	-1.928293	27682.578229

HLA A*0203	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-2.708336
	0.779687	-1.928649	510.900048

HLA B*2705	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.217387
	2.288348	-1.929039	16496.304537

HLA A*3001	1:18-26	9	SGVATAAPK	0.424227	0.140104	-2.493908
	0.564331	-1.929577	311.822784

HLA A*0216	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.345673
	2.415459	-1.930214	22165.281212

HLA B*5301	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.618230
	1.687135	-1.931095	4151.742389

HLA B*0801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-3.857483
	1.925846	-1.931637	7202.498142

HLA A*0201	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.347804
	2.415459	-1.932345	22274.308404

HLA A*0219	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.348833
	2.415459	-1.933374	22327.150659

HLA A*0211	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.450019
	2.513913	-1.936105	28185.034678

HLA A*6802	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.224759
	2.288348	-1.936411	16778.740196

HLA A*6901	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.274717
	1.338234	-1.936483	1882.421589

HLA B*4501	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.610105
	2.672978	-1.937128	40747.918898

HLA B*4403	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.563189
	2.626012	-1.937176	36575.356433

HLA A*6901	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-3.416123
	1.478828	-1.937295	2606.891760

HLA B*4601	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.226272	2.288348	-1.937924	16837.298749
HLA B*1502	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.316276	2.377639	-1.938637	20714.597032
HLA A*0301	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.356401	2.415459	-1.940942	22719.616383
HLA B*0802	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.911526	1.970572	-1.940954	8156.916357
HLA B*0802	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.270736	2.329547	-1.941190	18652.473062
HLA B*4001	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.379478	2.438276	-1.941201	23959.493660
HLA A*6901	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.230473	2.288348	-1.942125	17000.954183
HLA A*0250	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.554733	2.611929	-1.942804	35870.115127
HLA B*4501	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.580154	2.636993	-1.943161	38032.440831
HLA A*0202	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.569196	2.626012	-1.943184	37084.822121
HLA B*3901	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.122959	1.179033	-1.943926	1327.269027
HLA A*3001	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-2.830772	0.886699	-1.944073	677.286323
HLA B*1503	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.043393	2.098630	-1.944763	11050.786900
HLA B*3901	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.738064	1.793265	-1.944799	5470.959896
HLA B*1509	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.274418	2.329547	-1.944872	18811.267726
HLA B*5101	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-3.021142	1.076055	-1.945087	1049.884871

HLA A*3201	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.459142	2.513913	-1.945228	28783.368896
HLA A*0250	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.579111	2.633172	-1.945939	37941.196887
HLA A*2402	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.572135	2.626012	-1.946123	37336.654929
HLA B*4002	1:51-59	9	NINISLPSY	1.394333	1.278645	-4.619144	2.672978	-1.946166	41604.844380
HLA A*0250	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.572201	2.626012	-1.946189	37342.310998
HLA B*4601	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.367643	2.415459	-1.952184	23315.421969
HLA B*5401	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.564319	2.611929	-1.952390	36670.655178
HLA A*2301	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.193676	2.240828	-1.952848	15619.806981
HLA B*0801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.368585	2.415459	-1.953127	23366.056545
HLA B*5301	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-3.322228	1.368668	-1.953560	2100.042968
HLA B*3801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.283198	2.329547	-1.953652	19195.440813
HLA A*2602	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.165599	2.208753	-1.956846	14641.963405
HLA B*0702	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.395891	2.438276	-1.957615	24882.335296
HLA A*1101	1:18-26	9	SGVATAAPK	0.424227	0.140104	-2.521965	0.564331	-1.957635	332.633048
HLA B*0803	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.246222	2.288348	-1.957874	17628.765263
HLA B*0803	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.374706	2.415459	-1.959247	23697.680057

HLA B*7301	1:192-200	9	VTNDGVIFF	1.493493	1.143500	-4.596330	2.636993	-1.959338	39475.751146
HLA A*0212	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.753725	1.793265	-1.960461	5671.856027
HLA A*2603	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.216196	1.254764	-1.961432	1645.113713
HLA A*2301	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-3.800381	1.838116	-1.962266	6315.115114
HLA B*2705	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.291858	2.329547	-1.962312	19582.056153
HLA A*0206	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.476389	2.513913	-1.962476	29949.473576
HLA B*4601	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.340786	2.377639	-1.963147	21917.262885
HLA B*5801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.342459	2.377639	-1.964820	22001.847497
HLA B*4001	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.810874	1.845985	-1.964889	6469.549967
HLA B*7301	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.600090	2.633172	-1.966917	39818.929348
HLA B*0801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.175932	2.208753	-1.967179	14994.512553
HLA A*6901	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.210108	2.240828	-1.969280	16222.133121
HLA A*0201	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.407737	2.438276	-1.969461	25570.383492
HLA A*0250	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.257934	2.288348	-1.969586	18110.651670
HLA B*0801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.299344	2.329547	-1.969797	19922.496116
HLA B*5401	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-2.697340	0.725355	-1.971985	498.127311

HLA A*3301	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.489781	2.513913	-1.975868	30887.393267
HLA B*4801	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.391455	2.415459	-1.975996	24629.483835
HLA A*2402	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.821992	1.845985	-1.976007	6637.305910
HLA A*3201	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.139091	1.161468	-1.977623	1377.496562
HLA A*0211	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.265983	2.288348	-1.977635	18449.449551
HLA A*0101	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.355910	2.377639	-1.978271	22693.942583
HLA A*2403	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.419041	2.438276	-1.980764	26244.639629
HLA A*2501	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.189973	2.208753	-1.981220	15487.198847
HLA A*3001	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.269825	2.288348	-1.981477	18613.361893
HLA B*1509	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.828631	1.845985	-1.982647	6739.558992
HLA B*0801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.361116	2.377639	-1.983477	22967.642020
HLA B*3901	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.422494	2.438276	-1.984218	26454.183195
HLA A*2601	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.363158	2.377639	-1.985519	23075.871558
HLA B*1801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.315590	2.329547	-1.986044	20681.900272
HLA A*2501	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.401878	2.415459	-1.986419	25227.698139
HLA B*3801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.195198	2.208753	-1.986445	15674.659994

HLA B*1501	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.227489	2.240828	-1.986661	16884.548465
HLA B*7301	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.613226	2.626012	-1.987213	41041.719625
HLA A*0301	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.364911	2.377639	-1.987272	23169.188814
HLA B*0702	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.403179	2.415459	-1.987720	25303.420949
HLA B*5801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.167068	1.179033	-1.988035	1469.156941
HLA A*0212	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.196800	2.208753	-1.988047	15732.599167
HLA B*4501	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.624207	2.633172	-1.991035	42092.725005
HLA A*8001	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.279523	2.288348	-1.991176	19033.712073
HLA A*2501	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.232029	2.240828	-1.991201	17061.949651
HLA A*2902	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.200484	2.208753	-1.991731	15866.621817
HLA B*4402	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.322427	2.329547	-1.992881	21010.067176
HLA B*1517	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.370813	2.377639	-1.993174	23486.198932
HLA B*0803	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.370918	2.377639	-1.993279	23491.917226
HLA A*0101	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.282131	2.288348	-1.993783	19148.352938
HLA A*3301	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.620561	2.626012	-1.994548	41740.787785
HLA A*2402	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-3.997235	2.001898	-1.995338	9936.540839

HLA B*4801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.204610	2.208753	-1.995857	16018.069219
HLA B*4002	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.622903	2.626012	-1.996891	41966.531626
HLA A*2902	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.374786	2.377639	-1.997147	23702.039320
HLA B*3501	1:24-32	9	APKTYCEEL	1.537287	0.413098	-3.947670	1.950385	-1.997285	8864.831523
HLA B*1501	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.791420	1.793265	-1.998156	6186.148422
HLA B*5101	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.436941	2.438276	-1.998665	27348.992994
HLA A*0206	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.123593	1.122935	-2.000658	1329.209145
HLA A*6901	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.689984	1.687135	-2.002849	4897.604036
HLA A*0203	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-2.806981	0.804086	-2.002896	641.182146
HLA B*2705	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.068984	2.064774	-2.004210	11721.516273
HLA B*1503	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.783850	1.779223	-2.004627	6079.254080
HLA A*2602	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.420173	2.415459	-2.004714	26313.163576
HLA A*6901	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.382494	2.377639	-2.004855	24126.502811
HLA B*7301	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.618340	2.611929	-2.006412	41527.939009
HLA B*1517	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.247697	2.240828	-2.006869	17688.759268
HLA B*1801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.295218	2.288348	-2.006870	19734.133197

HLA B*4002	1:179-187	9	NAGLDPVNY	1.458021	1.175151	-4.641072	2.633172	-2.007899	43759.428900
HLA A*0203	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.423545	2.415459	-2.008086	26518.232653
HLA A*2601	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.250808	2.240828	-2.009980	17815.913263
HLA B*3901	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.075854	2.064774	-2.011079	11908.407538
HLA A*1101	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-3.601450	1.590000	-2.011451	3994.389177
HLA B*4501	1:121-129	9	GGTHPTTTY	1.498809	1.127203	-4.638849	2.626012	-2.012837	43536.050943
HLA A*8001	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.390527	2.377639	-2.012888	24576.909132
HLA B*3501	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.165820	2.152457	-2.013364	14649.411170
HLA A*0201	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.392101	2.377639	-2.014462	24666.152869
HLA B*4002	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.626820	2.611929	-2.014891	42346.709476
HLA B*1503	1:85-93	9	TPREAPYEL	1.651184	0.319388	-3.985502	1.970572	-2.014930	9671.679439
HLA A*2403	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.355502	1.339576	-2.015925	2267.261364
HLA A*6901	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-2.869111	0.852998	-2.016113	739.794677
HLA B*5401	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.530082	2.513913	-2.016169	33890.811967
HLA A*2902	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.018944	2.001898	-2.017047	10445.866309
HLA A*3201	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.263219	1.245899	-2.017320	1833.236584

HLA A*3101	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.395569	2.377639	-2.017930	24863.900466
HLA B*4801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.395872	2.377639	-2.018233	24881.258434
HLA B*1503	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.021377	1.002409	-2.018968	1050.453001
HLA A*6802	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.349153	2.329547	-2.019606	22343.583791
HLA A*0206	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-3.019652	0.999064	-2.020588	1046.290071
HLA A*6901	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.350215	2.329547	-2.020668	22398.286739
HLA B*4402	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.119780	2.098630	-2.021150	13175.880903
HLA A*3001	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.262638	2.240828	-2.021810	18307.866910
HLA B*0802	1:24-32	9	APKTYCEEL	1.537287	0.413098	-3.972458	1.950385	-2.022072	9385.503003
HLA B*3901	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.310772	2.288348	-2.022424	20453.688892
HLA B*3901	1:219-227	9	PRSAIDSML	1.524069	0.315829	-3.862398	1.839898	-2.022500	7284.475342
HLA A*0206	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.354364	2.329547	-2.024817	22613.302409
HLA B*0802	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.179240	2.152457	-2.026784	15109.163715
HLA B*4402	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.267717	2.240828	-2.026889	18523.256183
HLA B*0803	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.029653	2.001898	-2.027756	10706.645317
HLA B*5401	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-2.782580	0.754093	-2.028487	606.149386

HLA A*2301	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.095326	2.064774	-2.030552	12454.497812
HLA B*5701	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.408907	2.377639	-2.031268	25639.366178
HLA A*0203	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-2.072312	0.040514	-2.031797	118.116769
HLA A*2403	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.362124	2.329547	-2.032578	23021.008202
HLA B*4001	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.412878	2.377639	-2.035239	25874.854396
HLA A*0203	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.413883	2.377639	-2.036244	25934.835290
HLA B*4501	1:151-159	9	DTDPLPVVF	1.668283	0.943646	-4.648195	2.611929	-2.036267	44483.124440
HLA B*4001	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.367420	2.329547	-2.037874	23303.442332
HLA B*0802	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.042237	2.001898	-2.040340	11021.412512
HLA A*0206	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.059232	1.017829	-2.041403	1146.123793
HLA B*0702	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.371168	2.329547	-2.041621	23505.392488
HLA A*0202	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-3.881706	1.838116	-2.043591	7615.638931
HLA B*3801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.332002	2.288348	-2.043654	21478.383493
HLA B*5101	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.459151	2.415459	-2.043692	28783.991762
HLA B*4002	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.459452	2.415459	-2.043993	28803.930595
HLA B*0802	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.285458	2.240828	-2.044630	19295.600306

HLA B*0802	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.422516	2.377639	-2.044876	26455.471254
HLA A*0212	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.422797	2.377639	-2.045158	26472.651370
HLA A*8001	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.143979	2.098630	-2.045350	13930.905817
HLA A*2603	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.333956	2.288348	-2.045608	21575.276188
HLA B*4001	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.334295	2.288348	-2.045947	21592.090395
HLA B*4801	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.375495	2.329547	-2.045949	23740.795043
HLA B*1517	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.302384	1.254764	-2.047620	2006.247139
HLA A*0212	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.293903	1.245899	-2.048004	1967.445856
HLA A*0203	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.256947	2.208753	-2.048194	18069.548204
HLA A*2501	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.425875	2.377639	-2.048236	26660.928220
HLA A*0219	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.336611	2.288348	-2.048263	21707.573588
HLA A*2402	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.486915	2.438276	-2.048638	30684.205734
HLA A*3301	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.464188	2.415459	-2.048729	29119.795287
HLA A*6802	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.426681	2.377639	-2.049042	26710.445953
HLA A*0201	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.895117	1.845985	-2.049133	7854.475795
HLA A*2402	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.290294	2.240828	-2.049466	19511.629226

HLA B*1509 1:182-190 9 LDPVNYQNF 1.429067 0.948572 -4.428836
2.377639 -2.051196 26843.282177

HLA A*3301 1:83-91 9 SSTPREAPY 1.031192 1.298355 -4.381663
2.329547 -2.052116 24080.342342

HLA A*0216 1:69-77 9 YIAQTRDKF 1.072862 1.215486 -4.340937
2.288348 -2.052589 21924.852677

HLA A*6802 1:48-56 9 PAYNINISL 1.435478 0.251657 -3.742358
1.687135 -2.055223 5525.332143

HLA B*1517 1:58-66 9 SYYPDQKSL 1.636422 0.572331 -4.264576
2.208753 -2.055823 18389.760439

HLA B*0702 1:6-14 9 FMLVTAVVL 1.561991 0.439907 -4.058167
2.001898 -2.056269 11433.172759

HLA A*6802 1:5-13 9 IFMLVTAVV 1.049669 0.289907 -3.396679
1.339576 -2.057102 2492.749636

HLA A*0219 1:182-190 9 LDPVNYQNF 1.429067 0.948572 -4.435109
2.377639 -2.057470 27233.831224

HLA B*3501 1:58-66 9 SYYPDQKSL 1.636422 0.572331 -4.266310
2.208753 -2.057557 18463.328286

HLA A*0250 1:52-60 9 INISLPSYY 1.208811 1.305102 -4.572563
2.513913 -2.058650 37373.434696

HLA A*2902 1:61-69 9 PDQKSLENY 1.207586 0.891044 -4.158715
2.098630 -2.060085 14411.703748

HLA B*0803 1:83-91 9 SSTPREAPY 1.031192 1.298355 -4.390107
2.329547 -2.060560 24553.121106

HLA A*0216 1:182-190 9 LDPVNYQNF 1.429067 0.948572 -4.438252
2.377639 -2.060613 27431.676632

HLA A*0201 1:69-77 9 YIAQTRDKF 1.072862 1.215486 -4.349916
2.288348 -2.061568 22382.903148

HLA A*3101 1:124-132 9 HPTTTYKAF 1.324492 0.916336 -4.303721
2.240828 -2.062893 20124.302711

HLA A*2603 1:193-201 9 TNDGVIFFF 1.447213 0.968246 -4.478739
2.415459 -2.063280 30111.935964

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HLA A*3101	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.065568
	2.001898	-2.063670	11629.676752

HLA A*0201	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.393511
	2.329547	-2.063965	24746.347643

HLA B*4403	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.502523
	2.438276	-2.064246	31806.985790

HLA B*7301	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.578310
	2.513913	-2.064397	37871.268542

HLA A*3101	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.353953
	2.288348	-2.065605	22591.903834

HLA A*0203	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.397179
	2.329547	-2.067632	24956.211400

HLA A*0301	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.356359
	2.288348	-2.068011	22717.404100

HLA A*0202	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.313967
	1.245899	-2.068069	2060.475199

HLA B*1517	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-3.800602
	1.732070	-2.068532	6318.327354

HLA B*4403	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.448564
	2.377639	-2.070925	28090.808707

HLA A*0206	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-3.356244
	1.285203	-2.071041	2271.140619

HLA B*1509	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.939349
	1.867525	-2.071824	8696.582282

HLA B*5801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.227189
	2.152457	-2.074732	16872.860540

HLA A*3002	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.173710
	2.098630	-2.075080	14917.970339

HLA B*4801	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.363760
	2.288348	-2.075412	23107.852202

HLA B*2705	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.453820
	2.377639	-2.076181	28432.826847
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HLA A*0212	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.405860	2.329547	-2.076313	25460.094008
HLA B*0702	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.454097	2.377639	-2.076458	28450.983218
HLA A*3101	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.285893	2.208753	-2.077140	19314.921579
HLA A*2301	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.515966	2.438276	-2.077690	32806.981070
HLA A*3101	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.230417	2.152457	-2.077960	16998.746968
HLA A*0202	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.231902	2.152457	-2.079445	17056.966003
HLA B*4002	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.594517	2.513913	-2.080603	39311.227062
HLA A*0203	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.233079	2.152457	-2.080622	17103.259134
HLA A*0206	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.234928	2.152457	-2.082471	17176.232911
HLA A*1101	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.461475	2.377639	-2.083835	28938.409796
HLA A*2902	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.326142	2.240828	-2.085314	21190.537695
HLA A*0212	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.374450	2.288348	-2.086102	23683.710178
HLA B*4001	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.327942	2.240828	-2.087114	21278.532954
HLA B*5301	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.240066	2.152457	-2.087610	17380.659209
HLA A*6802	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.210726	1.122935	-2.087791	1624.524709
HLA B*5301	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.466084	2.377639	-2.088445	29247.203839

HLA B*1509	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.153561	2.064774	-2.088786	14241.658116
HLA B*3801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.331696	2.240828	-2.090868	21463.283366
HLA B*1503	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.958464	1.867525	-2.090939	9087.910060
HLA B*3501	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.778973	1.687135	-2.091838	6011.360373
HLA B*3501	1:89-97	9	APYELNITS	1.361001	-1.037258	-2.416079	0.323743	-2.092336	260.662649
HLA B*0803	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.301282	2.208753	-2.092529	20011.612096
HLA B*2705	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.333526	2.240828	-2.092698	21553.927025
HLA A*3101	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.019668	1.925846	-2.093822	10463.286200
HLA A*0216	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.424451	2.329547	-2.094905	26573.666342
HLA A*3002	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-3.934800	1.838116	-2.096684	8605.973558
HLA A*6901	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.305802	2.208753	-2.097049	20220.993291
HLA B*1517	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.584012	1.486927	-2.097086	3837.182884
HLA B*5801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.338500	2.240828	-2.097672	21802.197420
HLA A*6901	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.277043	1.179033	-2.098010	1892.530491
HLA B*1501	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.307421	2.208753	-2.098668	20296.505943
HLA A*2603	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.477392	2.377639	-2.099753	30018.737509

HLA	B*4402	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.389437	2.288348	-2.101089	24515.293821
HLA	B*5101	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.103526	2.001898	-2.101628	12691.879009
HLA	B*3901	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.431777	2.329547	-2.102231	27025.713715
HLA	A*2402	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.029221	1.925846	-2.103375	10695.993015
HLA	A*0206	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.482042	2.377639	-2.104403	30341.849795
HLA	A*3002	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.856445	1.751039	-2.105406	7185.296312
HLA	B*4001	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.170721	2.064774	-2.105947	14815.666530
HLA	A*0201	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.314956	2.208753	-2.106203	20651.712891
HLA	B*1501	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.258662	2.152457	-2.106206	18141.049904
HLA	B*5801	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.593439	1.486927	-2.106512	3921.377318
HLA	B*1503	1:62-70	9	DQKSLENYI	1.150042	0.062507	-3.319273	1.212549	-2.106723	2085.799354
HLA	B*5401	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-2.942227	0.835252	-2.106975	875.441591
HLA	B*5801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.033394	1.925846	-2.107547	10799.254996
HLA	A*6802	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-2.861687	0.754093	-2.107594	727.255191
HLA	B*5801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.902029	1.793265	-2.108765	7980.486928
HLA	B*4001	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.111289	2.001898	-2.109391	12920.776724

HLA A*3001	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.888722	1.779223	-2.109499	7739.660442
HLA B*3801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.487920	2.377639	-2.110281	30755.335259
HLA B*4601	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.351399	2.240828	-2.110571	22459.440885
HLA A*0202	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.290026	1.179033	-2.110993	1949.961960
HLA A*0219	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.441217	2.329547	-2.111671	27619.601148
HLA A*0250	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.979403	1.867525	-2.111878	9536.799027
HLA B*5401	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.550581	2.438276	-2.112305	35528.856555
HLA A*3201	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.179024	2.064774	-2.114250	15101.645607
HLA B*5301	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.406483	2.288348	-2.118135	25496.620300
HLA B*3901	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.495881	2.377639	-2.118241	31324.238411
HLA A*0203	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.373066	1.254764	-2.118302	2360.838817
HLA A*1101	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.408583	2.288348	-2.120235	25620.231876
HLA A*0301	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.361459	2.240828	-2.120631	22985.790036
HLA B*4501	1:52-60	9	INISLPSYY	1.208811	1.305102	-4.634683	2.513913	-2.120770	43120.461047
HLA A*0219	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-3.988617	1.867525	-2.121093	9741.308803
HLA A*0212	1:77-85	9	FLSAATSST	0.627583	-0.297236	-2.452439	0.330347	-2.122092	283.425835

HLA A*1101	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-3.077285	0.954978	-2.122307	1194.771822
HLA A*0206	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.099680	0.977336	-2.122344	1257.998903
HLA A*0211	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.809864	1.687135	-2.122729	6454.517653
HLA B*3801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.189141	2.064774	-2.124367	15457.567684
HLA B*4501	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.563503	2.438276	-2.125227	36601.880441
HLA A*3101	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.660559	1.534232	-2.126327	4576.766121
HLA B*4601	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.335512	2.208753	-2.126759	21652.683258
HLA A*6802	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.337116	2.208753	-2.128363	21732.836924
HLA B*3901	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.879850	1.751039	-2.128811	7583.160571
HLA B*5801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.337622	2.208753	-2.128869	21758.129662
HLA B*1503	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-2.909316	0.779687	-2.129628	811.550574
HLA A*2301	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.470659	1.339576	-2.131083	2955.692470
HLA B*4801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.372495	2.240828	-2.131667	23577.348688
HLA A*0101	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.374769	2.240828	-2.133941	23701.141759
HLA A*2403	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.061395	1.925846	-2.135549	11518.474316
HLA A*2402	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.288846	2.152457	-2.136390	19446.715106

HLA B*5701	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.377532	2.240828	-2.136704	23852.409801
HLA B*4001	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.345603	2.208753	-2.136850	22161.684153
HLA A*0250	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.552696	2.415459	-2.137237	35702.264824
HLA B*5301	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.466928	2.329547	-2.137381	29304.061497
HLA A*6801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.005726	1.867525	-2.138202	10132.725104
HLA A*0202	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.516110	2.377639	-2.138470	32817.809267
HLA A*0250	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.478276	1.339576	-2.138700	3007.989221
HLA A*0203	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.985018	1.845985	-2.139033	9660.906964
HLA B*0802	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.348448	2.208753	-2.139695	22307.350309
HLA A*8001	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.381649	2.240828	-2.140821	24079.560723
HLA A*0211	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.519704	2.377639	-2.142065	33090.573850
HLA A*6901	1:199-207	9	FFFNPGELL	1.344812	0.501173	-3.988237	1.845985	-2.142252	9732.775240
HLA B*0803	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.295366	2.152457	-2.142909	19740.860190
HLA B*4402	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.352273	2.208753	-2.143520	22504.685544
HLA A*2902	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.069740	1.925846	-2.143894	11741.952765
HLA B*4501	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.561088	2.415459	-2.145629	36398.888965

HLA A*3001	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.210766	2.064774	-2.145992	16246.724525
HLA B*5401	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.561668	2.415459	-2.146210	36447.559222
HLA A*0211	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.898961	1.751039	-2.147922	7924.300992
HLA B*1501	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.015890	1.867525	-2.148366	10372.659764
HLA A*0301	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.357273	2.208753	-2.148520	22765.262009
HLA A*6802	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.301738	2.152457	-2.149281	20032.625678
HLA B*7301	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.276282	1.122935	-2.153346	1889.216161
HLA B*5101	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.482916	2.329547	-2.153370	30402.973608
HLA A*1101	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-3.807524	1.653995	-2.153529	6419.832630
HLA A*0201	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.394792	2.240828	-2.153964	24819.417183
HLA A*0219	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.362801	2.208753	-2.154048	23056.903996
HLA A*3002	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.934264	1.779223	-2.155041	8595.365023
HLA B*1801	1:91-99	9	YELNITSAT	0.787532	-0.429583	-2.513094	0.357949	-2.155144	325.907038
HLA A*0206	1:147-155	9	LWQADTDPL	0.954861	0.515252	-3.625359	1.470113	-2.155246	4220.449768
HLA A*6802	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.402040	1.245899	-2.156142	2523.714287
HLA B*7301	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.129991	1.973182	-2.156808	13489.334445

HLA B*5101	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.446957	2.288348	-2.158609	27987.054567
HLA B*4002	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-3.954418	1.793265	-2.161154	9003.641767
HLA B*4801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.008137	1.845985	-2.162152	10189.123640
HLA B*7301	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.601248	2.438276	-2.162971	39925.271181
HLA A*0201	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.316086	2.152457	-2.163630	20705.521863
HLA B*5101	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.316175	2.152457	-2.163719	20709.778855
HLA A*8001	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.372775	2.208753	-2.164021	23592.532125
HLA A*6801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-3.499793	1.334657	-2.165136	3160.769742
HLA A*2301	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.136536	1.970572	-2.165964	13694.184905
HLA B*4801	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-3.898858	1.732070	-2.166787	7922.414954
HLA B*1502	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-3.900075	1.732070	-2.168004	7944.647253
HLA B*1503	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.329949	1.161468	-2.168481	2137.709014
HLA A*2402	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-3.758481	1.590000	-2.168481	5734.301925
HLA A*0212	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.410160	2.240828	-2.169332	25713.403235
HLA B*5701	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.379849	2.208753	-2.171096	23979.982092
HLA B*2705	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.379856	2.208753	-2.171103	23980.371282

HLA B*1502 1:198-206 9 IFFFNPGEL 1.210946 0.568277 -3.950518
1.779223 -2.171295 8923.147296

HLA A*3001 1:215-223 9 QVLVPRSAI 0.852479 0.308989 -3.333506
1.161468 -2.172038 2155.289974

HLA A*0301 1:7-15 9 MLVTAVVLL 1.492026 0.433820 -4.098268
1.925846 -2.172421 12539.140709

HLA A*2601 1:58-66 9 SYYPDQKSL 1.636422 0.572331 -4.383427
2.208753 -2.174674 24178.375613

HLA A*0212 1:70-78 9 IAQTRDKFL 1.739879 0.412578 -4.327237
2.152457 -2.174780 21244.026612

HLA A*0219 1:70-78 9 IAQTRDKFL 1.739879 0.412578 -4.327310
2.152457 -2.174853 21247.589673

HLA B*1501 1:44-52 9 QMSDPAYNI 1.440627 0.291443 -3.907382
1.732070 -2.175311 8079.444787

HLA A*3201 1:174-182 9 VSIAPNAGL 1.281479 0.469560 -3.926459
1.751039 -2.175421 8442.271905

HLA B*0702 1:58-66 9 SYYPDQKSL 1.636422 0.572331 -4.384896
2.208753 -2.176142 24260.265434

HLA A*0212 1:199-207 9 FFFNPGELL 1.344812 0.501173 -4.023930
1.845985 -2.177945 10566.473554

HLA A*3001 1:6-14 9 FMLVTAVVL 1.561991 0.439907 -4.179847
2.001898 -2.177949 15130.267075

HLA B*5401 1:182-190 9 LDPVNYQNF 1.429067 0.948572 -4.556025
2.377639 -2.178386 35977.003408

HLA B*1501 1:41-49 9 CQIQMSDPA 0.720301 -0.119784 -2.779276
0.600517 -2.178759 601.556320

HLA B*1502 1:209-217 9 EAAGPTQVL 1.572811 0.294714 -4.046997
1.867525 -2.179473 11142.876424

HLA A*6802 1:124-132 9 HPTTTYKAF 1.324492 0.916336 -4.420309
2.240828 -2.179481 26321.421246

HLA A*0211 1:83-91 9 SSTPREAPY 1.031192 1.298355 -4.509035
2.329547 -2.179489 32287.564538

HLA A*0203	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.421369	2.240828	-2.180541	26385.720238
HLA A*6802	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.152381	1.970572	-2.181809	14203.033600
HLA B*1501	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.280675	2.098630	-2.182045	19084.234440
HLA B*5401	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-3.517889	1.334657	-2.183232	3295.251700
HLA A*3001	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.284413	2.098630	-2.185783	19249.203935
HLA B*0702	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.338282	2.152457	-2.185825	21791.231064
HLA A*0203	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-3.965672	1.779223	-2.186449	9240.005725
HLA A*0219	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.427447	2.240828	-2.186619	26757.594696
HLA A*0206	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.442663	1.254764	-2.187899	2771.167531
HLA A*2602	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.286595	2.098630	-2.187966	19346.189845
HLA B*0702	1:140-148	9	KPITYDTLW	1.293618	0.385080	-3.867149	1.678698	-2.188451	7364.596144
HLA B*3801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.341014	2.152457	-2.188558	21928.767190
HLA A*0206	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.429465	2.240828	-2.188637	26882.229145
HLA A*3002	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.566633	2.377639	-2.188994	36866.585161
HLA A*6801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-3.264957	1.075247	-2.189710	1840.590323
HLA A*3201	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.567883	2.377639	-2.190244	36972.842277

HLA B*5101	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.679242	1.486927	-2.192315	4777.952465
HLA B*7301	1:193-201	9	TNDGVIFFF	1.447213	0.968246	-4.608839	2.415459	-2.193380	40629.273873
HLA A*0101	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.404366	2.208753	-2.195613	25372.644260
HLA B*4002	1:92-100	9	ELNITSATY	1.311755	1.126521	-4.633917	2.438276	-2.195641	43044.479794
HLA A*2601	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.122030	1.925846	-2.196184	13244.344454
HLA A*2603	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.295368	2.098630	-2.196739	19740.966986
HLA A*0206	1:148-156	9	WQADTDPLP	0.614046	0.092801	-2.903625	0.706847	-2.196778	800.986390
HLA A*2402	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.527375	2.329547	-2.197829	33680.254708
HLA A*0202	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.066136	1.867525	-2.198612	11644.912216
HLA A*2602	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.579736	2.377639	-2.202097	37995.834730
HLA B*4001	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.354573	2.152457	-2.202116	22624.192886
HLA A*0202	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-3.202400	1.000164	-2.202235	1593.674951
HLA A*0211	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.268218	2.064774	-2.203444	18544.612952
HLA A*0203	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.068648	0.864656	-2.203993	1171.246388
HLA A*2403	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.356535	2.152457	-2.204078	22726.623368
HLA B*2705	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.356561	2.152457	-2.204104	22727.975842

HLA A*3301	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.357526	2.152457	-2.205070	22778.566911
HLA A*0301	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.358114	2.152457	-2.205657	22809.395134
HLA B*1801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.414767	2.208753	-2.206014	25987.643505
HLA B*5101	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.415249	2.208753	-2.206495	26016.480498
HLA B*5401	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.209239	2.001898	-2.207341	16189.694419
HLA B*3901	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.053374	1.845985	-2.207389	11307.687986
HLA B*4601	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.359998	2.152457	-2.207541	22908.573965
HLA B*5301	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.158767	1.950385	-2.208382	14413.419096
HLA A*0250	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.586371	2.377639	-2.208732	38580.773954
HLA A*0211	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.361589	2.152457	-2.209132	22992.630335
HLA B*4403	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.538869	2.329547	-2.209323	34583.508297
HLA A*2301	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.540126	2.329547	-2.210579	34683.748014
HLA A*0216	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.363163	2.152457	-2.210706	23076.121235
HLA A*0206	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.697789	1.486927	-2.210862	4986.417744
HLA A*0101	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.364032	2.152457	-2.211575	23122.358020
HLA A*6901	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.364100	2.152457	-2.211644	23125.985897

HLA B*1801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.213891	2.001898	-2.211993	16364.043746
HLA B*1501	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.059102	1.845985	-2.213117	11457.816455
HLA A*0202	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.543873	2.329547	-2.214327	34984.321133
HLA A*0250	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.545974	2.329547	-2.216427	35153.930556
HLA A*1101	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.457598	2.240828	-2.216770	28681.245845
HLA B*5401	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.187919	1.970572	-2.217348	15414.144452
HLA A*0201	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.558178	1.339576	-2.218601	3615.576555
HLA B*5301	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-3.173487	0.954583	-2.218904	1491.032069
HLA A*0250	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.372089	2.152457	-2.219632	23555.292715
HLA A*2403	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-2.907967	0.687624	-2.220343	809.034394
HLA A*2601	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.373207	2.152457	-2.220750	23616.028287
HLA B*5401	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.551389	2.329547	-2.221843	35595.037385
HLA A*3001	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.195269	1.970572	-2.224697	15677.204146
HLA A*6802	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.005269	0.779687	-2.225581	1012.205184
HLA B*5401	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-3.302488	1.075247	-2.227240	2006.724753
HLA B*4801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.380119	2.152457	-2.227662	23994.905574

HLA A*3201	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.468641	2.240828	-2.227813	29419.859316
HLA A*0202	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.292836	2.064774	-2.228061	19626.175470
HLA B*4402	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.381341	2.152457	-2.228884	24062.501693
HLA A*0211	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.067396	1.838116	-2.229280	11678.727979
HLA A*0216	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.470111	2.240828	-2.229283	29519.661234
HLA B*1509	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.202505	1.973182	-2.229323	15940.613338
HLA B*1502	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.156544	1.925846	-2.230698	14339.843179
HLA A*0211	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.098404	1.867525	-2.230879	12543.075778
HLA A*8001	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.386329	2.152457	-2.233872	24340.457341
HLA B*7301	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.611698	2.377639	-2.234059	40897.652824
HLA A*0203	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.298890	2.064774	-2.234116	19901.705722
HLA B*5701	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.162766	1.925846	-2.236919	14546.745413
HLA B*3501	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.989280	1.751039	-2.238241	9756.181375
HLA A*3301	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.606662	1.368126	-2.238535	4042.607097
HLA B*5101	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.189583	1.950385	-2.239198	15473.296942
HLA B*1509	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.395055	2.152457	-2.242598	24834.460013

HLA B*4403	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.484666	2.240828	-2.243838	30525.756025
HLA A*3201	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.023488	1.779223	-2.244265	10555.732289
HLA A*0301	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.613926	1.368126	-2.245800	4110.798048
HLA B*1502	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-3.998161	1.751039	-2.247122	9957.743128
HLA B*5801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.345770	2.098630	-2.247140	22170.198138
HLA A*2603	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.489706	2.240828	-2.248878	30882.046614
HLA A*0203	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.000304	1.751039	-2.249265	10006.994227
HLA A*0206	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.937328	1.687135	-2.250193	8656.215369
HLA A*1101	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.460904	2.208753	-2.252151	28900.392268
HLA B*3501	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.098319	1.845985	-2.252335	12540.633176
HLA A*0101	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.351148	2.098630	-2.252518	22446.443817
HLA A*3301	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.633880	2.377639	-2.256241	43040.754101
HLA B*1517	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.321168	2.064774	-2.256394	20949.232515
HLA B*4501	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.587825	2.329547	-2.258279	38710.186779
HLA A*0202	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-3.258191	0.999064	-2.259127	1812.135288
HLA B*1801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.357780	2.098630	-2.259150	22791.879588

HLA B*3901	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.412939	2.152457	-2.260482	25878.494134
HLA A*2902	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.414586	2.152457	-2.262129	25976.820308
HLA B*5101	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.130028	1.867525	-2.262504	13490.502108
HLA A*3002	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.415014	2.152457	-2.262557	26002.409676
HLA A*0250	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.055878	1.793265	-2.262614	11373.087160
HLA B*0801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.328078	2.064774	-2.263304	21285.210643
HLA B*4001	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.798685	1.534232	-2.264453	6290.496764
HLA A*0301	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.363818	2.098630	-2.265188	23110.977687
HLA A*3002	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.506242	2.240828	-2.265414	32080.545881
HLA A*2601	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.364316	2.098630	-2.265687	23137.498792
HLA B*5401	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.555008	2.288348	-2.266660	35892.826555
HLA B*1509	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.237801	1.970572	-2.267230	17290.252703
HLA B*4001	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.134826	1.867525	-2.267301	13640.357803
HLA A*3301	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.476974	2.208753	-2.268221	29989.844571
HLA B*1517	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-2.887724	0.619394	-2.268330	772.189376
HLA A*0216	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.333862	2.064774	-2.269088	21570.607899

HLA A*0301	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.271420	2.001898	-2.269523	18681.860361
HLA B*4801	1:48-56	9	PAYNINISL	1.435478	0.251657	-3.956739	1.687135	-2.269604	9051.894807
HLA B*1502	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.368531	2.098630	-2.269902	23363.149347
HLA B*5301	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.368607	2.098630	-2.269977	23367.194242
HLA B*1501	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.336444	2.064774	-2.271670	21699.237264
HLA A*0201	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-3.076712	0.804086	-2.272626	1193.195748
HLA B*4501	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.651052	2.377639	-2.273413	44776.717979
HLA A*3301	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.561767	2.288348	-2.273419	36455.841607
HLA B*7301	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.603247	2.329547	-2.273701	40109.503530
HLA B*3501	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.053285	1.779223	-2.274062	11305.363638
HLA B*5301	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.278628	2.001898	-2.276731	18994.520803
HLA A*3002	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.010049	1.732070	-2.277979	10234.091912
HLA B*1509	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.119385	1.839898	-2.279487	13163.911294
HLA A*1101	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.432419	2.152457	-2.279962	27065.657474
HLA B*4601	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.378759	2.098630	-2.280129	23919.863301
HLA A*6801	1:182-190	9	LDPVNYQNF	1.429067	0.948572	-4.658394	2.377639	-2.280755	45540.143875

HLA B*4402	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.346296	2.064774	-2.281522	22197.080605
HLA B*5801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.328670	1.046875	-2.281796	2131.427028
HLA A*0206	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-3.488403	1.203934	-2.284469	3078.949430
HLA B*5801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.350074	2.064774	-2.285300	22391.017583
HLA A*6901	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.384412	2.098630	-2.285782	24233.243952
HLA B*1517	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.531953	1.245899	-2.286054	3403.710465
HLA B*1502	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.439824	2.152457	-2.287368	27531.137667
HLA A*3201	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.155675	1.867525	-2.288151	14311.168411
HLA B*5701	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.039986	1.751039	-2.288948	10964.439889
HLA A*6802	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-3.291920	1.000164	-2.291756	1958.483081
HLA A*3101	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.357033	2.064774	-2.292259	22752.703405
HLA B*3901	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.024513	1.732070	-2.292442	10580.659604
HLA A*0211	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.533764	2.240828	-2.292936	34179.335644
HLA A*0201	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.394044	2.098630	-2.295415	24776.755935
HLA B*3901	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.247784	1.950385	-2.297399	17692.300308
HLA A*0212	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.362331	2.064774	-2.297557	23031.970428

HLA B*1517	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.268262	1.970572	-2.297691	18546.519212
HLA B*7301	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.586460	2.288348	-2.298112	38588.706042
HLA B*2705	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.224280	1.925846	-2.298434	16760.233101
HLA A*2301	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.451172	2.152457	-2.298716	28260.000854
HLA B*7301	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.507546	2.208753	-2.298793	32177.012097
HLA B*5301	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.168198	1.867525	-2.300673	14729.833829
HLA B*4002	1:83-91	9	SSTPREAPY	1.031192	1.298355	-4.630680	2.329547	-2.301133	42724.783753
HLA B*5301	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.227988	1.925846	-2.302141	16903.924404
HLA A*0206	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-3.079005	0.776623	-2.302382	1199.512545
HLA A*0301	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.367404	2.064774	-2.302629	23302.559866
HLA B*0801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.276634	1.973182	-2.303451	18907.479091
HLA B*5801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.171341	1.867525	-2.303817	14836.841542
HLA A*6901	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.005687	0.701666	-2.304021	1013.180366
HLA A*2501	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.403283	2.098630	-2.304653	25309.444769
HLA B*4801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.404269	2.098630	-2.305640	25367.017093
HLA B*0803	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.371050	2.064774	-2.306276	23499.035270

HLA B*1801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.459059	2.152457	-2.306603	28777.919393
HLA A*3001	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.257925	1.950385	-2.307539	18110.259767
HLA A*2501	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.460197	2.152457	-2.307740	28853.369840
HLA B*3501	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.374769	2.064774	-2.309995	23701.141759
HLA B*3801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.312433	2.001898	-2.310535	20532.069790
HLA B*0801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.178249	1.867525	-2.310724	15074.709243
HLA A*3101	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.409469	2.098630	-2.310839	25672.538384
HLA A*3001	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.285273	1.973182	-2.312090	19287.355490
HLA A*6901	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.377013	2.064774	-2.312239	23823.909247
HLA B*4801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.154590	1.839898	-2.314691	14275.444186
HLA B*5301	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.525134	2.208753	-2.316381	33506.877548
HLA B*4601	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.096600	1.779223	-2.317377	12491.069982
HLA B*1517	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.004594	1.687135	-2.317459	10106.337768
HLA A*0201	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.382487	2.064774	-2.317713	24126.111249
HLA A*2603	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.527545	2.208753	-2.318791	33693.376127
HLA B*5701	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.417673	2.098630	-2.319043	26162.136876

HLA B*5801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.339995	1.020870	-2.319125	2187.736368
HLA B*3501	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.418756	2.098630	-2.320126	26227.465599
HLA A*3301	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.166948	1.845985	-2.320963	14687.501416
HLA A*6802	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.387292	2.064774	-2.322518	24394.505722
HLA B*0802	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.421176	2.098630	-2.322546	26374.017840
HLA B*4801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.293240	1.970572	-2.322668	19644.446143
HLA B*3801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.293912	1.970572	-2.323340	19674.864112
HLA A*0203	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.422125	2.098630	-2.323496	26431.723805
HLA B*5701	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.388420	2.064774	-2.323646	24457.934395
HLA B*4002	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.564984	2.240828	-2.324156	36726.840900
HLA A*0203	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-3.219462	0.895143	-2.324319	1657.531180
HLA B*5701	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.327025	2.001898	-2.325128	21233.685625
HLA A*3001	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.076356	1.751039	-2.325318	11922.202079
HLA A*0101	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.390156	2.064774	-2.325382	24555.910688
HLA A*2601	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.327627	2.001898	-2.325729	21263.113200
HLA A*2601	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.390978	2.064774	-2.326204	24602.450398

HLA A*2402	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.121363	1.793265	-2.328099	13224.011355
HLA B*4002	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.616769	2.288348	-2.328421	41377.912088
HLA A*3301	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.570505	2.240828	-2.329677	37196.738656
HLA A*0219	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.428410	2.098630	-2.329781	26817.010370
HLA B*4403	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.619165	2.288348	-2.330817	41606.870128
HLA B*1503	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.865114	1.534232	-2.330882	7330.173973
HLA A*2403	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.429768	2.098630	-2.331139	26900.996147
HLA A*3101	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.177225	1.845985	-2.331240	15039.194252
HLA B*1503	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.010684	1.678698	-2.331985	10249.051466
HLA A*3001	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.019433	1.687135	-2.332298	10457.627209
HLA B*4601	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.397082	2.064774	-2.332308	24950.676590
HLA A*0101	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.334297	2.001898	-2.332399	21592.207206
HLA B*1801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.258298	1.925846	-2.332452	18125.844414
HLA B*1503	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.821541	1.486927	-2.334614	6630.415328
HLA B*1801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-3.089249	0.754093	-2.335156	1228.141902
HLA B*0801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.433840	2.098630	-2.335210	27154.388036

HLA A*8001	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.401441	2.064774	-2.336666	25202.325803
HLA B*1501	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.287380	1.950385	-2.336995	19381.178134
HLA A*2403	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-3.278476	0.940065	-2.338411	1898.786219
HLA A*0212	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.678603	1.339576	-2.339026	4770.926927
HLA A*0206	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.118838	0.779687	-2.339151	1314.734208
HLA A*2301	1:147-155	9	LWQADTDPL	0.954861	0.515252	-3.809563	1.470113	-2.339450	6450.049667
HLA B*4001	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.090796	1.751039	-2.339758	12325.269199
HLA B*0803	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.310978	1.970572	-2.340407	20463.428603
HLA A*0212	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.439039	2.098630	-2.340410	27481.436489
HLA A*3002	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.343220	2.001898	-2.341323	22040.446244
HLA B*4002	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.550450	2.208753	-2.341697	35518.094583
HLA A*2602	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.494297	2.152457	-2.341840	31210.229907
HLA B*0803	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.441814	2.098630	-2.343184	27657.579657
HLA A*6802	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.442451	2.098630	-2.343821	27698.157618
HLA A*6801	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.584996	2.240828	-2.344169	38458.867100
HLA A*3001	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.363856	1.017829	-2.346027	2311.300195

HLA A*8001	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.347929	2.001898	-2.346031	22280.695901
HLA B*7301	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.185951	1.839898	-2.346052	15344.422787
HLA A*2602	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.525430	1.179033	-2.346398	3352.975959
HLA B*2705	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.445132	2.098630	-2.346502	27869.658344
HLA B*0702	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.445247	2.098630	-2.346617	27877.047140
HLA B*1517	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.445343	2.098630	-2.346713	27883.231107
HLA A*0202	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.587785	2.240828	-2.346957	38706.626840
HLA B*4001	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.445672	2.098630	-2.347042	27904.357432
HLA B*5401	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.558433	2.208753	-2.349680	36177.054942
HLA A*0201	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.100796	1.751039	-2.349757	12612.344412
HLA A*0202	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.129904	0.779687	-2.350217	1348.664846
HLA B*3501	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-3.426409	1.076055	-2.350355	2669.371656
HLA B*0802	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.415406	2.064774	-2.350632	26025.912207
HLA A*2501	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.321276	1.970572	-2.350704	20954.446483
HLA B*0702	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.415624	2.064774	-2.350850	26039.009651
HLA B*4801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.218655	1.867525	-2.351131	16544.566314

HLA A*0206	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-3.426940	1.075733	-2.351207	2672.637319
HLA B*1503	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.217657	0.864656	-2.353002	1650.658765
HLA A*0250	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.594082	2.240828	-2.353254	39271.902908
HLA A*1101	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.453451	2.098630	-2.354821	28408.687605
HLA A*2603	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.325848	1.970572	-2.355277	21176.212732
HLA A*0203	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.842320	1.486927	-2.355393	6955.359445
HLA A*6801	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.509402	2.152457	-2.356945	32314.824894
HLA B*4002	1:46-54	9	SDPAYNINI	1.266370	0.129806	-3.754181	1.396176	-2.358005	5677.811869
HLA A*0203	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.308749	1.950385	-2.358363	20358.638896
HLA A*0216	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.699142	1.339576	-2.359566	5001.980136
HLA A*2403	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.153321	1.793265	-2.360056	14233.801613
HLA A*6901	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.310861	1.950385	-2.360476	20457.894107
HLA A*0216	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.199178	1.838116	-2.361063	15818.968336
HLA A*0219	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.426080	2.064774	-2.361305	26673.479415
HLA B*4501	1:69-77	9	YIAQTRDKF	1.072862	1.215486	-4.649993	2.288348	-2.361645	44667.602224
HLA A*2501	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.427724	2.064774	-2.362950	26774.681313

HLA A*0206	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.334729	1.970572	-2.364158	21613.711214
HLA A*0202	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.341602	0.977336	-2.364266	2195.846785
HLA B*4001	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.290385	1.925846	-2.364539	19515.746334
HLA B*7301	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.605923	2.240828	-2.365095	40357.415842
HLA A*2301	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.464019	2.098630	-2.365389	29108.454986
HLA B*4403	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.464350	2.098630	-2.365721	29130.667222
HLA B*5101	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.431343	2.064774	-2.366568	26998.679115
HLA A*2402	1:147-155	9	LWQADTDPL	0.954861	0.515252	-3.838800	1.470113	-2.368687	6899.220896
HLA A*0250	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.233967	0.864656	-2.369312	1713.828762
HLA B*1509	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.468328	2.098630	-2.369698	29398.698892
HLA B*4501	1:66-74	9	LENYIAQTR	0.964649	0.569583	-3.904487	1.534232	-2.370255	8025.774476
HLA B*0801	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.709771	1.338234	-2.371537	5125.910663
HLA B*4601	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.342654	1.970572	-2.372082	22011.729003
HLA B*0802	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.298099	1.925846	-2.372252	19865.455327
HLA B*1501	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.627027	1.254764	-2.372263	4236.691779
HLA A*2501	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.374182	2.001898	-2.372284	23669.108289

HLA B*3801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.472668	2.098630	-2.374038	29693.925113
HLA A*0206	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.324554	1.950385	-2.374168	21113.183628
HLA A*6801	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.583432	2.208753	-2.374679	38320.549661
HLA B*5101	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.473419	2.098630	-2.374790	29745.374704
HLA A*0211	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.347076	1.970572	-2.376504	22236.984233
HLA B*5101	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-3.304504	0.927533	-2.376971	2016.060988
HLA B*5801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.347936	1.970572	-2.377364	22281.057512
HLA B*5801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.352545	1.973182	-2.379363	22518.812727
HLA A*2403	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.330336	1.950385	-2.379950	21396.158552
HLA B*4801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.353777	1.973182	-2.380594	22582.739216
HLA B*0702	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.306559	1.925846	-2.380713	20256.248643
HLA A*0206	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.248393	1.867525	-2.380868	17717.107450
HLA B*1509	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.160360	1.779223	-2.381137	14466.383220
HLA B*5701	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.402745	1.020870	-2.381875	2527.813516
HLA B*4001	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.332509	1.950385	-2.382124	21503.496428
HLA A*0203	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.353152	1.970572	-2.382580	22550.265337

HLA B*5401	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.535077	2.152457	-2.382620	34282.854779
HLA A*6802	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.162268	1.779223	-2.383045	14530.071365
HLA B*4501	1:124-132	9	HPTTTYKAF	1.324492	0.916336	-4.624007	2.240828	-2.383179	42073.373512
HLA B*4601	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.229181	1.845985	-2.383196	16950.444063
HLA B*1502	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.354420	1.970572	-2.383849	22616.238650
HLA B*4403	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.063246	1.678698	-2.384548	11567.682300
HLA A*0101	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.357938	1.973182	-2.384755	22800.142288
HLA B*5701	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.355351	1.970572	-2.384779	22664.741718
HLA B*5401	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.063721	1.678698	-2.385023	11580.330345
HLA A*3201	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.231352	1.845985	-2.385367	17035.387011
HLA A*0219	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.231455	1.845985	-2.385471	17039.442514
HLA B*4002	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.388013	2.001898	-2.386116	24435.054657
HLA A*0101	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.311970	1.925846	-2.386124	20510.199430
HLA A*2501	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.254328	1.867525	-2.386803	17960.880286
HLA A*6801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.233701	1.845985	-2.387717	17127.796303
HLA B*1501	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.359110	1.970572	-2.388538	22861.775216

HLA A*3201	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.541305	2.152457	-2.388849	34778.068919
HLA A*3101	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.360087	1.970572	-2.389516	22913.283897
HLA A*0216	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.488536	2.098630	-2.389906	30798.958501
HLA A*0203	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.077052	1.687135	-2.389917	11941.308719
HLA B*4402	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.392181	2.001898	-2.390284	24670.690285
HLA B*4402	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.341089	1.950385	-2.390704	21932.563749
HLA B*4403	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.599984	2.208753	-2.391231	39809.236808
HLA B*4601	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.258785	1.867525	-2.391260	18146.153957
HLA B*1501	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.256316	0.864656	-2.391660	1804.328996
HLA A*2902	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.456503	2.064774	-2.391729	28609.031250
HLA B*3901	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.079101	1.687135	-2.391966	11997.774008
HLA B*3501	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-3.629118	1.236794	-2.392324	4257.139795
HLA A*0301	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.363576	1.970572	-2.393005	23098.103408
HLA B*0803	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.319289	1.925846	-2.393442	20858.762010
HLA A*3002	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.187398	1.793265	-2.394133	15395.643247
HLA B*4001	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.364892	1.970572	-2.394320	23168.186093

HLA A*0203	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.261851	1.867525	-2.394326	18274.717375
HLA B*5101	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.073523	1.678698	-2.394825	11844.670937
HLA A*0301	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.368066	1.973182	-2.394884	23338.137120
HLA A*2403	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.127256	1.732070	-2.395185	13404.657499
HLA A*0201	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.368256	1.970572	-2.397685	23348.366156
HLA B*5101	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.323616	1.925846	-2.397770	21067.659006
HLA B*4002	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-3.684500	1.285203	-2.399297	4836.152333
HLA A*2403	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.371550	1.970572	-2.400979	23526.128965
HLA B*5801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.351404	1.950385	-2.401018	22459.683892
HLA A*2602	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.372300	1.970572	-2.401728	23566.764345
HLA B*3901	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.501517	2.098630	-2.402887	31733.424056
HLA A*1101	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.468521	2.064774	-2.403747	29411.743369
HLA B*4002	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.469602	2.064774	-2.404827	29485.027081
HLA A*0101	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.376449	1.970572	-2.405877	23792.996989
HLA A*0219	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.376623	1.970572	-2.406051	23802.523989
HLA B*4001	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.379412	1.973182	-2.406229	23955.864625

HLA A*3001	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.252373	1.845985	-2.406388	17880.219530
HLA A*0216	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.274404	1.867525	-2.406879	18810.657135
HLA A*0212	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.378745	1.970572	-2.408173	23919.086891
HLA B*1517	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.359552	1.950385	-2.409166	22885.038822
HLA A*0206	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.570855	1.161468	-2.409388	3722.677227
HLA A*3101	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.360268	1.950385	-2.409883	22922.830677
HLA A*3001	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.277928	1.867525	-2.410404	18963.923514
HLA B*0702	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.572787	1.161468	-2.411319	3739.268571
HLA A*3101	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-3.746291	1.334657	-2.411635	5575.597667
HLA A*1101	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.414055	2.001898	-2.412157	25945.079548
HLA A*0202	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.252549	1.839898	-2.412651	17887.475752
HLA A*6802	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-3.426790	1.013420	-2.413370	2671.712124
HLA A*0301	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-3.369039	0.954978	-2.414061	2339.049000
HLA A*6901	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.659990	1.245899	-2.414092	4570.778171
HLA B*4601	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.340032	1.925846	-2.414186	21879.234956
HLA A*0202	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.537173	1.122935	-2.414238	3444.872603

HLA A*2402	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.385638	1.970572	-2.415066	24301.774434
HLA A*3002	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.480393	2.064774	-2.415618	30226.837804
HLA B*5701	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.283196	1.867525	-2.415671	19195.336968
HLA A*1101	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.341992	1.925846	-2.416145	21978.173759
HLA A*0301	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.366743	1.950385	-2.416358	23267.162719
HLA B*4501	1:58-66	9	SYYPDQKSL	1.636422	0.572331	-4.625199	2.208753	-2.416445	42188.931346
HLA A*2601	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.387327	1.970572	-2.416756	24396.485376
HLA B*1801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.482648	2.064774	-2.417874	30384.229043
HLA B*4001	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.197190	1.779223	-2.417968	15746.734042
HLA A*0250	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.483456	2.064774	-2.418682	30440.826798
HLA A*3001	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.256884	1.838116	-2.418768	18066.909032
HLA A*2603	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.571567	2.152457	-2.419110	37287.806018
HLA A*0216	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.389860	1.970572	-2.419288	24539.177952
HLA A*0203	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-3.624085	1.203934	-2.420152	4208.092860
HLA A*3101	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.199667	1.779223	-2.420444	15836.778758
HLA A*3301	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.422957	2.001898	-2.421060	26482.391721

HLA B*4402	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.392022	1.970572	-2.421450	24661.616287
HLA B*1501	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.395165	1.973182	-2.421983	24840.775344
HLA A*0201	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.395614	1.973182	-2.422431	24866.456306
HLA A*0201	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.373820	1.950385	-2.423435	23649.397224
HLA A*8001	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.349454	1.925846	-2.423607	22359.061317
HLA A*8001	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.394451	1.970572	-2.423879	24799.955624
HLA A*2601	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.397094	1.973182	-2.423912	24951.351501
HLA A*6901	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.397235	1.973182	-2.424053	24959.451858
HLA B*0702	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.397259	1.973182	-2.424076	24960.802173
HLA A*3101	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.399568	1.973182	-2.426386	25093.895324
HLA B*4601	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.377053	1.950385	-2.426668	23826.100387
HLA A*0219	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.220685	1.793265	-2.427421	16622.079015
HLA B*5401	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-3.632746	1.203934	-2.428812	4292.848051
HLA A*6801	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.430929	2.001898	-2.429031	26972.984813
HLA B*4601	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.402242	1.973182	-2.429059	25248.861263
HLA A*0203	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.267400	1.838116	-2.429285	18509.732939

HLA B*7301	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.494591	2.064774	-2.429816	31231.342530
HLA A*0212	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-3.325048	0.895143	-2.429905	2113.720516
HLA A*0250	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-3.759289	1.328019	-2.431269	5744.983408
HLA B*5701	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.404572	1.973182	-2.431390	25384.726296
HLA A*0219	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.405094	1.973182	-2.431912	25415.231550
HLA B*5801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.278001	1.845985	-2.432016	18967.104155
HLA A*3001	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.164721	1.732070	-2.432650	14612.368292
HLA B*4801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.383117	1.950385	-2.432732	24161.115868
HLA A*2601	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.383129	1.950385	-2.432743	24161.769422
HLA A*0101	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.383234	1.950385	-2.432849	24167.652200
HLA B*3501	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.801218	1.368126	-2.433092	6327.289243
HLA A*2601	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.279159	1.845985	-2.433175	19017.758370
HLA A*2603	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.279820	1.845985	-2.433835	19046.690750
HLA B*4402	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.407260	1.973182	-2.434078	25542.317319
HLA A*2902	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.404728	1.970572	-2.434156	25393.791599
HLA A*8001	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.407676	1.973182	-2.434494	25566.787088

HLA A*2902	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.273711	1.838116	-2.435595	18780.660824
HLA B*3801	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.361810	1.925846	-2.435963	23004.325742
HLA A*2403	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.409316	1.973182	-2.436134	25663.512408
HLA A*2403	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.305004	1.867525	-2.437479	20183.833744
HLA B*1509	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.388248	1.950385	-2.437863	24448.277327
HLA B*5801	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.170312	1.732070	-2.438242	14801.726799
HLA B*4801	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.189428	1.751039	-2.438389	15467.773146
HLA A*0206	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.537053	2.098630	-2.438423	34439.187423
HLA B*3501	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.411929	1.973182	-2.438746	25818.364193
HLA B*4402	1:87-95	9	REAPYELNI	1.162222	0.222672	-3.825587	1.384894	-2.440693	6692.471749
HLA A*2603	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.367039	1.925846	-2.441193	23283.028095
HLA A*3301	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.367587	1.925846	-2.441741	23312.394953
HLA A*3002	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.367859	1.925846	-2.442013	23327.029171
HLA B*3801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.415526	1.973182	-2.442343	26033.093860
HLA B*0801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.283081	1.839898	-2.443182	19190.249254
HLA A*0202	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.308112	0.864656	-2.443457	2032.883425

HLA B*1503	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-3.371497	0.927533	-2.443964	2352.322601
HLA A*6802	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.283020	1.838116	-2.444904	19187.550199
HLA A*3301	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.224355	1.779223	-2.445132	16763.134824
HLA A*0212	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.418514	1.973182	-2.445332	26212.855239
HLA A*3001	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.285625	1.839898	-2.445727	19303.013211
HLA B*1509	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.133106	1.687135	-2.445971	13586.448268
HLA A*3301	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.785580	1.339576	-2.446003	6103.507969
HLA A*0206	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-3.402961	0.956718	-2.446243	2529.071947
HLA B*3501	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.284481	1.838116	-2.446365	19252.224117
HLA A*0202	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.397033	1.950385	-2.446648	24947.842163
HLA B*1502	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.608146	1.161468	-2.446679	4056.452628
HLA B*1517	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.785659	1.338234	-2.447426	6104.630728
HLA B*2705	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.293588	1.845985	-2.447603	19660.181035
HLA A*0203	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.421071	1.973182	-2.447888	26367.597998
HLA A*0211	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.547125	2.098630	-2.448495	35247.241824
HLA A*0203	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-3.405719	0.956718	-2.449001	2545.185731

HLA A*0250	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.137645	1.687135	-2.450510	13729.197246
HLA A*3001	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.471740	1.020870	-2.450870	2963.057015
HLA A*0216	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.231051	1.779223	-2.451828	17023.594672
HLA A*3101	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.289983	1.838116	-2.451868	19497.700840
HLA A*6802	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.403576	1.950385	-2.453191	25326.565719
HLA A*0206	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.292119	1.838116	-2.454003	19593.818664
HLA B*5701	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.404523	1.950385	-2.454138	25381.842561
HLA B*7301	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.607032	2.152457	-2.454576	40460.598880
HLA B*1801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.301146	1.845985	-2.455161	20005.333966
HLA A*3101	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.249845	1.793265	-2.456580	17776.440388
HLA A*3301	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-3.791355	1.334657	-2.456698	6185.211434
HLA A*2402	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.555348	2.098630	-2.456718	35920.993152
HLA B*4403	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.609236	2.152457	-2.456779	40666.437037
HLA A*2603	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.521629	2.064774	-2.456854	33237.513512
HLA A*0216	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.430086	1.973182	-2.456903	26920.650063
HLA A*0216	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.144590	1.687135	-2.457455	13950.514415

HLA B*2705	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.428229	1.970572	-2.457658	26805.841764
HLA A*0212	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.326767	1.867525	-2.459242	21221.053477
HLA A*0211	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-3.744872	1.285203	-2.459669	5557.408728
HLA B*4002	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.558365	2.098630	-2.459735	36171.379686
HLA A*0219	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.410211	1.950385	-2.459826	25716.463764
HLA B*0702	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.211348	1.751039	-2.460310	16268.536613
HLA B*0803	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.192407	1.732070	-2.460337	15574.242799
HLA B*1501	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.239852	1.779223	-2.460629	17372.104818
HLA B*1801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.411160	1.950385	-2.460775	25772.731010
HLA B*0802	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.434547	1.973182	-2.461365	27198.641628
HLA B*4402	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.387612	1.925846	-2.461765	24412.460460
HLA A*8001	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.413637	1.950385	-2.463251	25920.107492
HLA A*0212	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.214939	1.751039	-2.463900	16403.574754
HLA B*5301	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.528750	2.064774	-2.463976	33787.014324
HLA A*6802	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.437249	1.973182	-2.464067	27368.381971
HLA A*6901	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-3.189933	0.725355	-2.464579	1548.579049

HLA B*5401	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.563283	2.098630	-2.464653	36583.272034
HLA A*0202	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-3.951937	1.486927	-2.465011	8952.352020
HLA A*0202	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.319052	0.852998	-2.466054	2084.738933
HLA A*0250	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.245606	1.779223	-2.466383	17603.796110
HLA B*5101	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.153763	1.687135	-2.466627	14248.285596
HLA B*5401	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.392834	1.925846	-2.466988	24707.821665
HLA A*3201	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.320405	0.852998	-2.467407	2091.245312
HLA A*0203	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-3.354139	0.886699	-2.467440	2260.158446
HLA B*4002	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.620812	2.152457	-2.468355	41764.956774
HLA A*6901	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.248329	1.779223	-2.469106	17714.519754
HLA B*2705	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.202045	1.732070	-2.469974	15923.719854
HLA B*3801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.420615	1.950385	-2.470229	26339.939233
HLA A*2902	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.443522	1.973182	-2.470340	27766.570815
HLA A*3002	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-3.410461	0.940065	-2.470396	2573.124148
HLA A*2902	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.421002	1.950385	-2.470617	26363.461595
HLA B*1509	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.264045	1.793265	-2.470780	18367.290214

HLA B*1517	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.264355	1.793265	-2.471091	18380.411079
HLA A*0201	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.250618	1.779223	-2.471395	17808.108022
HLA A*2602	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.474122	2.001898	-2.472224	29793.528474
HLA A*6801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-3.842667	1.368668	-2.473999	6960.930578
HLA A*0203	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.654309	1.179033	-2.475276	4511.376676
HLA A*0212	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.256569	1.779223	-2.477346	18053.816622
HLA A*0250	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-2.518014	0.040514	-2.477499	329.620005
HLA A*0202	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.576313	2.098630	-2.477683	37697.520870
HLA B*5101	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.324457	1.845985	-2.478473	21108.501128
HLA A*1101	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.449462	1.970572	-2.478890	28148.920570
HLA A*0212	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.430137	1.950385	-2.479752	26923.854284
HLA A*2402	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.211875	1.732070	-2.479804	16288.263022
HLA B*5101	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.453634	1.973182	-2.480452	28420.677786
HLA B*1502	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.274895	1.793265	-2.481630	18831.937749
HLA B*4002	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.016769	1.534232	-2.482537	10393.667997
HLA B*5401	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.547515	2.064774	-2.482741	35278.909530

HLA A*2501	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.408696	1.925846	-2.482849	25626.885665
HLA A*0203	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-3.554855	1.071973	-2.482883	3588.024416
HLA B*5801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.262588	1.779223	-2.483365	18305.787114
HLA B*0801	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.170773	1.687135	-2.483638	14817.429960
HLA B*4402	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.354418	1.867525	-2.486893	22616.116299
HLA B*0803	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.460086	1.973182	-2.486904	28846.034377
HLA B*2705	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.438412	1.950385	-2.488027	27441.769847
HLA B*4402	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.335014	1.845985	-2.489029	21627.864107
HLA B*1509	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.415815	1.925846	-2.489968	26050.422472
HLA A*0216	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-3.170066	0.680076	-2.489990	1479.333643
HLA A*3002	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.144040	1.653995	-2.490046	13932.865436
HLA B*4501	1:91-99	9	YELNITSAT	0.787532	-0.429583	-2.849770	0.357949	-2.491821	707.571353
HLA A*2402	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.465387	1.973182	-2.492204	29200.249005
HLA A*3201	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.591138	2.098630	-2.492508	39006.594959
HLA B*4002	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.338524	1.845985	-2.492539	21803.376926
HLA A*0206	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.539692	1.046875	-2.492817	3464.908844

HLA A*0203 1:112-120 9 VVLKVYQNA 1.087232 -0.069403 -3.510746 1.017829 -2.492917 3241.500988

HLA A*0216 1:24-32 9 APKTYCEEL 1.537287 0.413098 -4.443724 1.950385 -2.493339 27779.492230

HLA B*4001 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.331891 1.838116 -2.493776 21472.922990

HLA A*0301 1:209-217 9 EAAGPTQVL 1.572811 0.294714 -4.362646 1.867525 -2.495121 23048.672936

HLA B*4001 1:219-227 9 PRSAIDSML 1.524069 0.315829 -4.335169 1.839898 -2.495271 21635.587773

HLA B*1503 1:12-20 9 VVLLCCSGV 1.181551 0.297277 -3.974746 1.478828 -2.495918 9435.087919

HLA A*0301 1:199-207 9 FFFNPGELL 1.344812 0.501173 -4.342050 1.845985 -2.496066 21981.146447

HLA A*0202 1:85-93 9 TPREAPYEL 1.651184 0.319388 -4.466653 1.970572 -2.496081 29285.519155

HLA A*2402 1:209-217 9 EAAGPTQVL 1.572811 0.294714 -4.363764 1.867525 -2.496240 23108.102226

HLA A*0250 1:61-69 9 PDQKSLENY 1.207586 0.891044 -4.595875 2.098630 -2.497245 39434.342349

HLA A*0201 1:209-217 9 EAAGPTQVL 1.572811 0.294714 -4.364817 1.867525 -2.497292 23164.175646

HLA A*6801 1:110-118 9 QAVVLKVYQ 1.073710 0.019058 -3.590469 1.092768 -2.497701 3894.654020

HLA B*4601 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.335885 1.838116 -2.497770 21671.316311

HLA B*1502 1:139-147 9 RKPITYDTL 1.549612 0.515162 -4.562554 2.064774 -2.497780 36521.970903

HLA A*0201 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.336336 1.838116 -2.498221 21693.837974

HLA A*2301 1:24-32 9 APKTYCEEL 1.537287 0.413098 -4.449072 1.950385 -2.498686 28123.653016

HLA B*4501	1:70-78	9	IAQTRDKFL	1.739879	0.412578	-4.652605	2.152457	-2.500149	44937.123318
HLA A*0206	1:87-95	9	REAPYELNI	1.162222	0.222672	-3.885451	1.384894	-2.500558	7681.595326
HLA B*0802	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.368736	1.867525	-2.501211	23374.148043
HLA B*1509	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.339518	1.838116	-2.501402	21853.328538
HLA A*6801	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-3.733205	1.231508	-2.501697	5410.093816
HLA A*1101	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.475120	1.973182	-2.501938	29862.108650
HLA B*5801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.340060	1.838116	-2.501945	21880.655373
HLA A*3101	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.253308	1.751039	-2.502269	17918.759548
HLA A*6802	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.296390	1.793265	-2.503126	19787.478144
HLA B*1517	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.476535	1.973182	-2.503352	29959.520708
HLA A*2501	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.454710	1.950385	-2.504325	28491.183842
HLA A*2301	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.237442	1.732070	-2.505372	17275.947257
HLA A*0101	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.373014	1.867525	-2.505490	23605.554282
HLA A*0250	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.343730	1.838116	-2.505615	22066.335730
HLA B*3501	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.346486	1.839898	-2.506588	22206.809520
HLA B*4402	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.185335	1.678698	-2.506637	15322.689147

HLA A*3101	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.374255	1.867525	-2.506730	23673.078087
HLA A*0201	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.194865	1.687135	-2.507729	15662.623278
HLA B*0801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.353934	1.845985	-2.507949	22590.926098
HLA A*1101	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.458777	1.950385	-2.508392	28759.243213
HLA B*7301	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.511582	2.001898	-2.509685	32477.465419
HLA B*5801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.350410	1.839898	-2.510512	22408.346293
HLA A*0206	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.290442	1.779223	-2.511219	19518.280371
HLA A*6801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.290639	1.779223	-2.511416	19527.152093
HLA A*0211	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-2.899335	0.387379	-2.511956	793.112833
HLA A*2603	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.514211	2.001898	-2.512314	32674.669447
HLA B*4601	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.200062	1.687135	-2.512926	15851.178738
HLA B*4402	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.353065	1.839898	-2.513167	22545.751994
HLA A*3101	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-3.853630	1.339576	-2.514054	7138.878647
HLA A*0101	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.355254	1.839898	-2.515356	22659.715113
HLA B*3901	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-3.269496	0.754093	-2.515403	1859.928886
HLA B*5301	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.309064	1.793265	-2.515799	20373.402736

HLA B*1801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.383904	1.867525	-2.516380	24204.943072
HLA A*2402	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.466961	1.950385	-2.516575	29306.281026
HLA A*3002	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-3.995713	1.478828	-2.516884	9901.768206
HLA A*2602	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.581691	2.064774	-2.516917	38167.240499
HLA A*0211	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.563802	1.046875	-2.516927	3662.707423
HLA A*0250	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.487566	1.970572	-2.516994	30730.221692
HLA B*3801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.357876	1.839898	-2.517978	22796.935512
HLA A*0203	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.359028	1.839898	-2.519130	22857.446837
HLA A*0101	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.365174	1.845985	-2.519189	23183.231455
HLA A*0206	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.493038	1.973182	-2.519855	31119.860670
HLA A*0219	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.207007	1.687135	-2.519872	16106.702636
HLA A*0203	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.523988	1.002409	-2.521579	3341.856950
HLA A*2601	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.359975	1.838116	-2.521859	22907.334670
HLA B*0801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.301287	1.779223	-2.522064	20011.828619
HLA A*3101	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.254553	1.732070	-2.522483	17970.210680
HLA A*3301	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.493771	1.970572	-2.523199	31172.431783

HLA B*4801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.361382	1.838116	-2.523266	22981.686833
HLA B*7301	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.621937	2.098630	-2.523308	41873.324195
HLA A*3002	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.703268	1.179033	-2.524235	5049.724193
HLA B*1801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.499066	1.973182	-2.525884	31554.871970
HLA A*6901	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.365073	1.838116	-2.526957	23177.839077
HLA B*4402	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.320348	1.793265	-2.527084	20909.716605
HLA A*0301	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.365254	1.838116	-2.527138	23187.496083
HLA B*1501	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.214412	1.687135	-2.527277	16383.708693
HLA B*1801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.306519	1.779223	-2.527296	20254.385799
HLA A*0211	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.500587	1.973182	-2.527404	31665.513799
HLA A*0301	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.367328	1.839898	-2.527430	23298.526158
HLA B*3501	1:147-155	9	LWQADTDPL	0.954861	0.515252	-3.997752	1.470113	-2.527639	9948.374108
HLA B*0803	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.374400	1.845985	-2.528416	23681.019679
HLA A*3001	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.896875	1.368126	-2.528748	7886.324089
HLA A*0211	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.479143	1.950385	-2.528757	30139.968188
HLA B*4501	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.627654	2.098630	-2.529024	42428.114928

HLA B*1501	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.016863	1.486927	-2.529936	10395.917384
HLA A*2501	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.504374	1.973182	-2.531191	31942.868163
HLA B*5401	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.378740	1.845985	-2.532755	23918.828093
HLA A*6901	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.788281	1.254764	-2.533517	6141.598530
HLA A*3201	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.507416	1.973182	-2.534234	32167.439448
HLA A*0219	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.374248	1.839898	-2.534349	23672.693884
HLA A*3201	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.505332	1.970572	-2.534761	32013.451441
HLA B*5301	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.508478	1.973182	-2.535296	32246.193767
HLA A*2301	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.222480	1.687135	-2.535345	16690.922822
HLA B*5701	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.328717	1.793265	-2.535452	21316.554670
HLA A*0211	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.022920	1.486927	-2.535993	10541.921838
HLA B*0801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.329398	1.793265	-2.536134	21350.023775
HLA A*3301	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.634791	2.098630	-2.536162	43131.193120
HLA A*2902	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.190245	1.653995	-2.536251	15496.920845
HLA B*3801	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.404173	1.867525	-2.536649	25361.391174
HLA A*2301	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.659713	1.122935	-2.536778	4567.861269

HLA B*1501	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.375035	1.838116	-2.536919	23715.635111
HLA A*0101	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.375256	1.838116	-2.537140	23727.698280
HLA B*1509	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.289596	1.751039	-2.538557	19480.304340
HLA B*4801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.317980	1.779223	-2.538757	20796.002735
HLA A*1101	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.271390	1.732070	-2.539319	18680.546539
HLA A*0301	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.333045	1.793265	-2.539780	21530.036382
HLA A*8001	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.386127	1.845985	-2.540142	24329.135565
HLA B*1517	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.386138	1.845985	-2.540154	24329.793664
HLA B*0702	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.380053	1.839898	-2.540155	23991.271175
HLA A*0206	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.405367	0.864656	-2.540711	2543.121193
HLA A*8001	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.379464	1.838116	-2.541348	23958.715964
HLA B*0702	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.334642	1.793265	-2.541378	21609.385319
HLA B*0803	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.408947	1.867525	-2.541423	25641.724291
HLA A*2301	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.514759	1.973182	-2.541576	32715.881973
HLA A*2902	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.410016	1.867525	-2.542492	25704.919129
HLA B*1503	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.012662	1.470113	-2.542549	10295.843685

HLA A*8001	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.410392	1.867525	-2.542868	25727.178483
HLA B*4403	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.607942	2.064774	-2.543167	40545.397023
HLA A*0219	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.323160	1.779223	-2.543938	21045.559707
HLA A*3002	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.514554	1.970572	-2.543983	32700.487527
HLA A*0250	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.494457	1.950385	-2.544071	31221.713403
HLA B*3501	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.276237	1.732070	-2.544166	18890.200426
HLA B*4001	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.231810	1.687135	-2.544675	17053.367607
HLA B*4002	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.515720	1.970572	-2.545148	32788.350738
HLA A*6801	1:61-69	9	PDQKSLENY	1.207586	0.891044	-4.643924	2.098630	-2.545294	44047.769379
HLA A*0250	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.518624	1.973182	-2.545441	33008.328713
HLA B*0702	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.232654	1.687135	-2.545518	17086.519991
HLA B*0801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.383749	1.838116	-2.545633	24196.302174
HLA B*1501	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.385871	1.839898	-2.545972	24314.793440
HLA A*0202	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.549282	1.002409	-2.546874	3542.276119
HLA A*2601	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.387351	1.839898	-2.547453	24397.805234
HLA A*2602	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.498051	1.950385	-2.547666	31481.212066

HLA A*8001	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.327204	1.779223	-2.547981	21242.417683
HLA A*3101	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.388723	1.839898	-2.548825	24475.008950
HLA A*6802	1:94-102	9	NITSATYQS	1.243610	-0.899139	-2.893663	0.344471	-2.549192	782.822537
HLA B*5101	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.281377	1.732070	-2.549307	19115.129255
HLA B*0702	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.395431	1.845985	-2.549446	24855.965587
HLA B*4402	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.388154	1.838116	-2.550039	24442.987401
HLA A*0201	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.389996	1.839898	-2.550098	24546.878906
HLA A*2601	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.303148	1.751039	-2.552109	20097.755896
HLA A*6901	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.393415	1.839898	-2.553517	24740.859377
HLA B*0802	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.399599	1.845985	-2.553614	25095.660203
HLA A*0206	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.407087	0.852998	-2.554089	2553.212018
HLA A*2902	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-3.923386	1.368668	-2.554718	8382.744111
HLA A*6802	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.394994	1.839898	-2.555095	24830.967115
HLA B*0802	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.396020	1.839898	-2.556122	24889.739985
HLA A*0206	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.300425	0.742712	-2.557713	1997.215647
HLA B*5401	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.508255	1.950385	-2.557870	32229.625434

HLA A*2902	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.398358	1.839898	-2.558460	25024.078703
HLA B*4601	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.398499	1.839898	-2.558601	25032.202671
HLA A*0216	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-3.362761	0.804086	-2.558676	2305.480727
HLA B*3901	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.028986	1.470113	-2.558873	10690.208166
HLA A*2603	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.246158	1.687135	-2.559023	17626.190470
HLA A*3301	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.093386	1.534232	-2.559154	12398.968197
HLA A*2501	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.352926	1.793265	-2.559661	22538.556912
HLA B*0803	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.400003	1.839898	-2.560105	25119.022606
HLA A*0301	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.341080	1.779223	-2.561857	21932.089143
HLA B*0702	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.400578	1.838116	-2.562463	25152.338006
HLA B*5301	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.408924	1.845985	-2.562939	25640.337140
HLA A*6802	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.818087	1.254764	-2.563323	6577.895813
HLA B*5701	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.409711	1.845985	-2.563726	25686.847585
HLA B*1517	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.343343	1.779223	-2.564120	22046.647407
HLA B*5701	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.404049	1.839898	-2.564150	25354.120494
HLA A*6901	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.582222	1.017829	-2.564393	3821.397288

HLA B*2705 1:209-217 9 EAAGPTQVL 1.572811 0.294714 -4.432513
1.867525 -2.564988 27071.514996

HLA A*2403 1:219-227 9 PRSAIDSML 1.524069 0.315829 -4.405115
1.839898 -2.565217 25416.469023

HLA A*0301 1:131-139 9 AFDWDQAYR 0.906877 0.747118 -4.219285
1.653995 -2.565290 16568.570856

HLA A*2602 1:106-114 9 PRGTQAVVL 1.809522 0.163660 -4.538709
1.973182 -2.565527 34570.788316

HLA B*0803 1:168-176 9 KQTGQQVSI 1.475491 0.317774 -4.359018
1.793265 -2.565754 22856.952218

HLA A*0216 1:174-182 9 VSIAPNAGL 1.281479 0.469560 -4.319220
1.751039 -2.568182 20855.489803

HLA B*4501 1:139-147 9 RKPITYDTL 1.549612 0.515162 -4.633018
2.064774 -2.568243 42955.384502

HLA A*8001 1:219-227 9 PRSAIDSML 1.524069 0.315829 -4.408522
1.839898 -2.568624 25616.628461

HLA A*3001 1:5-13 9 IFMLVTAVV 1.049669 0.289907 -3.908382
1.339576 -2.568806 8098.086251

HLA A*0301 1:174-182 9 VSIAPNAGL 1.281479 0.469560 -4.322014
1.751039 -2.570975 20990.072160

HLA A*0206 1:9-17 9 VTAVVLLCC 1.208701 0.051365 -3.831192
1.260066 -2.571126 6779.418088

HLA A*6901 1:168-176 9 KQTGQQVSI 1.475491 0.317774 -4.364476
1.793265 -2.571212 23146.012006

HLA A*0216 1:219-227 9 PRSAIDSML 1.524069 0.315829 -4.411113
1.839898 -2.571215 25769.942609

HLA A*3301 1:139-147 9 RKPITYDTL 1.549612 0.515162 -4.636629
2.064774 -2.571855 43314.047582

HLA A*3002 1:199-207 9 FFFNPGELL 1.344812 0.501173 -4.418291
1.845985 -2.572306 26199.386879

HLA A*0212 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.410862
1.838116 -2.572746 25755.029785

HLA B*5701	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.411990	1.838116	-2.573874	25821.995985
HLA A*0250	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.325602	1.751039	-2.574563	21164.187246
HLA B*1801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.253266	1.678698	-2.574567	17917.014740
HLA A*3001	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.820620	1.245899	-2.574721	6616.369260
HLA B*5101	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.412953	1.838116	-2.574838	25879.334147
HLA B*0702	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.354155	1.779223	-2.574932	22602.417174
HLA A*0202	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.548471	1.973182	-2.575289	35356.673090
HLA B*1517	1:79-87	9	SAATSSTPR	0.650358	0.717768	-3.943587	1.368126	-2.575461	8781.871566
HLA B*3901	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.063275	1.486927	-2.576348	11568.433283
HLA B*0802	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.358201	1.779223	-2.578978	22813.961254
HLA A*0250	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.626228	1.046875	-2.579353	4228.906130
HLA A*3002	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.530784	1.950385	-2.580399	33945.676643
HLA A*1101	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.448755	1.867525	-2.581230	28103.120825
HLA A*0212	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.268509	1.687135	-2.581374	18557.057339
HLA A*0301	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.313513	1.732070	-2.581443	20583.228480
HLA B*1517	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.061860	1.478828	-2.583032	11530.819033

HLA B*4601	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.376834	1.793265	-2.583570	23814.116022
HLA A*0219	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.334962	1.751039	-2.583923	21625.290164
HLA A*6901	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.071056	1.486927	-2.584129	11777.579395
HLA A*0212	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.424945	1.839898	-2.585047	26603.873221
HLA B*4002	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-3.038669	0.452621	-2.586048	1093.122506
HLA B*3501	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.379398	1.793265	-2.586133	23955.087047
HLA B*4601	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.337732	1.751039	-2.586693	21763.662691
HLA A*0206	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.426618	1.839898	-2.586720	26706.544723
HLA B*0801	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.318924	1.732070	-2.586854	20841.278585
HLA A*3002	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.561114	1.973182	-2.587931	36401.055083
HLA A*0250	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.606178	1.017829	-2.588349	4038.104374
HLA A*2601	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.075666	1.486927	-2.588739	11903.254800
HLA B*5101	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.368501	1.779223	-2.589278	23361.506308
HLA B*5401	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.562493	1.973182	-2.589311	36516.834190
HLA A*8001	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.382647	1.793265	-2.589382	24134.988214
HLA A*0301	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.928179	1.338234	-2.589945	8475.769913

HLA A*3002	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.430118	1.839898	-2.590220	26922.689068
HLA B*0802	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.428382	1.838116	-2.590267	26815.269502
HLA A*0101	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.342111	1.751039	-2.591073	21984.238470
HLA A*1101	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.437677	1.845985	-2.591692	27395.342146
HLA B*1502	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.542156	1.950385	-2.591771	34846.244324
HLA B*4501	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.593748	2.001898	-2.591851	39241.745650
HLA B*4403	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.517792	1.925846	-2.591945	32945.174930
HLA A*2902	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.343953	1.751039	-2.592915	22077.679405
HLA A*0203	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.193702	0.600517	-2.593185	1562.075256
HLA B*7301	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.387243	1.793265	-2.593978	24391.734476
HLA B*1502	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.432268	1.838116	-2.594153	27056.288075
HLA A*0101	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.388563	1.793265	-2.595298	24466.006924
HLA B*1503	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.434479	1.838116	-2.596363	27194.374856
HLA B*4002	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-3.935317	1.338234	-2.597083	8616.222276
HLA A*2603	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.570357	1.973182	-2.597174	37184.063312
HLA B*4402	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.376421	1.779223	-2.597198	23791.452429

HLA B*4501	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.547861	1.950385	-2.597475	35306.976372
HLA B*4403	1:6-14	9	FMLVTAVVL	1.561991	0.439907	-4.599577	2.001898	-2.597680	39771.996343
HLA A*2501	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.436143	1.838116	-2.598027	27298.734523
HLA A*0203	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.721354	1.122935	-2.598419	5264.461984
HLA B*4402	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.349700	1.751039	-2.598661	22371.765730
HLA A*2601	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.378005	1.779223	-2.598782	23878.360725
HLA A*0219	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.437038	1.838116	-2.598922	27355.059823
HLA B*1501	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-3.598072	0.999064	-2.599008	3963.435700
HLA B*7301	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.569769	1.970572	-2.599198	37133.806890
HLA B*4601	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.331675	1.732070	-2.599605	21462.238365
HLA B*0802	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.351049	1.751039	-2.600010	22441.344220
HLA B*0802	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.394075	1.793265	-2.600810	24778.498510
HLA A*0101	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.380356	1.779223	-2.601133	24008.019944
HLA A*2601	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.394543	1.793265	-2.601278	24805.188612
HLA A*2301	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.395064	1.793265	-2.601799	24834.997425
HLA B*4002	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.552451	1.950385	-2.602066	35682.183363

HLA A*3001	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.256435	1.653995	-2.602441	18048.250339
HLA A*0203	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-3.930811	1.328019	-2.602791	8527.281143
HLA B*3901	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.725832	1.122935	-2.602897	5319.025989
HLA B*5101	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.442991	1.839898	-2.603093	27732.643180
HLA B*5301	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.443468	1.839898	-2.603570	27763.116106
HLA A*3101	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.291687	1.687135	-2.604552	19574.324297
HLA A*2501	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.337422	1.732070	-2.605352	21748.126691
HLA A*0212	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.092869	1.486927	-2.605942	12384.220026
HLA B*3801	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.452056	1.845985	-2.606071	28317.543544
HLA B*5301	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-3.533893	0.927533	-2.606360	3418.954212
HLA A*3002	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.196650	1.590000	-2.606651	15727.152967
HLA B*1503	1:78-86	9	LSAATSSTP	0.733359	0.025119	-3.366262	0.758478	-2.607784	2324.139697
HLA A*6801	1:139-147	9	RKPITYDTL	1.549612	0.515162	-4.672625	2.064774	-2.607851	47057.107554
HLA B*3901	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.387348	1.779223	-2.608125	24397.673245
HLA A*2501	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.454222	1.845985	-2.608237	28459.141971
HLA B*5801	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.295491	1.687135	-2.608355	19746.521182

HLA B*2705	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.446797	1.838116	-2.608682	27976.760794
HLA B*0803	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.446856	1.838116	-2.608741	27980.544829
HLA A*2902	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-3.840318	1.231508	-2.608810	6923.374394
HLA B*1517	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.448900	1.839898	-2.609002	28112.548562
HLA A*8001	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.360200	1.751039	-2.609161	22919.234669
HLA A*3001	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.287944	1.678698	-2.609246	19406.358483
HLA B*4501	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.402954	1.793265	-2.609689	25290.283046
HLA B*1801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.449932	1.838116	-2.611816	28179.393560
HLA A*2403	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.363341	1.751039	-2.612303	23085.610969
HLA B*5401	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-3.336311	0.723137	-2.613174	2169.256931
HLA B*4402	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.345725	1.732070	-2.613655	22167.919427
HLA A*2902	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.292382	1.678698	-2.613684	19605.694305
HLA A*2902	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.406957	1.793265	-2.613693	25524.498175
HLA A*1101	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.365096	1.751039	-2.614058	23179.093007
HLA A*3201	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.564725	1.950385	-2.614340	36704.991707
HLA B*5301	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.347682	1.732070	-2.615612	22268.043205

HLA B*3501	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-3.691111	1.075247	-2.615864	4910.338400
HLA A*1101	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.409607	1.793265	-2.616343	25680.733941
HLA A*0219	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.469508	0.852998	-2.616510	2947.867761
HLA A*2602	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.103502	1.486927	-2.616576	12691.192411
HLA B*3501	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-3.951331	1.334657	-2.616674	8939.865479
HLA A*0206	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.318422	0.701666	-2.616756	2081.718564
HLA B*5701	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.395992	1.779223	-2.616769	24888.124229
HLA B*3801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.410098	1.793265	-2.616834	25709.786717
HLA A*2402	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.296158	1.678698	-2.617460	19776.883224
HLA B*2705	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.368834	1.751039	-2.617796	23379.459612
HLA B*4002	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.543688	1.925846	-2.617841	34969.372685
HLA B*3801	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.351049	1.732070	-2.618979	22441.344220
HLA A*1101	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.459654	1.839898	-2.619756	28817.334755
HLA B*1517	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.458063	1.838116	-2.619948	28711.984452
HLA B*1503	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-3.428984	0.809025	-2.619960	2685.246012
HLA B*1502	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.593762	1.973182	-2.620580	39243.019431

HLA B*5401	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.488456	1.867525	-2.620932	30793.293978
HLA A*2301	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.461846	1.839898	-2.621948	28963.155837
HLA B*3801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.460375	1.838116	-2.622260	28865.235388
HLA B*4501	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.490101	1.867525	-2.622576	30910.126872
HLA B*4001	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.356178	1.732070	-2.624107	22707.942875
HLA A*0202	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-3.519331	0.895143	-2.624188	3306.215644
HLA A*3001	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-2.866217	0.241980	-2.624237	734.880353
HLA A*0216	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-3.909562	1.285203	-2.624359	8120.108635
HLA A*0101	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.367240	0.742712	-2.624527	2329.376096
HLA B*3901	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.463065	1.838116	-2.624950	29044.590901
HLA B*3901	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.303655	1.678698	-2.624957	20121.254575
HLA B*1801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.465323	1.839898	-2.625425	29195.984123
HLA B*0801	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.376886	1.751039	-2.625847	23816.950489
HLA B*5101	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.419311	1.793265	-2.626046	26260.972477
HLA A*0202	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-3.832151	1.203934	-2.628217	6794.398382
HLA A*2603	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.789729	1.161468	-2.628261	6162.099497

HLA B*1503	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.218350	1.590000	-2.628350	16532.934850
HLA A*3101	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.307551	1.678698	-2.628852	20302.545943
HLA A*0211	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-3.706078	1.075733	-2.630344	5082.502986
HLA A*2403	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.284873	1.653995	-2.630879	19269.625427
HLA A*3002	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.499503	1.867525	-2.631979	31586.639705
HLA B*3501	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.811386	1.179033	-2.632354	6477.184370
HLA A*1101	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.653656	1.020870	-2.632786	4504.596894
HLA A*6802	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.611938	0.977336	-2.634602	4092.026875
HLA B*5701	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.322042	1.687135	-2.634907	20991.434852
HLA A*2301	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.502548	1.867525	-2.635024	31808.878641
HLA A*8001	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.368383	1.732070	-2.636313	23355.188005
HLA A*2402	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.005820	1.368668	-2.637152	10134.918018
HLA A*2602	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.369760	1.732070	-2.637690	23429.345991
HLA A*1101	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.477045	1.838116	-2.638929	29994.712218
HLA B*1501	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.317813	1.678698	-2.639115	20788.016480
HLA A*2402	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.479249	1.839898	-2.639350	30147.306506

HLA A*2601	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.373284	1.732070	-2.641214	23620.244746
HLA A*0211	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.481666	1.839898	-2.641768	30315.597792
HLA B*3801	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.393361	1.751039	-2.642322	24737.781127
HLA A*2501	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.484204	1.839898	-2.644305	30493.240587
HLA A*6801	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.614877	1.970572	-2.644306	41198.104716
HLA A*2603	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.014687	1.368668	-2.646019	10343.968669
HLA A*0101	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.378141	1.732070	-2.646070	23885.854299
HLA A*2902	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.667175	1.020870	-2.646305	4647.023511
HLA A*2603	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.378730	1.732070	-2.646660	23918.310506
HLA B*4403	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.492775	1.845985	-2.646790	31101.010622
HLA B*1502	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.134196	1.486927	-2.647270	13620.595655
HLA A*2501	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.399265	1.751039	-2.648226	25076.389013
HLA A*2601	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.335892	1.687135	-2.648757	21671.668032
HLA B*3801	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.428361	1.779223	-2.649138	26813.963925
HLA B*5101	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.400249	1.751039	-2.649211	25133.295228
HLA B*4403	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.600005	1.950385	-2.649620	39811.175128

HLA A*3301	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.517782	1.867525	-2.650258	32944.462019
HLA B*0802	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.337415	1.687135	-2.650280	21747.773729
HLA B*0803	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.429569	1.779223	-2.650346	26888.628821
HLA B*0702	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.383476	1.732070	-2.651406	24181.122618
HLA A*2902	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.338900	1.687135	-2.651765	21822.257713
HLA A*0301	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.242467	1.590000	-2.652468	17477.021395
HLA B*5701	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.385405	1.732070	-2.653335	24288.762398
HLA B*2705	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.432776	1.779223	-2.653553	27087.922802
HLA B*4403	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.624846	1.970572	-2.654274	42154.709617
HLA B*4002	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.628001	1.973182	-2.654819	42462.099178
HLA A*0301	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.342459	1.687135	-2.655324	22001.847497
HLA B*4801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.040649	1.384894	-2.655755	10981.179881
HLA B*0802	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.388020	1.732070	-2.655950	24435.451233
HLA A*2301	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.408513	1.751039	-2.657474	25616.074135
HLA A*0212	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-3.461618	0.804086	-2.657533	2894.799087
HLA A*2501	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.436831	1.779223	-2.657608	27342.039992

HLA B*1501	1:78-86	9	LSAATSSTP	0.733359	0.025119	-3.417913	0.758478	-2.659435	2617.660423
HLA A*0202	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.706383	1.046875	-2.659508	5086.078694
HLA B*1517	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.507180	0.847335	-2.659844	3214.990101
HLA B*4501	1:85-93	9	TPREAPYEL	1.651184	0.319388	-4.630635	1.970572	-2.660064	42720.392388
HLA A*3301	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.610843	1.950385	-2.660458	40817.196424
HLA A*3201	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.000186	1.339576	-2.660610	10004.287757
HLA B*1503	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.000910	1.339576	-2.661333	10020.971255
HLA B*0801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.340455	1.678698	-2.661757	21900.550895
HLA B*7301	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.612396	1.950385	-2.662011	40963.417418
HLA B*3501	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-2.940681	0.278445	-2.662236	872.330815
HLA A*2501	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-3.917108	1.254764	-2.662344	8262.441266
HLA B*1801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.455843	1.793265	-2.662578	28565.573446
HLA A*0101	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.352616	1.687135	-2.665481	22522.467752
HLA B*4403	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.639291	1.973182	-2.666108	43580.352207
HLA A*2402	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.417762	1.751039	-2.666724	26167.515730
HLA A*3301	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.640616	1.973182	-2.667433	43713.526662

HLA A*3001	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.146418	1.478828	-2.667590	14009.354387
HLA A*2403	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.354756	1.687135	-2.667621	22633.741662
HLA B*4801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.138303	1.470113	-2.668190	13750.009567
HLA B*4402	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.355987	1.687135	-2.668852	22697.994412
HLA B*0803	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.420598	1.751039	-2.669560	26338.941779
HLA B*7301	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.595675	1.925846	-2.669829	39416.213007
HLA B*4403	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.040193	1.368668	-2.671525	10969.660975
HLA A*2301	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.351378	1.678698	-2.672679	22458.347384
HLA B*4501	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.646177	1.973182	-2.672995	44276.886719
HLA B*1509	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.405555	1.732070	-2.673484	25442.194585
HLA B*5701	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.002258	1.328019	-2.674239	10052.137505
HLA B*5801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-3.935406	1.260066	-2.675340	8617.993744
HLA A*1101	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.455819	1.779223	-2.676597	28564.028122
HLA B*4501	1:7-15	9	MLVTAVVLL	1.492026	0.433820	-4.602585	1.925846	-2.676738	40048.359575
HLA A*2402	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.061724	1.384894	-2.676830	11527.201535
HLA B*1502	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.517970	1.839898	-2.678072	32958.723176

HLA B*2705	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.268316	1.590000	-2.678317	18548.827052
HLA A*6901	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-3.679303	1.000164	-2.679139	4778.624565
HLA A*0211	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.422692	0.742712	-2.679980	2646.623470
HLA A*3301	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.519523	1.838116	-2.681408	33076.792463
HLA A*0250	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.521704	1.839898	-2.681806	33243.267970
HLA A*0101	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.361185	1.678698	-2.682486	22971.245622
HLA A*3201	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.862464	1.179033	-2.683431	7285.578855
HLA A*0211	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-2.726934	0.040514	-2.686420	533.254424
HLA A*2603	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.636932	1.950385	-2.686547	43344.285954
HLA A*0301	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.365362	1.678698	-2.686664	23193.267123
HLA A*0203	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-3.706350	1.019585	-2.686766	5085.693497
HLA A*8001	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.365477	1.678698	-2.686779	23199.416115
HLA A*3201	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.365891	1.678698	-2.687192	23221.515738
HLA A*6801	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.438743	1.751039	-2.687705	27462.710260
HLA A*3201	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.073565	1.384894	-2.688671	11845.824403
HLA A*2402	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.376463	1.687135	-2.689328	23793.769306

HLA B*1501	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.159735	1.470113	-2.689622	14445.580624
HLA A*6901	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.369060	1.678698	-2.690362	23391.604872
HLA B*3801	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.378456	1.687135	-2.691320	23903.176033
HLA B*4601	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.030198	1.338234	-2.691965	10720.091603
HLA A*3002	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.379153	1.687135	-2.692018	23941.613023
HLA B*1501	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.031749	1.339576	-2.692173	10758.436392
HLA A*2602	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.539870	1.845985	-2.693885	34663.301803
HLA A*2501	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.372911	1.678698	-2.694212	23599.936000
HLA A*1101	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.942055	1.245899	-2.696157	8750.950295
HLA B*5301	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-3.771943	1.075247	-2.696696	5914.841413
HLA B*5401	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.717684	1.020870	-2.696814	5220.163412
HLA B*7301	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.543112	1.845985	-2.697128	34923.054182
HLA B*5801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.351796	1.653995	-2.697801	22479.984296
HLA A*6801	1:24-32	9	APKTYCEEL	1.537287	0.413098	-4.648313	1.950385	-2.697927	44495.158506
HLA A*2601	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.377194	1.678698	-2.698496	23833.835436
HLA B*1801	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.386608	1.687135	-2.699473	24356.132208

HLA A*3201	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-3.508975	0.809025	-2.699950	3228.305653
HLA A*0211	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-3.714343	1.013420	-2.700923	5180.159483
HLA B*4801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.380843	1.678698	-2.702144	24034.920314
HLA A*2403	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.380972	1.678698	-2.702274	24042.072822
HLA B*1517	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-3.137563	0.434427	-2.703136	1372.661202
HLA A*8001	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.391021	1.687135	-2.703886	24604.846253
HLA B*0803	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.391274	1.687135	-2.704139	24619.226278
HLA B*0702	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.191904	1.486927	-2.704978	15556.222677
HLA B*4403	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.572965	1.867525	-2.705440	37408.024523
HLA B*1503	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-3.659957	0.954256	-2.705701	4570.432000
HLA A*2501	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.393133	1.687135	-2.705998	24724.803153
HLA A*0201	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.385257	1.678698	-2.706559	24280.485639
HLA B*4001	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.385725	1.678698	-2.707027	24306.639307
HLA B*2705	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.394564	1.687135	-2.707429	24806.396381
HLA A*0212	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.572627	0.864656	-2.707971	3737.893250
HLA A*6801	1:106-114	9	PRGTQAVVL	1.809522	0.163660	-4.681314	1.973182	-2.708131	48008.001192

HLA B*5401 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.547130
1.838116 -2.709014 35247.623193

HLA A*2602 1:215-223 9 QVLVPRSAI 0.852479 0.308989 -3.871195
1.161468 -2.709727 7433.524025

HLA A*3201 1:158-166 9 VFPIVQGEL 1.307815 0.530301 -4.548159
1.838116 -2.710043 35331.242575

HLA B*3501 1:177-185 9 APNAGLDPV 0.672482 0.029184 -3.413534
0.701666 -2.711868 2591.396494

HLA A*2403 1:190-198 9 FAVTNDGVI 1.178752 0.308175 -4.198915
1.486927 -2.711988 15809.386406

HLA B*0702 1:147-155 9 LWQADTDPL 0.954861 0.515252 -4.183032
1.470113 -2.712920 15241.667943

HLA B*1801 1:174-182 9 VSIAPNAGL 1.281479 0.469560 -4.464830
1.751039 -2.713791 29162.834079

HLA B*4002 1:198-206 9 IFFFNPGEL 1.210946 0.568277 -4.493139
1.779223 -2.713916 31127.100777

HLA A*6801 1:68-76 9 NYIAQTRDK 0.633507 0.291193 -3.638849
0.924700 -2.714150 4353.609565

HLA B*4402 1:131-139 9 AFDWDQAYR 0.906877 0.747118 -4.368571
1.653995 -2.714577 23365.298110

HLA B*4403 1:168-176 9 KQTGQQVSI 1.475491 0.317774 -4.508871
1.793265 -2.715606 32275.339803

HLA A*0211 1:166-174 9 LSKQTGQQV 1.247032 0.080987 -4.043905
1.328019 -2.715886 11063.827398

HLA B*0801 1:190-198 9 FAVTNDGVI 1.178752 0.308175 -4.203567
1.486927 -2.716640 15979.640136

HLA A*6901 1:131-139 9 AFDWDQAYR 0.906877 0.747118 -4.371207
1.653995 -2.717213 23507.554334

HLA B*1801 1:44-52 9 QMSDPAYNI 1.440627 0.291443 -4.449511
1.732070 -2.717441 28152.118685

HLA A*0212 1:184-192 9 PVNYQNFAV 0.967153 -0.114155 -3.570522
0.852998 -2.717524 3719.818549

HLA B*4601	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.396241	1.678698	-2.717543	24902.400373
HLA B*5401	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.557470	1.839898	-2.717572	36096.901187
HLA B*5301	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.497652	1.779223	-2.718429	31452.272698
HLA A*2902	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.197815	1.478828	-2.718987	15769.410384
HLA B*1517	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.498933	0.779687	-2.719246	3154.517549
HLA A*0203	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.398057	1.678698	-2.719359	25006.756382
HLA A*2601	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.373919	1.653995	-2.719924	23654.771341
HLA B*0801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.048078	1.328019	-2.720059	11170.640550
HLA A*6801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-3.284430	0.564331	-2.720099	1924.995267
HLA A*1101	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.407716	1.687135	-2.720581	25569.138526
HLA B*1501	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.199596	1.478828	-2.720768	15834.208710
HLA B*5301	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.559702	1.838116	-2.721586	36282.894947
HLA A*2602	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.561791	1.839898	-2.721892	36457.813881
HLA A*6901	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.062184	1.339576	-2.722608	11539.430750
HLA A*0201	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.211132	1.486927	-2.724206	16260.441617
HLA A*6802	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.120470	1.396176	-2.724295	13196.853913

HLA B*4002	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.564281	1.839898	-2.724383	36667.481169
HLA B*1517	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.886499	1.161468	-2.725032	7700.151939
HLA B*5401	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.505081	1.779223	-2.725858	31994.925556
HLA A*0202	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-3.745464	1.019585	-2.725880	5564.990266
HLA A*2603	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.565952	1.839898	-2.726053	36808.791708
HLA A*0212	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.197284	1.470113	-2.727172	15750.141934
HLA B*5301	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.479124	1.751039	-2.728085	30138.663785
HLA A*0250	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.582260	0.852998	-2.729262	3821.728076
HLA A*0212	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.408522	1.678698	-2.729824	25616.628461
HLA B*2705	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.409293	1.678698	-2.730594	25662.124078
HLA B*7301	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.598288	1.867525	-2.730763	39654.047597
HLA A*0219	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.976940	1.245899	-2.731042	9482.882522
HLA A*3001	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.708549	0.977336	-2.731213	5111.511011
HLA A*3201	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.571116	1.839898	-2.731218	37249.095330
HLA B*4001	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.385349	1.653995	-2.731354	24285.609014
HLA A*0201	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.385678	1.653995	-2.731683	24304.009525

HLA A*3001	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.267262	1.534232	-2.733030	18503.825881
HLA A*0203	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.203431	1.470113	-2.733318	15974.626934
HLA B*2705	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.388023	1.653995	-2.734028	24435.583427
HLA A*2501	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.913664	1.179033	-2.734631	8197.171856
HLA B*0801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.913819	1.179033	-2.734786	8200.099201
HLA B*5401	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.422271	1.687135	-2.735136	26440.590839
HLA A*2602	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.574976	1.838116	-2.736860	37581.657764
HLA A*6801	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.424329	1.687135	-2.737194	26566.191843
HLA A*0216	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.391573	1.653995	-2.737578	24636.146875
HLA A*0101	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-3.985041	1.245899	-2.739143	9661.429623
HLA B*3901	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.329506	1.590000	-2.739507	21355.337494
HLA B*1517	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-3.976414	1.236794	-2.739620	9471.397981
HLA A*0211	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.393918	1.653995	-2.739923	24769.518859
HLA B*0802	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.419663	1.678698	-2.740965	26282.291469
HLA A*3002	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.081897	1.339576	-2.742320	12075.262052
HLA A*2603	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.580859	1.838116	-2.742743	38094.216334

HLA B*5401	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.536505	1.793265	-2.743241	34395.804032
HLA B*4801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.397282	1.653995	-2.743287	24962.152562
HLA B*1501	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.128383	1.384894	-2.743490	13439.511234
HLA A*6901	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.721147	0.977336	-2.743811	5261.956327
HLA A*2902	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.334001	1.590000	-2.744001	21577.493979
HLA A*0101	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.398753	1.653995	-2.744758	25046.832460
HLA B*4501	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.030335	1.285203	-2.745131	10723.455812
HLA A*6801	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.478008	1.732070	-2.745938	30061.315964
HLA B*1502	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.433814	1.687135	-2.746679	27152.772160
HLA B*1517	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.132425	1.384894	-2.747531	13565.149638
HLA A*3002	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.085787	1.338234	-2.747554	12183.927654
HLA B*4002	1:209-217	9	EAAGPTQVL	1.572811	0.294714	-4.617410	1.867525	-2.749885	41439.068265
HLA B*1501	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.405005	1.653995	-2.751010	25410.007331
HLA A*6802	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.429724	1.678698	-2.751025	26898.231192
HLA A*0219	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.430548	1.678698	-2.751850	26949.355990
HLA A*6801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.772841	1.020870	-2.751971	5927.077532

HLA B*0702	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.408221	1.653995	-2.754227	25598.895962
HLA B*3501	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.408449	1.653995	-2.754455	25612.332745
HLA B*7301	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.534259	1.779223	-2.755036	34218.373174
HLA A*2403	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-3.680238	0.924700	-2.755538	4788.924678
HLA A*2603	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.548812	1.793265	-2.755547	35384.418945
HLA B*1801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.345659	1.590000	-2.755660	22164.561754
HLA A*3301	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.442843	1.687135	-2.755708	27723.192867
HLA B*4601	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.409774	1.653995	-2.755780	25690.599860
HLA A*0212	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.410200	1.653995	-2.756205	25715.768157
HLA B*1509	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.411038	1.653995	-2.757044	25765.481794
HLA A*0250	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.880292	1.122935	-2.757357	7590.877018
HLA A*2603	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.537194	1.779223	-2.757971	34450.367969
HLA B*7301	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.596333	1.838116	-2.758217	39475.964706
HLA A*2602	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.551845	1.793265	-2.758581	35632.414646
HLA B*0801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.098268	1.339576	-2.758691	12539.140709
HLA A*0216	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.438762	1.678698	-2.760064	27463.898847

HLA B*5801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.146305	1.384894	-2.761411	14005.716984
HLA B*0803	1:62-70	9	DQKSLENYI	1.150042	0.062507	-3.974238	1.212549	-2.761689	9424.069117
HLA A*6901	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.351944	1.590000	-2.761944	22487.647298
HLA B*5701	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.416646	1.653995	-2.762652	26100.359457
HLA A*0201	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-3.658054	0.895143	-2.762911	4550.448137
HLA B*5801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.353250	1.590000	-2.763251	22555.389685
HLA B*0802	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.417972	1.653995	-2.763977	26180.117903
HLA B*4002	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.602477	1.838116	-2.764361	40038.394585
HLA B*5401	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.104593	1.339576	-2.765016	12723.089714
HLA A*0212	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.742593	0.977336	-2.765257	5528.322096
HLA A*0219	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.783113	1.017829	-2.765284	6068.935986
HLA A*6801	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-3.849594	1.083538	-2.766056	7072.835938
HLA A*0202	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.152165	1.384894	-2.767271	14195.966370
HLA A*3101	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.246628	1.478828	-2.767800	17645.271939
HLA B*0801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.422032	1.653995	-2.768037	26426.004716
HLA A*0219	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.422064	1.653995	-2.768070	26428.006257

HLA B*0702	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.107412	1.338234	-2.769178	12805.955004
HLA B*4402	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.137871	1.368668	-2.769202	13736.329347
HLA B*5801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.007282	1.236794	-2.770488	10169.078964
HLA B*4403	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.610596	1.839898	-2.770698	40794.017275
HLA A*3001	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.241847	1.470113	-2.771734	17452.078342
HLA A*2403	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-3.580267	0.808230	-2.772037	3804.235724
HLA A*0201	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.242973	1.470113	-2.772860	17497.361203
HLA A*2402	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.896560	1.122935	-2.773625	7880.609166
HLA B*0702	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.028479	1.254764	-2.773715	10677.723569
HLA B*4402	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.059163	1.285203	-2.773960	11459.428191
HLA A*0206	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.453188	1.678698	-2.774490	28391.479779
HLA B*1501	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.308941	1.534232	-2.774709	20367.672214
HLA A*1101	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.453484	1.678698	-2.774786	28410.839316
HLA B*5401	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.526600	1.751039	-2.775561	33620.180221
HLA A*3001	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.262645	1.486927	-2.775718	18308.164043
HLA A*2602	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.366729	1.590000	-2.776730	23266.407494

HLA A*2602	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.556279	1.779223	-2.777056	35998.029763
HLA A*0206	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.956152	1.179033	-2.777119	9039.660645
HLA A*3301	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.528177	1.751039	-2.777138	33742.444451
HLA A*0211	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-3.796791	1.019585	-2.777207	6263.127580
HLA A*6801	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.615528	1.838116	-2.777412	41259.887975
HLA A*0203	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.431641	1.653995	-2.777646	27017.235091
HLA B*3801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.456898	1.678698	-2.778200	28635.044713
HLA A*0216	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-3.854048	1.075733	-2.778315	7145.756415
HLA A*1101	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.118112	1.338234	-2.779878	13125.369134
HLA B*4002	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.026905	1.246912	-2.779993	10639.090874
HLA B*0803	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.434202	1.653995	-2.780207	27177.020406
HLA B*1501	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.960767	1.179033	-2.781734	9136.219301
HLA A*6802	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.829571	1.046875	-2.782697	6754.158890
HLA A*2601	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.373155	1.590000	-2.783156	23613.217732
HLA A*3301	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.623702	1.839898	-2.783804	42043.794317
HLA A*2403	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-3.622243	0.837899	-2.784344	4190.282649

HLA A*6901	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.112506	1.328019	-2.784486	12957.035689
HLA A*6802	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.438638	1.653995	-2.784643	27456.025414
HLA B*0801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-3.946754	1.161468	-2.785286	8846.147716
HLA B*1501	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.375653	1.590000	-2.785653	23749.401752
HLA A*0211	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.639005	0.852998	-2.786007	4355.164310
HLA A*3001	1:96-104	9	TSATYQSAI	0.928477	0.250556	-3.965409	1.179033	-2.786376	9234.408831
HLA A*6801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-3.741592	0.954978	-2.786614	5515.596124
HLA A*2301	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.274390	1.486927	-2.787463	18810.046563
HLA B*1509	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.466404	1.678698	-2.787706	29268.730239
HLA B*1501	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.156596	1.368126	-2.788470	14341.549973
HLA A*3301	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.520764	1.732070	-2.788694	33171.408790
HLA B*0803	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.467471	1.678698	-2.788772	29340.705217
HLA A*0201	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.766643	0.977336	-2.789307	5843.091226
HLA B*2705	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.259941	1.470113	-2.789828	18194.517283
HLA B*4501	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.793408	1.002409	-2.790999	6214.525866
HLA A*0301	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.326118	1.534232	-2.791886	21189.391341

HLA B*3901	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.029169	1.236794	-2.792376	10694.720080
HLA B*1503	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.047890	1.254764	-2.793126	11165.807042
HLA A*0202	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-3.869386	1.075733	-2.793652	7402.623234
HLA B*0801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-3.647138	0.853458	-2.793681	4437.500977
HLA A*3101	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-3.865814	1.071973	-2.793842	7342.000821
HLA B*4001	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.153488	0.357949	-2.795539	1423.928452
HLA A*0203	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-3.842465	1.046875	-2.795590	6957.692755
HLA A*0202	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.449786	1.653995	-2.795791	28169.943407
HLA B*0802	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.386096	1.590000	-2.796097	24327.424593
HLA B*1509	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.386860	1.590000	-2.796860	24370.235034
HLA A*3001	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-3.722482	0.924700	-2.797782	5278.150224
HLA A*6802	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.166008	1.368126	-2.797882	14655.752678
HLA B*4601	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.387966	1.590000	-2.797967	24432.410982
HLA B*1503	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.775787	0.977336	-2.798451	5967.423530
HLA B*5801	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.136912	1.338234	-2.798678	13706.043480
HLA B*4403	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.578120	1.779223	-2.798897	37854.676949

HLA A*3101	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-3.608090	0.809025	-2.799066	4055.925983
HLA A*3201	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.278407	1.478828	-2.799579	18984.863983
HLA A*8001	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.453599	1.653995	-2.799605	28418.371589
HLA A*3002	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.270304	1.470113	-2.800191	18633.915262
HLA A*2602	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.487758	1.687135	-2.800623	30743.856978
HLA B*5401	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.279775	1.478828	-2.800947	19044.733081
HLA A*0216	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.288076	1.486927	-2.801149	19412.238604
HLA B*4402	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.197421	1.396176	-2.801245	15755.084687
HLA B*0702	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.280630	1.478828	-2.801802	19082.272913
HLA B*4501	1:199-207	9	FFFNPGELL	1.344812	0.501173	-4.647848	1.845985	-2.801863	44447.522676
HLA A*6801	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.642425	1.839898	-2.802527	43896.000162
HLA B*4001	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.392823	1.590000	-2.802823	24707.153341
HLA A*0201	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.392919	1.590000	-2.802919	24712.634130
HLA A*6901	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.199333	1.396176	-2.803158	15824.617549
HLA B*1509	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.337506	1.534232	-2.803274	21752.362682
HLA B*1503	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-3.422687	0.619394	-2.803294	2646.594834

HLA B*1801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.457523	1.653995	-2.803528	28676.281079
HLA B*1503	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-3.691445	0.886699	-2.804746	4914.111993
HLA B*4501	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.405381	0.600517	-2.804864	2543.203742
HLA B*5401	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.538209	1.732070	-2.806139	34530.975119
HLA B*3801	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.460446	1.653995	-2.806451	28869.920500
HLA A*2902	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.146070	1.339576	-2.806494	13998.142096
HLA B*4403	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.644767	1.838116	-2.806652	44133.399890
HLA B*3901	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.191796	1.384894	-2.806902	15552.351917
HLA A*3201	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-3.426663	0.619394	-2.807269	2670.931740
HLA B*4501	1:219-227	9	PRSAIDSML	1.524069	0.315829	-4.647211	1.839898	-2.807313	44382.406798
HLA A*6901	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-3.663434	0.856017	-2.807417	4607.172674
HLA B*0801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.286342	1.478828	-2.807513	19334.889786
HLA A*2602	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.177351	1.368668	-2.808683	15043.588354
HLA A*2902	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.295812	1.486927	-2.808886	19761.161836
HLA A*3001	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.194052	1.384894	-2.809158	15633.333062
HLA A*6802	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.827095	1.017829	-2.809266	6715.756111

HLA B*1517	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.463686	1.653995	-2.809691	29086.102334
HLA A*3002	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.488574	1.678698	-2.809875	30801.624520
HLA B*4001	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.297361	1.486927	-2.810434	19831.738421
HLA B*3901	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.467830	1.653995	-2.813835	29365.000955
HLA A*0212	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.403865	1.590000	-2.813866	25343.424038
HLA B*4801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.405653	1.590000	-2.815654	25447.976099
HLA B*1503	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.469743	1.653995	-2.815748	29494.599278
HLA B*0801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-3.939151	1.122935	-2.816216	8692.631186
HLA A*0203	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.201175	1.384894	-2.816281	15891.877876
HLA A*3201	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.351246	1.534232	-2.817014	22451.544573
HLA B*4601	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.156864	1.339576	-2.817288	14350.397528
HLA B*4501	1:158-166	9	VFPIVQGEL	1.307815	0.530301	-4.655465	1.838116	-2.817349	45233.958010
HLA B*3501	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.407467	1.590000	-2.817467	25554.480151
HLA B*7301	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.549898	1.732070	-2.817827	35472.968270
HLA A*0301	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.296759	1.478828	-2.817931	19804.291830
HLA A*2902	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-3.485438	0.666762	-2.818675	3058.000175

HLA B*5801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.353466	1.534232	-2.819235	22566.618518
HLA B*4801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.353579	1.534232	-2.819347	22572.479258
HLA A*2402	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.473910	1.653995	-2.819916	29779.025833
HLA B*0801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-3.748444	0.927533	-2.820911	5603.295882
HLA B*7301	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.508215	1.687135	-2.821080	32226.661472
HLA A*0101	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.411727	1.590000	-2.821727	25806.354981
HLA A*2603	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.500610	1.678698	-2.821912	31667.226915
HLA B*3501	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-3.547459	0.725355	-2.822104	3527.436553
HLA B*4001	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.292251	1.470113	-2.822138	19599.755585
HLA B*4402	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.412417	1.590000	-2.822418	25847.432838
HLA B*5701	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.412488	1.590000	-2.822488	25851.628131
HLA B*1502	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.293108	1.470113	-2.822995	19638.495685
HLA B*3901	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.162578	1.338234	-2.824344	14540.451072
HLA A*6901	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.358917	1.534232	-2.824685	22851.635732
HLA B*2705	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.359460	1.534232	-2.825228	22880.210916
HLA A*2602	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.504153	1.678698	-2.825455	31926.628399

HLA A*2501	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.480245	1.653995	-2.826250	30216.537557
HLA A*0203	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.804178	0.977336	-2.826842	6370.566290
HLA B*2705	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.211912	1.384894	-2.827018	16289.672967
HLA B*4002	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.578698	1.751039	-2.827659	37905.088730
HLA B*5101	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.306822	1.478828	-2.827994	20268.525776
HLA B*0801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.418484	1.590000	-2.828484	26211.011792
HLA A*3002	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.315734	1.486927	-2.828807	20688.726492
HLA B*7301	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.580168	1.751039	-2.829130	38033.675359
HLA A*6802	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.089645	1.260066	-2.829579	12292.640079
HLA B*4403	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.580911	1.751039	-2.829872	38098.750485
HLA B*1517	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-3.639164	0.809025	-2.830140	4356.766750
HLA A*3001	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.227391	1.396176	-2.831215	16880.712472
HLA A*3301	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.624691	1.793265	-2.831426	42139.660851
HLA A*6802	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.422217	1.590000	-2.832218	26437.301109
HLA A*0201	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.575108	0.742712	-2.832396	3759.308360
HLA B*4801	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.170975	1.338234	-2.832741	14824.325380

HLA A*0101	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.320459	1.486927	-2.833532	20915.033886
HLA A*0206	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-2.874426	0.040514	-2.833911	748.903288
HLA B*4801	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.321201	1.486927	-2.834274	20950.819238
HLA A*0206	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.163945	1.328019	-2.835926	14586.304638
HLA A*0203	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.096275	1.260066	-2.836209	12481.748071
HLA A*2301	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.222386	1.384894	-2.837492	16687.311371
HLA B*1502	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.516528	1.678698	-2.837829	32849.426734
HLA B*1501	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.618104	0.779687	-2.838416	4150.529701
HLA B*1801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.223364	1.384894	-2.838470	16724.908688
HLA A*1101	1:160-168	9	PIVQGELSK	0.947962	0.037882	-3.825013	0.985844	-2.839169	6683.643427
HLA B*4002	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.526621	1.687135	-2.839486	33621.817194
HLA A*0203	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.430109	1.590000	-2.840109	26922.106480
HLA A*0216	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.430506	1.590000	-2.840507	26946.731843
HLA B*0702	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.430546	1.590000	-2.840546	26949.210197
HLA B*0801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.311822	1.470113	-2.841709	20503.210273
HLA B*4501	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.573881	1.732070	-2.841811	37487.033416

HLA A*0203	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.694880	0.852998	-2.841882	4953.133082
HLA A*0203	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-3.619823	0.776623	-2.843201	4166.998547
HLA A*3101	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-3.799347	0.954978	-2.844370	6300.100799
HLA A*6901	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.314973	1.470113	-2.844860	20652.494970
HLA B*0803	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.434956	1.590000	-2.844956	27224.256327
HLA A*0211	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.006732	1.161468	-2.845264	10156.213929
HLA B*1503	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-3.003398	0.157927	-2.845472	1007.855725
HLA B*5101	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-3.922052	1.075247	-2.846804	8357.025008
HLA A*2501	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.438168	1.590000	-2.848168	27426.334668
HLA A*0219	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.335274	1.486927	-2.848348	21640.855490
HLA B*4601	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.382656	1.534232	-2.848425	24135.510490
HLA A*2601	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.383246	1.534232	-2.849014	24168.305930
HLA A*2403	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.233936	1.384894	-2.849043	17137.064758
HLA A*0206	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-3.597273	0.748062	-2.849211	3956.152206
HLA B*5701	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.336860	1.486927	-2.849934	21720.025328
HLA A*0206	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.246177	1.396176	-2.850002	17626.953333

HLA A*3002	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-3.933630	1.083538	-2.850092	8582.819196
HLA A*0202	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.178559	1.328019	-2.850540	15085.478018
HLA A*2501	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.189254	1.338234	-2.851020	15461.582144
HLA B*5701	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.385419	1.534232	-2.851188	24289.550808
HLA B*4601	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.321697	1.470113	-2.851584	20974.747972
HLA A*2501	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.338679	1.486927	-2.851752	21811.163271
HLA A*0201	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.386622	1.534232	-2.852390	24356.922804
HLA B*3501	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.331778	1.478828	-2.852950	21467.347740
HLA B*1509	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.323311	1.470113	-2.853198	21052.847634
HLA A*0250	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.340316	1.486927	-2.853390	21893.561717
HLA B*1509	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-3.920844	1.067238	-2.853606	8333.819049
HLA A*0250	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.108568	1.254764	-2.853804	12840.085574
HLA B*5801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.333519	1.478828	-2.854691	21553.577214
HLA A*2301	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.508702	1.653995	-2.854707	32262.770618
HLA A*0101	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.390323	1.534232	-2.856091	24565.344477
HLA B*1502	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.196462	1.339576	-2.856886	15720.347867

HLA A*0206	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.511368	1.653995	-2.857374	32461.480700
HLA B*5101	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.511761	1.653995	-2.857766	32490.821325
HLA A*6901	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.143467	1.285203	-2.858264	13914.486006
HLA B*0803	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.393076	1.534232	-2.858844	24721.593158
HLA B*3901	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.198920	1.339576	-2.859343	15809.557461
HLA A*0219	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.329793	1.470113	-2.859680	21369.436807
HLA B*0801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.394369	1.534232	-2.860137	24795.260293
HLA A*0203	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.394688	1.534232	-2.860456	24813.509993
HLA A*8001	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.246899	1.384894	-2.862005	17656.253135
HLA A*2902	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.333526	1.470113	-2.863413	21553.927025
HLA A*0211	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.123647	1.260066	-2.863581	13293.731807
HLA A*0211	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.543028	1.678698	-2.864329	34916.253370
HLA B*1503	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-3.940641	1.076055	-2.864586	8722.496967
HLA A*0250	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.520336	1.653995	-2.866342	33138.764301
HLA A*6802	1:53-61	9	NISLPSYYP	0.515820	0.118220	-3.501564	0.634040	-2.867525	3173.689032
HLA A*2402	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.354512	1.486927	-2.867585	22621.010856

HLA B*4501	1:198-206	9	IFFFNPGEL	1.210946	0.568277	-4.647808	1.779223	-2.868585	44443.435109
HLA A*0219	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.459109	1.590000	-2.869109	28781.188971
HLA B*2705	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.207354	1.338234	-2.869121	16119.603851
HLA B*3801	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.459214	1.590000	-2.869215	28788.196461
HLA A*0202	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.469842	0.600517	-2.869324	2950.133196
HLA B*5801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.339755	1.470113	-2.869642	21865.272434
HLA B*3501	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.404105	1.534232	-2.869873	25357.412619
HLA A*0101	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.349799	1.478828	-2.870971	22376.849516
HLA B*1517	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-3.909139	1.037888	-2.871251	8112.205284
HLA B*5801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.117167	1.245899	-2.871269	13096.855420
HLA A*0203	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.032830	1.161468	-2.871362	10785.242629
HLA A*0211	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.256959	1.384894	-2.872065	18070.036982
HLA A*3001	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-3.492824	0.619394	-2.873431	3110.457608
HLA A*0211	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.343601	1.470113	-2.873488	22059.771003
HLA A*2301	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-3.798558	0.924700	-2.873858	6288.659364
HLA A*8001	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.464376	1.590000	-2.874377	29132.400804

HLA B*1502	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-3.874996	1.000164	-2.874832	7498.876758
HLA A*6801	1:168-176	9	KQTGQQVSI	1.475491	0.317774	-4.668215	1.793265	-2.874951	46581.690517
HLA B*4501	1:174-182	9	VSIAPNAGL	1.281479	0.469560	-4.626371	1.751039	-2.875332	42302.975693
HLA B*1503	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.896536	1.020870	-2.875667	7880.182846
HLA A*0212	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.410340	1.534232	-2.876108	25724.116680
HLA B*1501	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.113380	1.236794	-2.876586	12983.137705
HLA B*1517	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.467473	1.590000	-2.877473	29340.863948
HLA A*6901	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.246064	1.368126	-2.877938	17622.376653
HLA B*1517	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-3.961664	1.083538	-2.878126	9155.119531
HLA A*0201	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.896076	1.017829	-2.878247	7871.831614
HLA A*0301	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.366647	1.486927	-2.879721	23262.002507
HLA B*5801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.727655	0.847335	-2.880320	5341.402590
HLA A*6802	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.727839	0.847335	-2.880503	5343.656985
HLA B*1501	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.212108	0.330347	-2.881760	1629.700575
HLA A*2902	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.416242	1.534232	-2.882010	26076.084344
HLA A*6802	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.352158	1.470113	-2.882045	22498.720690

HLA B*3501	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.221644	1.339576	-2.882068	16658.808366
HLA A*3101	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.369091	1.486927	-2.882164	23393.250028
HLA B*0702	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.250362	1.368126	-2.882236	17797.610069
HLA B*4601	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.362547	1.478828	-2.883719	23043.436519
HLA A*6901	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-3.960395	1.076055	-2.884341	9128.413341
HLA A*0202	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.563203	1.678698	-2.884504	36576.543664
HLA A*8001	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.419830	1.534232	-2.885598	26292.388492
HLA A*6802	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.420648	1.534232	-2.886416	26341.934255
HLA B*0803	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.357158	1.470113	-2.887045	22759.228090
HLA B*4403	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.620471	1.732070	-2.888401	41732.207771
HLA B*4002	1:44-52	9	QMSDPAYNI	1.440627	0.291443	-4.620495	1.732070	-2.888425	41734.465499
HLA B*3501	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-3.744816	0.856017	-2.888799	5556.687215
HLA A*8001	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.258521	1.368668	-2.889853	18135.162395
HLA B*1503	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.288550	1.396176	-2.892375	19433.463847
HLA B*0802	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.427539	1.534232	-2.893307	26763.240761
HLA B*0702	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.428286	1.534232	-2.894054	26809.322389

HLA A*2601	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.373336	1.478828	-2.894508	23623.056137
HLA A*1101	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.126076	1.231508	-2.894568	13368.302996
HLA B*4402	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-3.414859	0.519628	-2.895231	2599.315379
HLA A*8001	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.374440	1.478828	-2.895612	23683.197678
HLA A*0219	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.429956	1.534232	-2.895724	26912.641179
HLA B*1517	1:78-86	9	LSAATSSTP	0.733359	0.025119	-3.654873	0.758478	-2.896395	4517.237932
HLA B*0801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.264541	1.368126	-2.896415	18388.268201
HLA A*1101	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.431124	1.534232	-2.896892	26985.098964
HLA A*0301	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.367291	1.470113	-2.897178	23296.509566
HLA B*0802	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.384604	1.486927	-2.897678	24243.996468
HLA A*6801	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.385114	1.486927	-2.898187	24272.474322
HLA A*0202	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.916803	1.017829	-2.898974	8256.632453
HLA A*3101	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.370625	1.470113	-2.900512	23476.036513
HLA A*3101	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-3.993993	1.092768	-2.901225	9862.634356
HLA B*5801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.241217	1.339576	-2.901641	17426.793775
HLA B*4001	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.380967	1.478828	-2.902139	24041.812693

HLA B*3801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.287180	1.384894	-2.902287	19372.267930
HLA A*0101	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.372732	1.470113	-2.902619	23590.234844
HLA A*0216	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.373000	1.470113	-2.902887	23604.788074
HLA B*5701	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.382560	1.478828	-2.903732	24130.157696
HLA A*3001	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.272717	1.368668	-2.904049	18737.732614
HLA B*0802	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.374436	1.470113	-2.904323	23682.941433
HLA A*8001	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.391991	1.486927	-2.905064	24659.881932
HLA B*1509	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.392151	1.486927	-2.905224	24668.955292
HLA A*2601	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.375770	1.470113	-2.905657	23755.826703
HLA B*2705	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.392733	1.486927	-2.905807	24702.074670
HLA B*5801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.233906	1.328019	-2.905886	17135.859575
HLA A*0202	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.166332	1.260066	-2.906266	14666.698231
HLA B*1509	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.245996	1.339576	-2.906420	17619.612152
HLA B*5101	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.497180	1.590000	-2.907180	31418.090471
HLA A*3001	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.119916	1.212549	-2.907367	13180.015794
HLA B*1801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.247077	1.339576	-2.907501	17663.514024

HLA A*2501	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.441819	1.534232	-2.907587	27657.878907
HLA A*1101	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.386470	1.478828	-2.907641	24348.359374
HLA A*2403	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.442378	1.534232	-2.908146	27693.512845
HLA A*2301	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.387717	1.478828	-2.908889	24418.404275
HLA B*4501	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.563198	1.653995	-2.909203	36576.147916
HLA B*3901	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.443720	1.534232	-2.909488	27779.191664
HLA B*1503	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-3.866341	0.956718	-2.909622	7350.903362
HLA A*2403	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.388784	1.478828	-2.909956	24478.451776
HLA A*8001	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.380251	1.470113	-2.910138	24002.176023
HLA A*3101	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.156211	1.245899	-2.910312	14328.831480
HLA A*0203	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.307539	1.396176	-2.911363	20301.996778
HLA A*2403	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.280109	1.368668	-2.911440	19059.368947
HLA A*3301	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-3.949348	1.037888	-2.911460	8899.139579
HLA B*5101	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.445733	1.534232	-2.911501	27908.282655
HLA B*5401	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.565667	1.653995	-2.911673	36784.704683
HLA B*1801	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.251212	1.338234	-2.912979	17832.498702

HLA A*3002	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.282284	1.368668	-2.913616	19155.087503
HLA A*0211	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.503855	1.590000	-2.913855	31904.700554
HLA B*4002	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.592830	1.678698	-2.914131	39158.826623
HLA B*4403	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.602434	1.687135	-2.915299	40034.495916
HLA B*1502	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.243522	1.328019	-2.915503	17519.525384
HLA A*0250	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.595299	1.678698	-2.916601	39382.109793
HLA A*2501	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.395581	1.478828	-2.916753	24864.573030
HLA A*0203	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.766647	0.847335	-2.919312	5843.154447
HLA A*2602	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.573547	1.653995	-2.919553	37458.246776
HLA A*0202	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.317439	1.396176	-2.921264	20770.142890
HLA B*7301	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.600367	1.678698	-2.921668	39844.356551
HLA A*0216	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.306773	1.384894	-2.921879	20266.223247
HLA B*4801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.401072	1.478828	-2.922243	25180.929230
HLA B*5701	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.392607	1.470113	-2.922494	24694.859408
HLA B*4402	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.410693	1.486927	-2.923766	25744.999844
HLA B*1503	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.160571	1.236794	-2.923778	14473.428472

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HLA B*5301	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.170702
	1.246912	-2.923791	14815.025335

HLA B*0801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-3.995934
	1.071973	-2.923961	9906.804828

HLA A*6802	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-3.595229
	0.671022	-2.924207	3937.575916

HLA A*0206	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.514411
	1.590000	-2.924411	32689.698041

HLA B*3901	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.292631
	1.368126	-2.924505	19616.940380

HLA B*1801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.403677
	1.478828	-2.924849	25332.458002

HLA A*6802	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.293726
	1.368668	-2.925058	19666.457241

HLA B*0702	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.259901
	1.334657	-2.925244	18192.844045

HLA B*0803	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.253277
	1.328019	-2.925258	17917.499392

HLA A*0216	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.459734
	1.534232	-2.925502	28822.635795

HLA B*1517	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.459802
	1.534232	-2.925570	28827.158040

HLA A*0211	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-3.606408
	0.680076	-2.926331	4040.245820

HLA A*0216	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.187285
	1.260066	-2.927219	15391.645908

HLA A*2601	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.106538
	1.179033	-2.927505	12780.209207

HLA A*0206	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-3.731955
	0.804086	-2.927869	5394.545621

HLA B*2705	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.407068
	1.478828	-2.928239	25530.988981
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HLA A*2402	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.409666	1.478828	-2.930838	25684.207424
HLA A*6801	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.609657	1.678698	-2.930958	40705.836275
HLA B*0702	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.271044	1.339576	-2.931468	18665.696670
HLA B*5301	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.587271	1.653995	-2.933276	38660.795710
HLA A*3201	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.587830	1.653995	-2.933835	38710.605617
HLA A*0250	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.010378	1.076055	-2.934324	10241.845990
HLA B*1501	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.180866	1.245899	-2.934968	15165.833043
HLA A*2601	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.303340	1.368126	-2.935214	20106.673458
HLA B*4402	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.414783	1.478828	-2.935955	25988.627655
HLA B*3801	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.470823	1.534232	-2.936591	29568.089438
HLA A*0211	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.717632	0.779687	-2.937945	5219.542157
HLA B*0801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-3.339581	0.401614	-2.937967	2185.654326
HLA A*2301	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.306658	1.368668	-2.937989	20260.851696
HLA A*6802	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.142147	1.203934	-2.938213	13872.245238
HLA A*3301	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.617114	1.678698	-2.938416	41410.831114
HLA B*4601	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.306693	1.368126	-2.938567	20262.495897

HLA B*4402	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.408722	1.470113	-2.938609	25628.410735
HLA A*6802	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.681333	0.742712	-2.938620	4801.012828
HLA A*0201	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.324100	1.384894	-2.939206	21091.150675
HLA A*0101	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.308286	1.368668	-2.939618	20336.953272
HLA A*0219	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.917094	0.977336	-2.939758	8262.173077
HLA B*4601	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.267821	1.328019	-2.939801	18527.665894
HLA B*0801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.324941	1.384894	-2.940047	21132.038339
HLA B*5101	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.268873	1.328019	-2.940854	18572.624566
HLA B*1501	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.154007	1.212549	-2.941458	14256.304343
HLA A*0211	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.337730	1.396176	-2.941554	21763.544953
HLA A*0101	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.121265	1.179033	-2.942232	13221.006998
HLA A*0211	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.065234	1.122935	-2.942299	11620.746215
HLA A*0202	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.155285	1.212549	-2.942736	14298.322155
HLA A*0202	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.790189	0.847335	-2.942854	6168.636872
HLA A*0203	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.311004	1.368126	-2.942878	20464.646393
HLA B*1503	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.961072	1.017829	-2.943243	9142.646933

HLA A*2902	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.189221	1.245899	-2.943323	15460.411152
HLA B*1502	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.597381	1.653995	-2.943386	39571.327731
HLA A*0203	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.156286	1.212549	-2.943737	14331.312251
HLA B*1801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.414008	1.470113	-2.943895	25942.272499
HLA B*4403	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.598344	1.653995	-2.944349	39659.196507
HLA A*3101	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.314035	1.368668	-2.945367	20607.963693
HLA A*1101	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.021581	1.075247	-2.946333	10509.464449
HLA B*0702	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.274773	1.328019	-2.946753	18826.640802
HLA A*3301	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.427165	1.478828	-2.948337	26740.229659
HLA A*0201	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.344635	1.396176	-2.948459	22112.343551
HLA B*1502	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.279294	0.330347	-2.948946	1902.364319
HLA B*1502	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.539012	1.590000	-2.949013	34594.922850
HLA B*1501	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.021247	1.071973	-2.949274	10501.394134
HLA A*0250	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-3.970014	1.019585	-2.950430	9332.845762
HLA B*4501	1:48-56	9	PAYNINISL	1.435478	0.251657	-4.637637	1.687135	-2.950502	43414.689404
HLA A*3201	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.421261	1.470113	-2.951148	26379.154839

HLA A*6901	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.953864	1.002409	-2.951455	8992.153848
HLA B*2705	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-3.908030	0.954978	-2.953052	8091.517454
HLA B*5401	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.553770	0.600517	-2.953253	3579.067818
HLA B*2705	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.321744	1.368126	-2.953618	20977.017516
HLA A*0201	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.214121	1.260066	-2.954055	16372.721757
HLA B*4501	1:140-148	9	KPITYDTLW	1.293618	0.385080	-4.632942	1.678698	-2.954244	42947.948862
HLA B*0803	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.433363	1.478828	-2.954535	27124.583253
HLA A*2403	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-3.289932	0.335272	-2.954660	1949.540043
HLA B*5801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.350992	1.396176	-2.954817	22438.430684
HLA A*3101	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.283633	1.328019	-2.955613	19214.661793
HLA A*2902	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.340577	1.384894	-2.955683	21906.712699
HLA A*3001	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.290627	1.334657	-2.955971	19526.623901
HLA B*1501	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.352207	1.396176	-2.956031	22501.276862
HLA A*6901	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.341216	1.384894	-2.956322	21938.971933
HLA B*1501	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.958774	1.002409	-2.956366	9094.402103
HLA B*2705	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.291059	1.334657	-2.956403	19546.070763

HLA A*3002	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.977833	1.020870	-2.956963	9502.397084
HLA B*3901	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.699678	0.742712	-2.956965	5008.153658
HLA B*1501	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.118802	1.161468	-2.957334	13146.261741
HLA A*2902	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.212439	1.254764	-2.957675	16309.425005
HLA A*2603	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.353866	1.396176	-2.957690	22587.382158
HLA A*2402	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.137255	1.179033	-2.958222	13716.873390
HLA A*0211	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-3.845520	0.886699	-2.958821	7006.797677
HLA A*2902	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.297431	1.338234	-2.959198	19834.957307
HLA B*7301	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.613886	1.653995	-2.959891	41104.157826
HLA B*0803	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.447103	1.486927	-2.960176	27996.443367
HLA B*0702	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.345091	1.384894	-2.960197	22135.563047
HLA B*1801	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.447791	1.486927	-2.960865	28040.855649
HLA A*0216	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.289163	1.328019	-2.961144	19460.922911
HLA B*2705	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.207368	1.245899	-2.961470	16120.127091
HLA B*4001	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.357745	1.396176	-2.961569	22790.030140
HLA B*3901	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.440562	1.478828	-2.961734	27577.944698

HLA B*5401	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.551742	1.590000	-2.961742	35623.933889
HLA A*3001	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.046682	1.083538	-2.963145	11134.801600
HLA A*1101	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.433464	1.470113	-2.963351	27130.893849
HLA A*3201	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.359606	1.396176	-2.963430	22887.886526
HLA A*0250	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.554329	1.590000	-2.964329	35836.753475
HLA B*5401	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.498733	1.534232	-2.964501	31530.640691
HLA A*2403	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.360689	1.396176	-2.964513	22945.039213
HLA A*0301	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.304534	1.339576	-2.964957	20162.007093
HLA A*0101	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.361650	1.396176	-2.965474	22995.864640
HLA B*1509	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.145037	1.179033	-2.966004	13964.861227
HLA B*4001	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.305913	1.339576	-2.966337	20226.135432
HLA A*2501	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.351265	1.384894	-2.966371	22452.516277
HLA B*1509	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.351533	1.384894	-2.966639	22466.367628
HLA B*1502	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-3.906799	0.940065	-2.966734	8068.612248
HLA A*0212	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.351695	1.384894	-2.966801	22474.755492
HLA B*1509	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.294840	1.328019	-2.966820	19716.952405

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HLA A*0101	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.295089
	1.328019	-2.967069	19728.262299

HLA A*0201	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-3.969615
	1.002409	-2.967206	9324.266466

HLA A*0212	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.171285
	1.203934	-2.967351	14834.915291

HLA A*0202	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.501745
	1.534232	-2.967513	31750.080834

HLA A*0250	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.438656
	1.470113	-2.968544	27457.213712

HLA B*2705	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.200531
	1.231508	-2.969023	15868.338643

HLA A*0202	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.559220
	1.590000	-2.969221	36242.678532

HLA B*4402	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.216203
	1.246912	-2.969291	16451.387239

HLA B*1502	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.448280
	1.478828	-2.969452	28072.426576

HLA A*3201	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.559866
	1.590000	-2.969867	36296.637600

HLA A*3101	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-3.990784
	1.020870	-2.969914	9790.019030

HLA B*5801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.338590
	1.368126	-2.970463	21806.679884

HLA A*0201	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.017384
	1.046875	-2.970510	10408.410334

HLA A*0211	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.225380
	1.254764	-2.970616	16802.720894

HLA B*0801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.366861
	1.396176	-2.970685	23273.457209

HLA B*1517	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.231007
	1.260066	-2.970940	17021.844942
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HLA A*0301	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.367187	1.396176	-2.971012	23290.964839
HLA B*0801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.048322	1.076055	-2.972268	11176.927239
HLA B*5101	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.442430	1.470113	-2.972317	27696.809055
HLA B*5101	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.312313	1.339576	-2.972737	20526.405684
HLA B*3901	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.368975	1.396176	-2.972800	23387.049660
HLA A*2603	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.626855	1.653995	-2.972860	42350.145981
HLA A*3001	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.233116	1.260066	-2.973050	17104.739626
HLA A*0203	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.258862	1.285203	-2.973659	18149.393813
HLA B*1503	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.219802	1.245899	-2.973903	16588.302104
HLA A*0301	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.358898	1.384894	-2.974005	22850.646755
HLA B*1501	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.342814	1.368668	-2.974146	22019.828001
HLA A*0212	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.302419	1.328019	-2.974400	20064.078887
HLA A*6901	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.343408	1.368668	-2.974740	22049.987218
HLA A*0206	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.509653	1.534232	-2.975421	32333.536009
HLA A*0101	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.230344	1.254764	-2.975580	16995.896406
HLA A*0206	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-3.975860	1.000164	-2.975695	9459.313243

HLA A*3001	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.260941	1.285203	-2.975738	18236.496955
HLA A*3201	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.230595	1.254764	-2.975831	17005.737467
HLA B*3501	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.314799	1.338234	-2.976565	20644.228775
HLA A*6802	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-3.833396	0.856017	-2.977379	6813.907516
HLA A*6802	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.305525	1.328019	-2.977506	20208.088998
HLA A*3001	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.181609	1.203934	-2.977675	15191.781587
HLA B*1517	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.448264	1.470113	-2.978151	28071.363515
HLA B*5101	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.374889	1.396176	-2.978713	23707.681909
HLA A*6801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.158100	1.179033	-2.979067	14391.291199
HLA A*0301	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.348042	1.368668	-2.979373	22286.482385
HLA A*0203	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.559277	0.579719	-2.979558	3624.742171
HLA B*7301	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.513948	1.534232	-2.979716	32654.877613
HLA B*0802	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.458691	1.478828	-2.979862	28753.487170
HLA A*6802	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.227062	1.246912	-2.980150	16867.932123
HLA A*2301	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.514970	1.534232	-2.980738	32731.814888
HLA A*0216	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.376999	1.396176	-2.980823	23823.135951

HLA A*0212	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-3.998814	1.017829	-2.980985	9972.730334
HLA A*0101	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.241582	1.260066	-2.981516	17441.412842
HLA B*0802	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.350880	1.368668	-2.982211	22432.604748
HLA A*1101	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.469378	1.486927	-2.982452	29469.877455
HLA A*3001	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.219976	1.236794	-2.983182	16594.944258
HLA B*1517	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-3.960823	0.977336	-2.983487	9137.405601
HLA A*0201	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.162935	1.179033	-2.983902	14552.412648
HLA B*1517	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-3.997367	1.013420	-2.983947	9939.551608
HLA A*2601	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.352658	1.368668	-2.983990	22524.661052
HLA A*3101	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.369448	1.384894	-2.984554	23412.494283
HLA B*5701	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.369765	1.384894	-2.984871	23429.599493
HLA A*6901	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.232557	1.246912	-2.985646	17082.730528
HLA A*3002	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.231632	1.245899	-2.985733	17046.357529
HLA B*4002	1:131-139	9	AFDWDQAYR	0.906877	0.747118	-4.640036	1.653995	-2.986041	43655.153793
HLA A*0216	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.109061	1.122935	-2.986126	12854.681186
HLA A*2403	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.315196	1.328019	-2.987176	20663.111831

HLA B*3901	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.690158	0.701666	-2.988492	4899.565095
HLA A*2601	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.384719	1.396176	-2.988544	24250.424030
HLA B*1503	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.061160	1.071973	-2.989187	11512.244635
HLA B*1517	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.569079	0.579719	-2.989360	3707.483031
HLA A*0211	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.065723	1.076055	-2.989668	11633.829901
HLA B*4001	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.328024	1.338234	-2.989790	21282.562343
HLA A*2402	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.524074	1.534232	-2.989842	33425.225108
HLA B*5101	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.275402	1.285203	-2.990199	18853.956410
HLA A*2602	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.469042	1.478828	-2.990214	29447.087957
HLA A*0203	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.692338	0.701666	-2.990672	4924.224608
HLA A*0250	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-3.731358	0.740601	-2.990757	5387.138003
HLA B*1517	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.063251	1.071973	-2.991278	11567.807460
HLA A*0301	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.326217	1.334657	-2.991561	21194.206443
HLA A*0212	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.277244	1.285203	-2.992041	18934.092519
HLA A*0211	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.526438	1.534232	-2.992206	33607.632744
HLA B*4801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.389437	1.396176	-2.993261	24515.293821

HLA A*2601	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.248226	1.254764	-2.993462	17710.303578
HLA B*3501	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.378449	1.384894	-2.993555	23902.788096
HLA B*4001	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.363168	1.368668	-2.994499	23076.370915
HLA B*1503	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.280280	1.285203	-2.995077	19066.897396
HLA B*4002	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.595826	0.600517	-2.995308	3942.990305
HLA B*5701	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.333623	1.338234	-2.995389	21558.708334
HLA B*1503	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.842860	0.847335	-2.995525	6964.019207
HLA A*0216	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.363872	1.368126	-2.995746	23113.853506
HLA B*3501	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.392202	1.396176	-2.996027	24671.891506
HLA B*1503	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.365794	1.368668	-2.997126	23216.365650
HLA A*2501	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.468199	1.470113	-2.998086	29389.952790
HLA A*6801	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-3.784654	0.786460	-2.998194	6090.512219
HLA A*0206	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.356371	0.357949	-2.998421	2271.804193
HLA A*3101	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.395064	1.396176	-2.998888	24834.997425
HLA B*1503	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-3.998166	0.999064	-2.999102	9957.850869
HLA A*2402	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.395790	1.396176	-2.999614	24876.547711

HLA A*0301	1:160-168	9	PIVQGELSK	0.947962	0.037882	-3.985695	0.985844	-2.999850	9675.970854
HLA A*3001	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.853033	0.852998	-3.000035	7129.075766
HLA B*2705	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.204150	1.203934	-3.000216	16001.093649
HLA A*8001	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.260605	1.260066	-3.000539	18222.394399
HLA B*3501	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.369530	1.368668	-3.000862	23416.927767
HLA B*1503	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-3.854429	0.853458	-3.000971	7152.021715
HLA A*0101	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.369119	1.368126	-3.000993	23394.768736
HLA B*1502	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.339623	1.338234	-3.001390	21858.649270
HLA B*0803	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.386336	1.384894	-3.001442	24340.852381
HLA B*0802	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.386604	1.384894	-3.001710	24355.868681
HLA A*0202	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-3.672753	0.671022	-3.001730	4707.090488
HLA B*3901	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.336846	1.334657	-3.002190	21719.320322
HLA A*3201	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.074195	1.071973	-3.002222	11863.011531
HLA A*2501	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.398692	1.396176	-3.002516	25043.309693
HLA A*1101	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.371435	1.368668	-3.002767	23519.893378
HLA A*0212	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.399126	1.396176	-3.002951	25068.386322

HLA A*2403	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.164655	1.161468	-3.003187	14610.155023
HLA A*0101	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.388241	1.384894	-3.003347	24447.880543
HLA A*3002	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.537591	1.534232	-3.003359	34481.879353
HLA B*4601	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.399810	1.396176	-3.003634	25107.882005
HLA B*4601	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.388554	1.384894	-3.003660	24465.477496
HLA A*0219	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.265662	1.260066	-3.005595	18435.780719
HLA A*0219	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.390525	1.384894	-3.005631	24576.776174
HLA B*4801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.374172	1.368126	-3.006046	23668.596105
HLA B*7301	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.596173	1.590000	-3.006173	39461.445257
HLA B*1503	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.607338	0.600517	-3.006821	4048.910582
HLA B*5101	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-3.961453	0.954583	-3.006870	9150.663079
HLA A*0202	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.262032	1.254764	-3.007267	18282.331504
HLA A*8001	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.403569	1.396176	-3.007394	25326.154680
HLA A*0101	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.345737	1.338234	-3.007503	22168.519065
HLA B*4402	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.347113	1.339576	-3.007537	22238.909110
HLA A*2501	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.377636	1.368668	-3.008967	23858.088188

HLA B*4601	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.377659	1.368668	-3.008991	23859.378919
HLA B*4001	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.294391	1.285203	-3.009188	19696.589620
HLA A*3101	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.240703	1.231508	-3.009195	17406.159333
HLA B*5701	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.246356	1.236794	-3.009562	17634.202172
HLA A*0101	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.349618	1.339576	-3.010042	22367.530124
HLA A*2601	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.394994	1.384894	-3.010100	24830.967115
HLA A*2601	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.256235	1.245899	-3.010337	18039.952929
HLA B*4402	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.339327	1.328019	-3.011308	21843.754485
HLA A*6901	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.345974	1.334657	-3.011317	22180.635227
HLA A*3001	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.030927	1.019585	-3.011342	10738.084984
HLA B*0802	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.379828	1.368126	-3.011702	23978.814559
HLA B*0803	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.381303	1.368126	-3.013177	24060.418976
HLA A*2603	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.603489	1.590000	-3.013490	40131.859519
HLA B*5301	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.603525	1.590000	-3.013525	40135.116285
HLA A*0201	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.381733	1.368126	-3.013607	24084.250819
HLA A*6901	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.794212	0.779687	-3.014524	6226.034513

HLA B*3801	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.501634	1.486927	-3.014708	31742.008932
HLA B*5401	1:89-97	9	APYELNITS	1.361001	-1.037258	-3.338491	0.323743	-3.014749	2180.174802
HLA A*1101	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.410933	1.396176	-3.014757	25759.210080
HLA B*7301	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.218956	1.203934	-3.015022	16556.026828
HLA B*1503	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.247242	1.231508	-3.015733	17670.204326
HLA B*0801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.384407	1.368668	-3.015739	24232.981755
HLA A*3101	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.270852	1.254764	-3.016087	18657.418200
HLA B*2705	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.412657	1.396176	-3.016481	25861.699612
HLA A*0201	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.385347	1.368668	-3.016678	24285.477632
HLA B*4001	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.344961	1.328019	-3.016942	22128.977725
HLA A*0212	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.178756	1.161468	-3.017289	15092.334880
HLA A*2601	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.355633	1.338234	-3.017399	22679.460144
HLA B*5801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.352242	1.334657	-3.017586	22503.102878
HLA A*6802	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.403454	1.384894	-3.018560	25319.441997
HLA B*5701	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.414835	1.396176	-3.018659	25991.720942
HLA A*2601	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.359380	1.339576	-3.019804	22876.002803

HLA B*1509	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.389775	1.368668	-3.021107	24534.399265
HLA B*4501	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.611358	1.590000	-3.021358	40865.583897
HLA B*4002	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.611379	1.590000	-3.021379	40867.573650
HLA A*2403	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.268098	1.245899	-3.022199	18539.497119
HLA A*8001	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.360668	1.338234	-3.022434	22943.922069
HLA A*0219	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.350772	1.328019	-3.022752	22427.022979
HLA B*3801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.493005	1.470113	-3.022892	31117.503789
HLA B*1503	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-3.943907	0.920569	-3.023338	8788.335161
HLA B*5701	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.391772	1.368126	-3.023646	24647.478180
HLA A*0212	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.392369	1.368668	-3.023701	24681.369852
HLA A*0201	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.309482	1.285203	-3.024278	20393.030962
HLA A*3002	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.147583	1.122935	-3.024648	14046.996237
HLA A*0206	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.100730	1.076055	-3.024676	12610.434078
HLA B*1503	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-3.773809	0.748062	-3.025747	5940.302976
HLA B*1502	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.394540	1.368126	-3.026414	24805.054419
HLA A*0201	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.149421	1.122935	-3.026486	14106.548403

HLA A*0219	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.422694	1.396176	-3.026518	26466.350699
HLA A*0202	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.395950	1.368126	-3.027824	24885.700791
HLA B*4001	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.395978	1.368126	-3.027852	24887.316390
HLA A*3001	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.259377	1.231508	-3.027869	18170.909336
HLA B*1502	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.103935	1.076055	-3.027880	12703.831762
HLA A*0219	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.313638	1.285203	-3.028435	20589.131035
HLA A*8001	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.151968	1.122935	-3.029032	14189.516753
HLA B*1502	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.563550	1.534232	-3.029318	36605.840898
HLA A*6801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.369088	1.339576	-3.029512	23393.123474
HLA A*3002	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.357573	1.328019	-3.029554	22781.031634
HLA A*3002	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-3.839049	0.808230	-3.030819	6903.178377
HLA A*2403	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.369645	1.338234	-3.031411	23423.136056
HLA A*2602	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.052876	1.020870	-3.032006	11294.726673
HLA B*4601	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.292145	1.260066	-3.032079	19594.984703
HLA A*3001	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.279267	1.246912	-3.032356	19022.491622
HLA A*0301	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.287493	1.254764	-3.032729	19386.211588

HLA A*1101	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.367493	1.334657	-3.032836	23307.350800
HLA B*3901	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.194357	1.161468	-3.032889	15644.331627
HLA B*5301	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.269712	1.236794	-3.032918	18608.529102
HLA A*2501	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.245545	1.212549	-3.032996	17601.320185
HLA B*1509	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.401149	1.368126	-3.033023	25185.425090
HLA B*5101	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.417950	1.384894	-3.033057	26178.843250
HLA B*5301	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.567401	1.534232	-3.033169	36931.861115
HLA A*0301	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.361654	1.328019	-3.033635	22996.113452
HLA A*3201	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.054534	1.020870	-3.033665	11337.948032
HLA A*3002	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.246682	1.212549	-3.034133	17647.467631
HLA A*6901	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.294267	1.260066	-3.034200	19690.942942
HLA B*3501	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.196641	1.161468	-3.035173	15726.812642
HLA B*1509	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.514216	1.478828	-3.035388	32675.022981
HLA A*8001	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.404124	1.368126	-3.035998	25358.510089
HLA B*0801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.370768	1.334657	-3.036112	23483.784959
HLA A*2301	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.432296	1.396176	-3.036121	27058.044590

HLA B*4001	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.371055	1.334657	-3.036398	23499.289526
HLA A*2902	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.433262	1.396176	-3.037086	27118.274124
HLA B*7301	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.268873	1.231508	-3.037365	18572.624566
HLA B*5701	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.376952	1.339576	-3.037376	23820.558480
HLA B*1503	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.178047	1.138874	-3.039173	15067.697359
HLA A*8001	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.379055	1.339576	-3.039478	23936.173740
HLA B*0803	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.377819	1.338234	-3.039585	23868.157742
HLA B*0801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.244483	1.203934	-3.040550	17558.332786
HLA A*6901	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.272172	1.231508	-3.040664	18714.229745
HLA A*2603	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.519669	1.478828	-3.040841	33087.888714
HLA B*1517	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.437118	1.396176	-3.040942	27360.091872
HLA B*3501	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.273217	1.231508	-3.041709	18759.336668
HLA A*2601	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.376419	1.334657	-3.041762	23791.323720
HLA B*0801	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.254436	1.212549	-3.041886	17965.350495
HLA B*5101	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.744036	0.701666	-3.042370	5546.715900
HLA B*1501	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-3.999354	0.956718	-3.042636	9985.146872

HLA A*0216	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.785490	0.742712	-3.042778	6102.253364
HLA A*2603	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.381242	1.338234	-3.043008	24057.034944
HLA A*2902	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.411311	1.368126	-3.043185	25781.655923
HLA B*2705	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.371351	1.328019	-3.043331	23515.313184
HLA B*1501	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.303540	1.260066	-3.043474	20115.921448
HLA B*4402	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.411917	1.368126	-3.043791	25817.665830
HLA A*6901	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.280647	1.236794	-3.043853	19082.995557
HLA A*0201	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.371985	1.328019	-3.043966	23549.686396
HLA A*1101	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.428878	1.384894	-3.043984	26845.896250
HLA A*0203	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.787440	0.742712	-3.044728	6129.715360
HLA A*0206	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.257558	1.212549	-3.045009	18094.982193
HLA A*6901	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.058782	1.013420	-3.045362	11449.389525
HLA A*0211	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.625194	0.579719	-3.045475	4218.851819
HLA B*4402	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.384289	1.338234	-3.046056	24226.427755
HLA B*4001	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-3.798149	0.751912	-3.046237	6282.742504
HLA B*4801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.385929	1.339576	-3.046353	24318.082171

HLA A*2603	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.516664	1.470113	-3.046551	32859.735633
HLA B*2705	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.386178	1.339576	-3.046602	24332.031332
HLA A*6802	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-3.941848	0.895143	-3.046706	8746.785219
HLA A*2902	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.085031	1.037888	-3.047142	12162.721918
HLA A*0219	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.047627	1.000164	-3.047463	11159.043644
HLA A*0206	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.415866	1.368126	-3.047740	26053.523114
HLA A*3201	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.534760	1.486927	-3.047833	34257.825950
HLA B*1503	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.085740	1.037888	-3.047852	12182.609451
HLA B*4601	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.383225	1.334657	-3.048569	24167.129228
HLA B*4601	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.228025	1.179033	-3.048992	16905.387641
HLA B*1509	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.262074	1.212549	-3.049525	18284.111888
HLA A*6802	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.334852	1.285203	-3.049648	21619.792314
HLA A*2601	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.377821	1.328019	-3.049802	23868.286867
HLA A*6802	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.286602	1.236794	-3.049809	19346.503830
HLA B*4801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.418566	1.368668	-3.049898	26215.975215
HLA B*4403	1:99-107	9	TYQSAIPPR	0.787540	0.802460	-4.639953	1.590000	-3.049954	43646.888642

HLA A*2603	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-3.747095	0.696230	-3.050865	5585.923087
HLA A*0203	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.419825	1.368668	-3.051157	26292.104015
HLA A*0101	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.386251	1.334657	-3.051595	24336.112316
HLA B*0702	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-3.886955	0.835252	-3.051703	7708.237633
HLA B*2705	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.055009	1.002409	-3.052601	11350.344887
HLA B*5301	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.522994	1.470113	-3.052881	33342.148211
HLA A*0202	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.009918	0.956718	-3.053199	10230.991925
HLA A*0216	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.053731	1.000164	-3.053567	11316.990158
HLA B*5401	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.176576	1.122935	-3.053641	15016.755545
HLA B*3501	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.796627	0.742712	-3.053914	6260.756231
HLA B*5301	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.533110	1.478828	-3.054282	34127.970295
HLA B*0802	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.450507	1.396176	-3.054332	28216.767935
HLA A*6802	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.138063	1.083538	-3.054525	13742.424285
HLA A*0250	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.588838	1.534232	-3.054606	38800.551168
HLA A*3001	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.193793	1.138874	-3.054920	15624.032624
HLA A*2902	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.382957	1.328019	-3.054938	24152.229294

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HLA A*1101	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.394916
	1.339576	-3.055340	24826.534529

HLA B*0702	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.424127
	1.368668	-3.055459	26553.834784

HLA A*6801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.041438
	0.985844	-3.055594	11001.158774

HLA A*0216	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.424289
	1.368668	-3.055621	26563.748712

HLA B*0802	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.395346
	1.339576	-3.055770	24851.125210

HLA A*0301	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.301933
	1.245899	-3.056034	20041.622764

HLA A*2501	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.424334
	1.368126	-3.056208	26566.479284

HLA A*3101	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.070351
	1.013420	-3.056931	11758.480278

HLA A*2603	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.545039
	1.486927	-3.058112	35078.320795

HLA B*5101	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.393112
	1.334657	-3.058455	24723.599356

HLA B*3501	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.923466
	0.864656	-3.058810	8384.286143

HLA A*2602	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.529098
	1.470113	-3.058985	33814.077189

HLA B*5101	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.427682
	1.368668	-3.059014	26772.074175

HLA A*0211	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.053604
	0.994492	-3.059112	11313.684563

HLA B*4801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.296163
	1.236794	-3.059369	19777.097206

HLA B*5301	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.135484
	1.076055	-3.059429	13661.035450
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HLA A*2902	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.182530	1.122935	-3.059595	15224.032626
HLA A*0201	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.395125	1.334657	-3.060469	24838.490890
HLA A*6802	1:82-90	9	TSSTPREAP	0.792178	0.117162	-3.970536	0.909340	-3.061196	9344.061201
HLA B*0702	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.457553	1.396176	-3.061378	28678.297912
HLA A*0250	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.223209	1.161468	-3.061741	16718.938080
HLA A*0212	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.061912	1.000164	-3.061748	11532.191485
HLA A*0212	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.429999	1.368126	-3.061872	26915.262006
HLA B*1501	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.265842	1.203934	-3.061909	18443.461954
HLA A*0212	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.322211	1.260066	-3.062145	20999.612861
HLA A*0201	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.317019	1.254764	-3.062255	20750.039439
HLA B*1501	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.396951	1.334657	-3.062294	24943.118833
HLA A*2403	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.430628	1.368126	-3.062502	26954.313409
HLA A*0212	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.805433	0.742712	-3.062720	6388.996706
HLA B*0801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.322839	1.260066	-3.062772	21029.967468
HLA A*3001	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.155703	1.092768	-3.062936	14312.097503
HLA B*3501	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.391049	1.328019	-3.063029	24606.443618

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HLA B*0802	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.392527
	1.328019	-3.064507	24690.317546

HLA A*0219	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.433713
	1.368668	-3.065045	27146.456475

HLA B*5701	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.311307
	1.245899	-3.065409	20478.933157

HLA B*1509	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.403917
	1.338234	-3.065683	25346.440530

HLA B*0803	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.461916
	1.396176	-3.065741	28967.856843

HLA B*1503	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.400600
	1.334657	-3.065943	25153.562678

HLA B*3801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.544945
	1.478828	-3.066116	35070.730824

HLA A*0211	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.270111
	1.203934	-3.066178	18625.650887

HLA A*0201	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.270281
	1.203934	-3.066347	18632.907215

HLA A*3101	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.326447
	1.260066	-3.066381	21205.445936

HLA B*5301	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.401243
	1.334657	-3.066587	25190.875694

HLA A*0301	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.326699
	1.260066	-3.066633	21217.724435

HLA B*5801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.352031
	1.285203	-3.066828	22492.149008

HLA B*5701	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.401838
	1.334657	-3.067181	25225.378101

HLA B*1801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.402037
	1.334657	-3.067381	25236.980421

HLA B*0802	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.405677
	1.338234	-3.067443	25449.352844
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HLA A*3001	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.143232	1.075733	-3.067499	13906.960460
HLA A*3101	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.229143	1.161468	-3.067676	16948.976926
HLA B*5101	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.406224	1.338234	-3.067990	25481.452086
HLA A*3101	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.304926	1.236794	-3.068132	20180.230720
HLA A*0212	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.403102	1.334657	-3.068445	25298.904025
HLA B*4801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.403252	1.334657	-3.068596	25307.664855
HLA A*2902	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.305936	1.236794	-3.069143	20227.229673
HLA B*1801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.437526	1.368126	-3.069400	27385.858619
HLA B*0803	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.438478	1.368668	-3.069810	27445.926955
HLA A*0250	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-3.849650	0.779687	-3.069963	7073.754316
HLA B*4601	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.355543	1.285203	-3.070340	22674.798276
HLA B*0803	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.325543	1.254764	-3.070779	21161.325042
HLA A*3001	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.193868	1.122935	-3.070933	15626.737635
HLA A*0216	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.924016	0.852998	-3.071018	8394.906650
HLA B*5401	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.541789	1.470113	-3.071677	34816.848496
HLA A*0211	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.250970	1.179033	-3.071937	17822.564870

HLA B*5301	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.251337	1.179033	-3.072304	17837.612443
HLA B*5301	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.457525	1.384894	-3.072631	28676.436215
HLA A*0202	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.358508	1.285203	-3.073305	22830.135135
HLA A*6802	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.166182	1.092768	-3.073414	14661.621016
HLA B*4601	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.328428	1.254764	-3.073664	21302.375004
HLA B*7301	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.077390	1.002409	-3.074982	11950.614910
HLA B*4801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.403494	1.328019	-3.075475	25321.770686
HLA A*3301	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.097229	1.020870	-3.076360	12509.193299
HLA B*3901	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-3.929908	0.853458	-3.076451	8509.584979
HLA B*1501	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.361661	1.285203	-3.076458	22996.486674
HLA B*4001	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.323785	1.246912	-3.076874	21075.866710
HLA B*4801	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.290500	1.212549	-3.077951	19520.920343
HLA A*0219	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.446931	1.368126	-3.078805	27985.389141
HLA B*7301	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.566017	1.486927	-3.079091	36814.367812
HLA A*0301	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.310992	1.231508	-3.079484	20464.092843
HLA B*1801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.448322	1.368668	-3.079654	28075.160346

HLA A*8001	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.408315	1.328019	-3.080296	25604.436049
HLA A*2603	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.614534	1.534232	-3.080302	41165.577495
HLA B*1509	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.476540	1.396176	-3.080364	29959.844865
HLA A*6802	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.293158	1.212549	-3.080608	19640.726896
HLA B*1509	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.317649	1.236794	-3.080855	20780.145709
HLA B*1503	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.340948	1.260066	-3.080882	21925.445740
HLA B*7301	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.559751	1.478828	-3.080923	36287.017196
HLA B*4002	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-3.600600	0.519628	-3.080972	3986.574300
HLA A*0250	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.466463	1.384894	-3.081569	29272.689022
HLA B*4002	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.560442	1.478828	-3.081614	36344.777888
HLA B*0802	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.417081	1.334657	-3.082425	26126.494543
HLA B*1503	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.070408	0.987852	-3.082556	11760.007067
HLA A*0301	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.367850	1.285203	-3.082647	23326.524390
HLA B*5301	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.479124	1.396176	-3.082948	30138.663785
HLA B*5401	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.314498	1.231508	-3.082990	20629.938300
HLA B*3801	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.451839	1.368668	-3.083171	28303.453132

HLA B*1801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.288294	1.203934	-3.084360	19422.007740
HLA A*2602	1:66-74	9	LENYIAQTR	0.964649	0.569583	-4.618690	1.534232	-3.084458	41561.427074
HLA A*8001	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.330446	1.245899	-3.084548	21401.599534
HLA B*3801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.480980	1.396176	-3.084804	30267.746422
HLA A*2601	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.370122	1.285203	-3.084919	23448.873650
HLA B*4402	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.419875	1.334657	-3.085218	26295.091170
HLA A*2403	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.419971	1.334657	-3.085314	26300.924211
HLA A*3301	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.454086	1.368668	-3.085417	28450.213645
HLA A*0206	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.224623	1.138874	-3.085750	16773.476297
HLA B*1517	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.426174	1.339576	-3.086597	26679.252063
HLA B*0801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.323419	1.236794	-3.086625	21058.087390
HLA A*3101	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.372009	1.285203	-3.086805	23550.960442
HLA B*4801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.249347	1.161468	-3.087879	17756.064338
HLA A*0216	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.335253	1.246912	-3.088342	21639.801844
HLA A*3002	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.161154	1.071973	-3.089181	14492.859816
HLA A*1101	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.343975	1.254764	-3.089210	22078.754372

HLA B*5101	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.457737	1.368126	-3.089610	28690.401885
HLA A*1101	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.326711	1.236794	-3.089917	21218.298370
HLA A*6802	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.157588	1.067238	-3.090350	14374.328750
HLA A*2501	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.430588	1.339576	-3.091012	26951.834586
HLA A*3002	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.252530	1.161468	-3.091062	17886.701615
HLA A*3002	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.351242	1.260066	-3.091175	22451.301653
HLA A*0216	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.138373	1.046875	-3.091499	13752.241329
HLA A*2902	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.351892	1.260066	-3.091826	22484.971032
HLA A*0206	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.338817	1.246912	-3.091906	21818.126144
HLA A*0201	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-3.944917	0.852998	-3.091919	8808.802843
HLA A*1101	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.352090	1.260066	-3.092024	22495.191215
HLA B*1502	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-3.869024	0.776623	-3.092401	7396.458507
HLA B*4801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.271481	1.179033	-3.092448	18684.488282
HLA A*3002	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.092042	0.999064	-3.092978	12360.659431
HLA A*6802	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-3.365139	0.271476	-3.093663	2318.137405
HLA A*0212	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.348516	1.254764	-3.093752	22310.850312

HLA A*3002	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.479516	1.384894	-3.094622	30165.904910
HLA A*0202	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.166967	1.071973	-3.094994	14688.137091
HLA A*0203	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.429813	1.334657	-3.095156	26903.761386
HLA A*6901	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.178977	1.083538	-3.095439	15100.011731
HLA A*3001	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.081619	0.985844	-3.095775	12067.556064
HLA A*2403	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.381146	1.285203	-3.095942	24051.699555
HLA A*0212	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.308674	1.212549	-3.096124	20355.114786
HLA B*4402	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.328468	1.231508	-3.096960	21304.334233
HLA B*5801	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.344106	1.246912	-3.097195	22085.444227
HLA B*4801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.343131	1.245899	-3.097233	22035.915727
HLA A*0101	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.382868	1.285203	-3.097665	24147.264690
HLA A*0211	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.329274	1.231508	-3.097766	21343.903085
HLA A*0216	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.432682	1.334657	-3.098025	27082.061730
HLA B*5401	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.436568	1.338234	-3.098334	27325.478260
HLA A*2501	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.426597	1.328019	-3.098577	26705.244439
HLA B*3901	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.467442	1.368668	-3.098774	29338.800520

HLA B*4402	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.456938	0.357949	-3.098989	2863.770775
HLA B*1801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.427142	1.328019	-3.099122	26738.783081
HLA A*6801	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.578167	1.478828	-3.099338	37858.772963
HLA B*1509	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.346425	1.246912	-3.099513	22203.686194
HLA A*2902	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.278765	1.179033	-3.099732	19000.481716
HLA A*0219	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.354561	1.254764	-3.099797	22623.580922
HLA A*2602	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.027515	0.927533	-3.099982	10654.066042
HLA B*2705	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.469146	1.368668	-3.100478	29454.098233
HLA A*6802	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.435167	1.334657	-3.100511	27237.514773
HLA A*3301	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.439394	1.338234	-3.101161	27503.895061
HLA B*4001	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.313835	1.212549	-3.101286	20598.489494
HLA B*0801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.100782	0.999064	-3.101718	12611.935031
HLA B*4501	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-3.165597	0.063696	-3.101902	1464.189923
HLA B*5701	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.362124	1.260066	-3.102058	23021.008202
HLA B*3901	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.349639	1.246912	-3.102728	22368.619203
HLA A*0206	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.116345	1.013420	-3.102925	13072.080495

HLA A*3301	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.573583	1.470113	-3.103470	37461.286573
HLA B*1801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.499696	1.396176	-3.103520	31600.654991
HLA A*2902	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.150840	1.046875	-3.103965	14152.717970
HLA B*4601	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.349959	1.245899	-3.104060	22385.082857
HLA B*5401	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.432228	1.328019	-3.104209	27053.799873
HLA A*6901	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.227146	1.122935	-3.104211	16871.217574
HLA B*0803	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.444020	1.339576	-3.104444	27798.434466
HLA A*3001	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.099038	0.994492	-3.104546	12561.410460
HLA B*1509	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.104771	1.000164	-3.104607	12728.321908
HLA B*1501	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.188361	1.083538	-3.104823	15429.829523
HLA A*8001	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.359855	1.254764	-3.105091	22901.015309
HLA B*4402	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.341916	1.236794	-3.105123	21974.369305
HLA A*6901	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.317747	1.212549	-3.105198	20784.867814
HLA A*3101	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.284786	1.179033	-3.105754	19265.768691
HLA B*5801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.083109	0.977336	-3.105773	12109.017272
HLA A*3001	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.152931	1.046875	-3.106056	14221.024805

HLA B*0801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.352806	1.245899	-3.106908	22532.339284
HLA A*0203	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.354340	1.246912	-3.107429	22612.079087
HLA A*6802	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.437889	0.330347	-3.107541	2740.871206
HLA A*0206	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.954940	0.847335	-3.107605	9014.461595
HLA B*5801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.362655	1.254764	-3.107891	23049.171704
HLA A*3301	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.362874	1.254764	-3.108110	23060.771114
HLA A*3201	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.369354	1.260066	-3.109288	23407.428471
HLA B*2705	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.348060	1.236794	-3.111266	22287.446945
HLA A*3301	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.598212	1.486927	-3.111286	39647.183423
HLA A*2601	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.371503	1.260066	-3.111437	23523.583628
HLA B*4002	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.343874	1.231508	-3.112365	22073.618894
HLA A*2403	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.359321	1.246912	-3.112410	22872.909096
HLA B*4403	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.470565	0.357949	-3.112616	2955.052941
HLA A*2902	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.447357	1.334657	-3.112700	28012.805573
HLA B*4601	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.350231	1.236794	-3.113437	22399.134960
HLA B*4001	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.359343	1.245899	-3.113444	22874.022783

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HLA A*2402	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.053764
	0.940065	-3.113699	11317.847322

HLA B*7301	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.452530
	1.338234	-3.114296	28348.505803

HLA B*4002	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.602070
	1.486927	-3.115144	40000.939748

HLA B*4501	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-3.868253
	0.751912	-3.116341	7383.345546

HLA B*4402	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.330352
	1.212549	-3.117803	21396.968824

HLA A*3001	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.117068
	0.999064	-3.118005	13093.879952

HLA A*2402	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.446062
	1.328019	-3.118043	27929.427962

HLA A*0250	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.514228
	1.396176	-3.118052	32675.906835

HLA A*0211	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.256940
	1.138874	-3.118067	18069.254944

HLA B*2705	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.372974
	1.254764	-3.118210	23603.383424

HLA A*0301	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.355405
	1.236794	-3.118611	22667.562010

HLA A*3101	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.331393
	1.212549	-3.118844	21448.309887

HLA B*0702	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.202641
	1.083538	-3.119103	15945.615866

HLA B*4501	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.457699
	1.338234	-3.119465	28687.918603

HLA A*1101	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.298528
	1.179033	-3.119496	19885.132060

HLA A*0301	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.366553
	1.246912	-3.119642	23256.969258
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HLA A*0101 1:37-45 9 TGQACQIQM 1.304282 -0.067488 -4.356469 1.236794 -3.119675 22723.181070

HLA B*5101 1:1-9 9 VRIKIFMLV 0.881917 0.241018 -4.242719 1.122935 -3.119784 17487.141040

HLA B*1517 1:35-43 9 TDTGQACQI 1.187370 0.059542 -4.366708 1.246912 -3.119797 23265.274704

HLA B*5801 1:132-140 9 FDWDQAYRK 1.061895 0.169613 -4.351425 1.231508 -3.119917 22460.777458

HLA B*1501 1:15-23 9 LCCSGVATA 1.215808 -0.196223 -4.139581 1.019585 -3.119997 13790.535169

HLA A*2602 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -3.887491 0.767355 -3.120136 7717.751261

HLA B*1501 1:103-111 9 AIPPRGTQA 1.171695 -0.095962 -4.196096 1.075733 -3.120362 15707.086391

HLA B*1509 1:212-220 9 GPTQVLVPR 0.849469 0.485188 -4.455197 1.334657 -3.120540 28523.107482

HLA A*0216 1:72-80 9 QTRDKFLSA 1.401913 -0.147149 -4.375474 1.254764 -3.120710 23739.639156

HLA B*5401 1:79-87 9 SAATSSTPR 0.650358 0.717768 -4.488912 1.368126 -3.120786 30825.629075

HLA A*3301 1:68-76 9 NYIAQTRDK 0.633507 0.291193 -4.045658 0.924700 -3.120958 11108.568764

HLA A*0201 1:37-45 9 TGQACQIQM 1.304282 -0.067488 -4.358097 1.236794 -3.121303 22808.531376

HLA B*0801 1:35-43 9 TDTGQACQI 1.187370 0.059542 -4.368527 1.246912 -3.121615 23362.896564

HLA B*5301 1:207-215 9 LPEAAGPTQ 1.054236 -0.218984 -3.956979 0.835252 -3.121727 9056.891100

HLA B*4403 1:150-158 9 ADTDPLPVV 1.257750 0.027453 -4.406931 1.285203 -3.121728 25522.979288

HLA A*0216 1:215-223 9 QVLVPRSAI 0.852479 0.308989 -4.283215 1.161468 -3.121747 19196.167743

HLA B*0702	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.301310	1.179033	-3.122278	20012.911266
HLA B*4501	1:12-20	9	VVLLCCSGV	1.181551	0.297277	-4.601640	1.478828	-3.122812	39961.358025
HLA A*3002	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.378169	1.254764	-3.123405	23887.404988
HLA A*6801	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.461677	1.338234	-3.123443	28951.876537
HLA A*0216	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.355823	1.231508	-3.124315	22689.400485
HLA A*3001	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.127025	1.002409	-3.124617	13397.552647
HLA A*8001	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.459553	1.334657	-3.124896	28810.631896
HLA A*0212	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.247838	1.122935	-3.124903	17694.501853
HLA A*0219	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.361699	1.236794	-3.124905	22998.477295
HLA B*3501	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.372013	1.246912	-3.125102	23551.215260
HLA A*0219	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.459898	1.334657	-3.125242	28833.552770
HLA B*4002	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.595635	1.470113	-3.125522	39412.588138
HLA A*6901	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.329741	1.203934	-3.125808	21366.893620
HLA A*6901	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.218754	1.092768	-3.125986	16548.325921
HLA A*2602	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.380843	1.254764	-3.126079	24034.920314
HLA B*0801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.411757	1.285203	-3.126554	25808.169968

HLA B*4403	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.522923	1.396176	-3.126747	33336.737330
HLA A*3002	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.494988	1.368126	-3.126862	31259.909506
HLA A*2902	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.288351	1.161468	-3.126883	19424.529606
HLA B*1501	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.148030	1.020870	-3.127160	14061.442272
HLA A*2602	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.210996	1.083538	-3.127458	16255.340321
HLA B*5801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.288964	1.161468	-3.127496	19451.976046
HLA A*0203	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.128097	1.000164	-3.127933	13430.643996
HLA B*1502	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.364810	1.236794	-3.128016	23163.799703
HLA B*0702	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.364927	1.236794	-3.128133	23170.066230
HLA B*4601	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.267095	1.138874	-3.128221	18496.719887
HLA A*0201	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-3.992964	0.864656	-3.128308	9839.292199
HLA B*4402	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.374403	1.245899	-3.128504	23681.147792
HLA B*5701	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.375516	1.246912	-3.128605	23741.950987
HLA A*2601	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.375690	1.246912	-3.128779	23751.457547
HLA B*4501	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.383996	1.254764	-3.129232	24210.050507
HLA A*0101	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.361095	1.231508	-3.129587	22966.523776

HLA A*3201	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.497887	1.368126	-3.129761	31469.292632
HLA B*3901	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.415180	1.285203	-3.129977	26012.399176
HLA A*0219	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.342624	1.212549	-3.130074	22010.181004
HLA B*3801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.459113	1.328019	-3.131094	28781.500379
HLA A*0206	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.203088	1.071973	-3.131115	15962.014456
HLA B*1801	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.362702	1.231508	-3.131194	23051.665708
HLA B*4801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.416588	1.285203	-3.131384	26096.829695
HLA B*2705	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.203360	1.071973	-3.131388	15972.034516
HLA A*0219	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.292911	1.161468	-3.131443	19629.573378
HLA B*1801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.368470	1.236794	-3.131676	23359.863385
HLA A*2402	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.470558	1.338234	-3.132324	29550.019472
HLA A*6802	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.208651	1.076055	-3.132597	16167.813106
HLA A*0206	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.501686	1.368668	-3.133018	31745.787014
HLA A*1101	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.461324	1.328019	-3.133305	28928.392100
HLA A*0202	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-3.813552	0.680076	-3.133476	6509.572741
HLA A*0203	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-3.821978	0.688457	-3.133521	6637.090471

HLA B*4001	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.388631	1.254764	-3.133867	24469.845618
HLA A*1101	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.419203	1.285203	-3.133999	26254.438119
HLA B*0702	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.380070	1.245899	-3.134171	23992.179723
HLA B*1801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.388946	1.254764	-3.134182	24487.590856
HLA A*2301	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.462325	1.328019	-3.134306	28995.137724
HLA B*5801	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.347306	1.212549	-3.134757	22248.776721
HLA B*3501	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.219055	1.083538	-3.135517	16559.789039
HLA B*3901	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.381576	1.245899	-3.135677	24075.522761
HLA B*1517	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.023188	0.886699	-3.136489	10548.425335
HLA A*3201	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.341183	1.203934	-3.137250	21937.310372
HLA A*2601	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.374304	1.236794	-3.137510	23675.767683
HLA B*4001	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.397705	1.260066	-3.137639	24986.472047
HLA A*0101	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.384656	1.246912	-3.137744	24246.882102
HLA B*5701	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.423455	1.285203	-3.138252	26512.781707
HLA A*2603	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.350990	1.212549	-3.138441	22438.309295
HLA A*2501	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.473177	1.334657	-3.138521	29728.804646

HLA B*4801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.141517	1.002409	-3.139109	13852.147132
HLA B*1501	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.386108	1.246912	-3.139196	24328.082645
HLA A*0201	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.370707	1.231508	-3.139199	23480.482030
HLA A*2403	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.376193	1.236794	-3.139399	23778.970920
HLA A*2902	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.425941	1.285203	-3.140738	26664.967040
HLA B*4601	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.372246	1.231508	-3.140738	23563.832175
HLA A*2902	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.080924	0.940065	-3.140859	12048.247422
HLA B*0803	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.372537	1.231508	-3.141029	23579.644715
HLA A*2501	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.372923	1.231508	-3.141414	23600.574374
HLA A*3002	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-3.988843	0.847335	-3.141508	9746.369259
HLA B*4801	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.373089	1.231508	-3.141581	23609.641146
HLA B*0801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.217420	1.075733	-3.141686	16497.553989
HLA B*1502	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.537922	1.396176	-3.141747	34508.191971
HLA B*3901	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.470170	1.328019	-3.142151	29523.653957
HLA A*2501	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.388074	1.245899	-3.142176	24438.491863
HLA A*3002	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.379010	1.236794	-3.142216	23933.713517

HLA A*0219	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.373820	1.231508	-3.142312	23649.397224
HLA B*7301	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.612478	1.470113	-3.142365	40971.174417
HLA A*0301	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.321445	1.179033	-3.142413	20962.610082
HLA B*0702	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.427659	1.285203	-3.142455	26770.625874
HLA A*0202	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.029202	0.886699	-3.142503	10695.530112
HLA A*3301	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.374029	1.231508	-3.142521	23660.786681
HLA A*0211	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.510830	1.368126	-3.142704	32421.290221
HLA B*0803	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.477888	1.334657	-3.143232	30053.023060
HLA A*0201	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.390259	1.246912	-3.143348	24561.756552
HLA B*1517	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.478076	1.334657	-3.143420	30066.032557
HLA A*0219	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.348154	1.203934	-3.144221	22292.270372
HLA B*5701	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.399143	1.254764	-3.144379	25069.335660
HLA B*5101	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.391758	1.246912	-3.144847	24646.678153
HLA A*2403	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.399772	1.254764	-3.145008	25105.708805
HLA A*2501	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.430642	1.285203	-3.145439	26955.188342
HLA A*0206	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-3.954606	0.809025	-3.145582	9007.539307

HLA A*0201	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.358887	1.212549	-3.146337	22850.028666
HLA A*3001	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.159777	1.013420	-3.146357	14446.987374
HLA B*1801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.167592	1.020870	-3.146722	14709.288984
HLA B*3801	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.515026	1.368126	-3.146900	32736.064975
HLA A*2501	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.308486	1.161468	-3.147018	20346.307179
HLA B*4403	1:190-198	9	FAVTNDGVI	1.178752	0.308175	-4.633962	1.486927	-3.147036	43048.904472
HLA A*0212	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.378940	1.231508	-3.147432	23929.829470
HLA B*1517	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.432896	1.285203	-3.147692	27095.397509
HLA A*0211	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.395001	1.246912	-3.148089	24831.370116
HLA B*1503	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-3.934734	0.786460	-3.148275	8604.670051
HLA B*4601	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.395558	1.246912	-3.148646	24863.227921
HLA A*2501	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.408872	1.260066	-3.148806	25637.285671
HLA A*0219	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.396020	1.246912	-3.149109	24889.739985
HLA A*8001	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.221108	1.071973	-3.149136	16638.273147
HLA A*0202	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-3.897528	0.748062	-3.149466	7898.193643
HLA A*2601	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.362108	1.212549	-3.149559	23020.136431

HLA B*5101	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.409713	1.260066	-3.149647	25686.986549
HLA A*2601	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.381524	1.231508	-3.150016	24072.657522
HLA A*2602	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.488299	1.338234	-3.150065	30782.134584
HLA A*2603	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.478419	1.328019	-3.150400	30089.789408
HLA B*3501	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.410575	1.260066	-3.150509	25738.036906
HLA B*5101	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.312043	1.161468	-3.150575	20513.639414
HLA B*1801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.079082	0.927533	-3.151549	11997.254766
HLA A*0201	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.227635	1.075733	-3.151902	16890.212714
HLA A*2301	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.389002	1.236794	-3.152209	24490.770466
HLA A*3101	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.399429	1.246912	-3.152518	25085.887046
HLA B*4402	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.356528	1.203934	-3.152594	22726.254525
HLA B*3501	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.437839	1.285203	-3.152636	27405.570252
HLA A*0219	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.155158	1.002409	-3.152750	14294.145739
HLA B*5801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.356751	1.203934	-3.152817	22737.937446
HLA B*3901	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.228890	1.076055	-3.152835	16939.077073
HLA A*0206	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.733205	0.579719	-3.153486	5410.093816

HLA A*0301	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.366079	1.212549	-3.153529	23231.567979
HLA B*0802	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.408477	1.254764	-3.153713	25613.995517
HLA A*3101	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.229085	1.075247	-3.153837	16946.684779
HLA A*3002	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.550367	1.396176	-3.154192	35511.370006
HLA B*4001	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.391025	1.236794	-3.154232	24605.112473
HLA B*1503	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.174006	1.019585	-3.154421	14928.142581
HLA B*0801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.172737	1.017829	-3.154908	14884.596037
HLA B*1502	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.082893	0.927533	-3.155360	12102.991995
HLA B*1502	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.524044	1.368668	-3.155376	33422.874443
HLA A*0301	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.317002	1.161468	-3.155535	20749.253666
HLA A*2301	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.387076	1.231508	-3.155568	24382.367358
HLA B*2705	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.368130	1.212549	-3.155580	23341.546301
HLA A*2601	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.317282	1.161468	-3.155814	20762.615855
HLA B*4801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.359798	1.203934	-3.155865	22898.042095
HLA A*0201	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.317360	1.161468	-3.155892	20766.322860
HLA B*5401	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.441278	1.285203	-3.156075	27623.486315

HLA B*3801 1:4-12 9 KIFMLVTAV 1.048201 0.290033 -4.494960 1.338234 -3.156726 31257.880220

HLA A*0206 1:212-220 9 GPTQVLVPR 0.849469 0.485188 -4.491466 1.334657 -3.156809 31007.434747

HLA B*5401 1:46-54 9 SDPAYNINI 1.266370 0.129806 -4.553034 1.396176 -3.156858 35730.088582

HLA A*2402 1:62-70 9 DQKSLENYI 1.150042 0.062507 -4.369640 1.212549 -3.157091 23422.882624

HLA B*4402 1:96-104 9 TSATYQSAI 0.928477 0.250556 -4.336155 1.179033 -3.157123 21684.803039

HLA B*5701 1:96-104 9 TSATYQSAI 0.928477 0.250556 -4.336827 1.179033 -3.157795 21718.380349

HLA A*3101 1:3-11 9 IKIFMLVTA 1.316552 -0.112618 -4.361770 1.203934 -3.157836 23002.210174

HLA A*3101 1:8-16 9 LVTAVVLLC 0.979168 0.067707 -4.204732 1.046875 -3.157858 16022.575964

HLA A*2402 1:79-87 9 SAATSSTPR 0.650358 0.717768 -4.526781 1.368126 -3.158655 33634.188010

HLA B*5801 1:95-103 9 ITSATYQSA 0.951011 -0.171324 -3.938470 0.779687 -3.158783 8679.004288

HLA B*4501 1:190-198 9 FAVTNDGVI 1.178752 0.308175 -4.645850 1.486927 -3.158924 44243.604141

HLA B*1501 1:33-41 9 KGTDTGQAC 1.197565 -0.058691 -4.298124 1.138874 -3.159251 19866.637532

HLA A*0203 1:37-45 9 TGQACQIQM 1.304282 -0.067488 -4.396215 1.236794 -3.159422 24900.918506

HLA B*1801 1:62-70 9 DQKSLENYI 1.150042 0.062507 -4.372100 1.212549 -3.159551 23555.929882

HLA B*1501 1:220-228 9 RSAIDSMLA 1.010961 -0.163626 -4.007319 0.847335 -3.159984 10169.959220

HLA B*4403 1:12-20 9 VVLLCCSGV 1.181551 0.297277 -4.638830 1.478828 -3.160002 43534.166782

HLA B*1501	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.087723	0.927533	-3.160190	12238.361777
HLA B*4402	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.420281	1.260066	-3.160215	26319.712550
HLA A*0301	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.364171	1.203934	-3.160237	23129.739472
HLA A*8001	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.445526	1.285203	-3.160323	27894.999514
HLA A*6802	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.162846	1.002409	-3.160437	14549.421332
HLA A*2301	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.498975	1.338234	-3.160741	31548.215046
HLA B*4402	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.415552	1.254764	-3.160788	26034.643104
HLA B*5101	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.393011	1.231508	-3.161503	24717.848692
HLA A*6802	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.048524	0.886699	-3.161826	11182.128519
HLA B*4801	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.408841	1.246912	-3.161930	25635.482701
HLA B*4601	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.365919	1.203934	-3.161985	23223.023297
HLA B*3901	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-3.755069	0.592876	-3.162193	5689.434523
HLA A*2602	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.531057	1.368126	-3.162931	33966.985841
HLA B*2705	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.448376	1.285203	-3.163173	28078.653884
HLA A*2602	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.375878	1.212549	-3.163329	23761.739192
HLA A*8001	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.184456	1.020870	-3.163587	15291.718115

HLA A*0216	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.376191	1.212549	-3.163641	23778.842278
HLA B*3801	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.498364	1.334657	-3.163707	31503.871429
HLA B*4501	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.559974	1.396176	-3.163799	36305.671320
HLA A*2403	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.164194	1.000164	-3.164030	14594.671527
HLA B*0802	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.400896	1.236794	-3.164102	25170.714350
HLA A*2403	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.303216	1.138874	-3.164342	20100.909216
HLA B*1801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.424506	1.260066	-3.164439	26576.973041
HLA B*4001	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.343718	1.179033	-3.164686	22065.738856
HLA A*0250	1:149-157	9	QADTDPLPV	0.679726	0.062986	-3.907621	0.742712	-3.164909	8083.904325
HLA A*2403	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.344254	1.179033	-3.165221	22092.972738
HLA A*0301	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.186153	1.020870	-3.165283	15351.563448
HLA A*0211	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.867064	0.701666	-3.165399	7363.161985
HLA A*2403	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.377958	1.212549	-3.165408	23875.777279
HLA A*3101	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.249060	1.083538	-3.165522	17744.349087
HLA A*2902	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-3.973769	0.808230	-3.165539	9413.877998
HLA A*0101	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.288494	1.122935	-3.165559	19430.940821

HLA B*0802	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.411616	1.245899	-3.165718	25799.794167
HLA B*5101	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.344985	1.179033	-3.165952	22130.174911
HLA A*3201	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.494144	1.328019	-3.166125	31199.256983
HLA B*5101	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.412742	1.245899	-3.166843	25866.736824
HLA B*5101	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.421717	1.254764	-3.166953	26406.854783
HLA B*0702	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.427276	1.260066	-3.167209	26747.029622
HLA B*2705	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.427553	1.260066	-3.167487	26764.109492
HLA B*5101	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.371616	1.203934	-3.167683	23529.692900
HLA B*1801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.453038	1.285203	-3.167834	28381.651416
HLA A*6802	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-3.870908	0.702905	-3.168003	7428.619470
HLA A*2403	1:49-57	9	AYNINISLP	0.584960	0.117828	-3.871030	0.702788	-3.168243	7430.709540
HLA A*0216	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.372608	1.203934	-3.168674	23583.471924
HLA B*4801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.423648	1.254764	-3.168884	26524.545675
HLA B*5401	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.096590	0.927533	-3.169057	12490.799684
HLA A*0211	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.537779	1.368668	-3.169111	34496.806035
HLA B*3501	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.373096	1.203934	-3.169163	23610.024326

HLA A*6802	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.400748	1.231508	-3.169239	25162.137053
HLA B*4501	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-3.415531	0.245175	-3.170356	2603.340227
HLA B*0802	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.401997	1.231508	-3.170489	25234.659530
HLA A*2602	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.455735	1.285203	-3.170532	28558.465648
HLA A*0301	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.243226	1.071973	-3.171254	17507.587339
HLA B*7301	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-3.919510	0.748062	-3.171448	8308.250053
HLA B*0803	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.332965	1.161468	-3.171497	21526.076592
HLA A*3201	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-3.605971	0.434427	-3.171544	4036.182411
HLA B*1503	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.126241	0.954583	-3.171658	13373.366427
HLA A*2902	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.375702	1.203934	-3.171768	23752.100020
HLA A*2902	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.144374	0.972498	-3.171876	13943.572835
HLA B*4001	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.376019	1.203934	-3.172086	23769.453347
HLA A*2403	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.432635	1.260066	-3.172569	27079.131670
HLA B*7301	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.557888	1.384894	-3.172994	36131.677810
HLA B*4002	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.512715	1.339576	-3.173138	32562.263082
HLA B*7301	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.513659	1.339576	-3.174083	32633.155751

HLA A*0101	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.386686	1.212549	-3.174137	24360.480807
HLA A*3101	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.192172	1.017829	-3.174343	15565.819585
HLA B*5401	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.559260	1.384894	-3.174366	36246.011856
HLA A*3002	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.459644	1.285203	-3.174441	28816.711168
HLA B*0803	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.246466	1.071973	-3.174494	17638.686499
HLA B*0802	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.387168	1.212549	-3.174618	24387.512231
HLA A*0212	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.177116	1.002409	-3.174708	15035.452140
HLA A*6901	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.069891	0.895143	-3.174748	11746.018920
HLA A*0101	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.378763	1.203934	-3.174830	23920.122110
HLA A*2603	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.560026	1.384894	-3.175132	36309.992589
HLA A*2301	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.543634	1.368126	-3.175508	34965.021805
HLA B*4501	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.645672	1.470113	-3.175559	44225.417052
HLA A*0212	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.354658	1.179033	-3.175625	22628.599513
HLA A*3301	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.388413	1.212549	-3.175863	24457.537454
HLA A*0212	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.412908	1.236794	-3.176115	25876.674201
HLA A*6802	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.195818	1.019585	-3.176234	15697.062706

HLA A*2402	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.436389	1.260066	-3.176323	27314.245656
HLA B*5301	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.338061	1.161468	-3.176593	21780.152395
HLA A*8001	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.413533	1.236794	-3.176740	25913.938331
HLA A*0101	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.223669	1.046875	-3.176794	16736.675212
HLA A*0202	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.338277	1.161468	-3.176809	21790.995289
HLA B*4501	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.517129	1.339576	-3.177553	32894.952461
HLA A*0212	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.424618	1.246912	-3.177707	26583.875304
HLA B*3501	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.433001	1.254764	-3.178237	27101.994551
HLA A*0203	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.410122	1.231508	-3.178614	25711.177625
HLA B*1502	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.043276	0.864656	-3.178620	11047.798127
HLA A*0219	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.357874	1.179033	-3.178841	22796.812183
HLA B*4801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.301853	1.122935	-3.178918	20037.936722
HLA A*0216	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.416242	1.236794	-3.179449	26076.084344
HLA B*1517	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.383418	1.203934	-3.179484	24177.852409
HLA A*2902	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.426512	1.246912	-3.179600	26700.043939
HLA A*2301	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.383545	1.203934	-3.179611	24184.916614

HLA B*1503	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.255406	1.075247	-3.180159	18005.535070
HLA A*0202	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.548913	1.368668	-3.180245	35392.651211
HLA B*3501	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.392912	1.212549	-3.180363	24712.233055
HLA B*4601	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.393189	1.212549	-3.180640	24728.013564
HLA A*0202	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.417539	1.236794	-3.180745	26154.070666
HLA B*1501	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.412695	1.231508	-3.181187	25863.938252
HLA B*0802	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.360296	1.179033	-3.181264	22924.318845
HLA B*4801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.441499	1.260066	-3.181433	27637.537247
HLA A*3101	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.304407	1.122935	-3.181472	20156.117946
HLA B*4001	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.304513	1.122935	-3.181577	20161.025449
HLA B*0802	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.466841	1.285203	-3.181638	29298.196411
HLA A*8001	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.428657	1.246912	-3.181745	26832.247788
HLA A*1101	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.428786	1.246912	-3.181875	26840.232748
HLA B*5301	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.550675	1.368126	-3.182549	35536.545674
HLA B*2705	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.344151	1.161468	-3.182683	22087.714460
HLA A*0211	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.185373	1.002409	-3.182964	15324.015509

HLA A*2601	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.387012	1.203934	-3.183079	24378.806159
HLA B*1503	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-3.775975	0.592876	-3.183099	5970.006737
HLA B*1502	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.395673	1.212549	-3.183123	24869.819652
HLA B*5401	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.202773	1.019585	-3.183188	15950.447383
HLA A*0250	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.551350	1.368126	-3.183223	35591.763927
HLA A*0211	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.183460	1.000164	-3.183296	15256.682277
HLA A*2602	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.522954	1.339576	-3.183377	33339.081937
HLA B*5801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.323113	1.138874	-3.184240	21043.282747
HLA A*0301	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.231580	1.046875	-3.184705	17044.328834
HLA B*3801	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.524319	1.339576	-3.184742	33444.036383
HLA A*2602	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.445000	1.260066	-3.184934	27861.216404
HLA A*8001	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.364100	1.179033	-3.185068	23125.985897
HLA B*1502	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.570272	1.384894	-3.185378	37176.822197
HLA A*0216	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.050230	0.864656	-3.185574	11226.133579
HLA A*6801	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.656108	1.470113	-3.185995	45301.058461
HLA B*5301	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.417542	1.231508	-3.186034	26154.212157

HLA B*5701	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.417575	1.231508	-3.186066	26156.193112
HLA A*6802	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.185349	0.999064	-3.186285	15323.186520
HLA B*7301	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.555132	1.368668	-3.186464	35903.119370
HLA B*3901	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.417979	1.231508	-3.186471	26180.542801
HLA B*5701	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.390551	1.203934	-3.186617	24578.238751
HLA A*2402	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.111430	0.924700	-3.186730	12924.971403
HLA A*0206	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.181336	0.994492	-3.186844	15182.251018
HLA B*5401	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.555623	1.368668	-3.186955	35943.736794
HLA B*5401	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.186331	0.999064	-3.187268	15357.876565
HLA B*4403	1:147-155	9	LWQADTDPL	0.954861	0.515252	-4.657574	1.470113	-3.187461	45454.242865
HLA B*1503	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.434599	1.246912	-3.187687	27201.878937
HLA A*0206	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.424917	1.236794	-3.188123	26602.146189
HLA B*5301	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.527935	1.339576	-3.188358	33723.647771
HLA A*1101	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.349851	1.161468	-3.188383	22379.512912
HLA A*2402	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.434432	1.245899	-3.188534	27191.432644
HLA B*0802	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.435539	1.246912	-3.188627	27260.806332

HLA A*0201	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.261165	1.071973	-3.189192	18245.871820
HLA B*4601	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.350790	1.161468	-3.189323	22427.993622
HLA A*0250	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.449520	1.260066	-3.189454	28152.727891
HLA B*5801	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.203337	1.013420	-3.189917	15971.170470
HLA B*3801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.426770	1.236794	-3.189977	26715.937538
HLA B*0803	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.436150	1.245899	-3.190251	27299.177576
HLA B*0702	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.421787	1.231508	-3.190279	26411.140875
HLA A*2301	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.525033	1.334657	-3.190376	33499.083909
HLA A*2602	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.587170	1.396176	-3.190994	38651.803280
HLA A*0203	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.267104	1.076055	-3.191050	18497.120152
HLA B*5701	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.275379	1.083538	-3.191841	18852.936459
HLA B*0702	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.395966	1.203934	-3.192033	24886.643211
HLA B*3501	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.285209	1.092768	-3.192442	19284.538450
HLA A*6802	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.268718	1.075733	-3.192985	18565.994345
HLA B*4001	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.424618	1.231508	-3.193110	26583.875304
HLA A*6802	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-3.881871	0.688457	-3.193414	7618.523460

HLA A*2403	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.211348	1.017829	-3.193520	16268.536613
HLA B*0802	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.454518	1.260066	-3.194452	28478.547645
HLA A*0202	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.896212	0.701666	-3.194546	7874.301975
HLA A*0211	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.529365	1.334657	-3.194709	33834.937688
HLA A*0250	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.208449	1.013420	-3.195029	16160.292773
HLA A*3301	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.003457	0.808230	-3.195227	10079.910085
HLA A*6901	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.082052	0.886699	-3.195353	12079.574327
HLA B*5701	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.407921	1.212549	-3.195371	25581.175738
HLA A*2301	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.441619	1.245899	-3.195721	27645.163616
HLA A*0212	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.334847	1.138874	-3.195973	21619.558393
HLA B*0801	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.427797	1.231508	-3.196289	26779.171979
HLA A*2403	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.400242	1.203934	-3.196309	25132.887326
HLA B*1801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.442547	1.245899	-3.196649	27704.301902
HLA B*4601	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.217636	1.020870	-3.196766	16505.767027
HLA A*0216	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.199474	1.002409	-3.197066	15829.754948
HLA A*8001	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.428650	1.231508	-3.197142	26831.812313

HLA A*6802	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.154157	0.956718	-3.197439	14261.241199
HLA A*3001	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.273163	1.075247	-3.197916	18757.002636
HLA A*0211	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.410524	1.212549	-3.197974	25734.973810
HLA A*2902	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.410531	1.212549	-3.197981	25735.391484
HLA A*0201	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.217922	1.019585	-3.198338	16516.664536
HLA B*3901	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.402364	1.203934	-3.198430	25255.965126
HLA A*3001	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.275706	1.076055	-3.199651	18867.118720
HLA B*1501	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.120790	0.920569	-3.200221	13206.567004
HLA A*2902	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.283868	1.083538	-3.200330	19225.059524
HLA B*0803	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.485665	1.285203	-3.200462	30596.021678
HLA B*3501	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.220356	1.019585	-3.200772	16609.494476
HLA B*3501	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.199963	0.999064	-3.200899	15847.577516
HLA A*0219	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.221080	1.019585	-3.201496	16637.193048
HLA A*2402	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.010040	0.808230	-3.201810	10233.870453
HLA A*3001	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.010153	0.808230	-3.201923	10236.528275
HLA B*1509	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.324958	1.122935	-3.202023	21132.838608

HLA B*7301	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.598215	1.396176	-3.202039	39647.397910
HLA A*2602	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.531125	1.328019	-3.203106	33972.315230
HLA A*2602	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.175979	0.972498	-3.203481	14996.135014
HLA B*0702	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.279249	1.075733	-3.203515	19021.668363
HLA B*2705	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.160623	0.956718	-3.203905	14475.151167
HLA B*1509	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.489243	1.285203	-3.204040	30849.151661
HLA B*2705	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.383133	1.179033	-3.204101	24162.030848
HLA B*2705	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.451576	1.246912	-3.204665	28286.309050
HLA B*1503	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.199272	0.994492	-3.204780	15822.391861
HLA A*2403	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.436650	1.231508	-3.205142	27330.652724
HLA A*6801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-3.786660	0.581216	-3.205444	6118.715762
HLA A*3001	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.272952	1.067238	-3.205714	18747.872262
HLA A*2603	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.545722	1.339576	-3.206146	35133.587306
HLA A*8001	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.418902	1.212549	-3.206353	26236.264111
HLA A*8001	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.410719	1.203934	-3.206785	25746.531944
HLA A*0301	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.282225	1.075247	-3.206978	19152.497005

HLA A*0219	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.330409	1.122935	-3.207473	21399.747130
HLA B*1509	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.439039	1.231508	-3.207531	27481.436489
HLA A*0202	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.454945	1.246912	-3.208034	28506.601426
HLA B*0702	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.420713	1.212549	-3.208164	26345.924752
HLA B*3501	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.347633	1.138874	-3.208759	22265.513528
HLA A*0202	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-3.985840	0.776623	-3.209218	9679.216846
HLA B*0702	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.456162	1.246912	-3.209251	28586.598155
HLA B*1501	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.333132	1.122935	-3.210197	21534.346392
HLA A*0250	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.414598	1.203934	-3.210664	25977.522976
HLA B*0803	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.138247	0.927533	-3.210714	13748.224418
HLA A*3101	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.135874	0.924700	-3.211174	13673.309139
HLA B*3901	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.278490	1.067238	-3.211252	18988.459033
HLA A*2602	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.596340	1.384894	-3.211446	39476.605393
HLA A*2501	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.458472	1.246912	-3.211560	28739.024363
HLA B*1501	1:148-156	9	WQADTDPLP	0.614046	0.092801	-3.918607	0.706847	-3.211760	8291.008430
HLA B*1501	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.230224	1.017829	-3.212395	16991.207811

HLA B*1801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.391874	1.179033	-3.212841	24653.212473
HLA A*0101	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.233805	1.020870	-3.212935	17131.873806
HLA A*2403	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.336600	1.122935	-3.213664	21706.986418
HLA A*0211	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.450582	1.236794	-3.213789	28221.653145
HLA A*0216	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.393138	1.179033	-3.214105	24725.070671
HLA B*5101	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.427160	1.212549	-3.214611	26739.940337
HLA B*1801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.068265	0.853458	-3.214807	11702.128222
HLA B*3501	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.460847	1.245899	-3.214949	28896.640162
HLA B*1503	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.307868	1.092768	-3.215100	20317.379020
HLA A*3201	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.462041	1.246912	-3.215129	28976.163817
HLA B*5801	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.307945	1.092768	-3.215178	20321.006531
HLA B*7301	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.136019	0.920569	-3.215450	13677.896115
HLA B*0803	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.452274	1.236794	-3.215480	28331.794243
HLA A*0250	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.584520	1.368668	-3.215851	38416.654467
HLA B*4002	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.420145	1.203934	-3.216211	26311.455415
HLA A*6901	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-3.864668	0.648272	-3.216395	7322.643312

HLA B*4001	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.377896	1.161468	-3.216429	23872.419217
HLA B*5401	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.471601	1.254764	-3.216837	29621.083660
HLA A*0219	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.021510	0.804086	-3.217424	10507.758936
HLA A*2902	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.310217	1.092768	-3.217450	20427.591638
HLA A*2403	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.293188	1.075733	-3.217455	19642.108248
HLA B*4501	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.421606	1.203934	-3.217673	26400.141303
HLA A*0206	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.449412	1.231508	-3.217904	28145.722818
HLA A*0101	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.380690	1.161468	-3.219222	24026.470093
HLA B*4501	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.174072	0.954256	-3.219816	14930.404020
HLA A*6901	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.240066	1.019585	-3.220482	17380.659209
HLA B*5301	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.558868	1.338234	-3.220634	36213.280130
HLA A*3002	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-3.988392	0.767355	-3.221037	9736.250974
HLA B*5301	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.922822	0.701666	-3.221157	8371.867242
HLA B*5801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.344181	1.122935	-3.221246	22089.267912
HLA A*2501	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.458141	1.236794	-3.221347	28717.110756
HLA A*6801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.481607	1.260066	-3.221541	30311.497968

HLA B*1509	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.467908	1.245899	-3.222009	29370.243849
HLA B*3901	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.482270	1.260066	-3.222204	30357.776140
HLA A*0216	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.298543	1.076055	-3.222488	19885.777528
HLA B*7301	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.243438	1.020870	-3.222568	17516.113684
HLA B*1503	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.236100	1.013420	-3.222680	17222.663389
HLA A*0211	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.031707	0.809025	-3.222682	10757.388808
HLA A*2601	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.269792	1.046875	-3.222917	18611.952199
HLA B*3901	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.435522	1.212549	-3.222973	27259.774006
HLA B*5101	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.459828	1.236794	-3.223034	28828.873560
HLA B*4002	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.469641	1.245899	-3.223743	29487.738888
HLA B*1517	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.151291	0.927533	-3.223758	14167.426017
HLA B*1517	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.455293	1.231508	-3.223785	28529.434764
HLA A*0101	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.362693	1.138874	-3.223819	23051.166886
HLA A*6901	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.270830	1.046875	-3.223956	18656.509811
HLA A*8001	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.271023	1.046875	-3.224148	18664.787878
HLA A*2402	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.428598	1.203934	-3.224665	26828.619046

HLA A*0202	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.456219	1.231508	-3.224711	28590.310004
HLA A*0216	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.244302	1.019585	-3.224718	17551.020185
HLA B*5101	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.202679	0.977336	-3.225343	15946.996150
HLA B*5301	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.553516	1.328019	-3.225496	35769.736206
HLA B*4501	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.593976	1.368126	-3.225850	39262.343523
HLA B*5701	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.388286	1.161468	-3.226818	24450.393619
HLA B*1801	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.473812	1.246912	-3.226900	29772.260350
HLA A*0202	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.241192	1.013420	-3.227772	17425.756759
HLA A*2403	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.295502	1.067238	-3.228265	19747.055322
HLA A*0301	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.367274	1.138874	-3.228401	23295.627362
HLA B*4402	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-3.980544	0.751912	-3.228632	9561.906229
HLA B*4002	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.557009	1.328019	-3.228990	36058.646546
HLA A*0219	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.276234	1.046875	-3.229359	18890.098233
HLA B*1501	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.322272	1.092768	-3.229505	21002.566814
HLA A*2301	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.037787	0.808230	-3.229557	10909.060065
HLA A*0202	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.564596	1.334657	-3.229939	36694.071985

HLA B*0803	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.490432	1.260066	-3.230366	30933.713937
HLA B*0803	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.477423	1.246912	-3.230511	30020.848758
HLA B*1517	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.323339	1.092768	-3.230571	21054.214401
HLA B*1502	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.476796	1.245899	-3.230897	29977.516734
HLA A*2301	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.409986	1.179033	-3.230953	25703.111403
HLA B*4601	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.353922	1.122935	-3.230987	22590.315034
HLA A*0301	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.249163	1.017829	-3.231334	17748.573368
HLA A*3101	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.370263	1.138874	-3.231389	23456.486234
HLA B*1801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.393058	1.161468	-3.231590	24720.523253
HLA A*6901	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.307525	1.075247	-3.232277	20301.337800
HLA A*3101	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.209962	0.977336	-3.232626	16216.692917
HLA B*3901	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.487596	1.254764	-3.232832	30732.382980
HLA B*1502	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.568200	1.334657	-3.233543	36999.854702
HLA A*3301	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.395036	1.161468	-3.233568	24833.385223
HLA A*1101	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.305709	1.071973	-3.233736	20216.618032
HLA B*7301	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.562190	1.328019	-3.234171	36491.358869

HLA A*2402	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.481222	1.246912	-3.234310	30284.616872
HLA B*4403	1:5-13	9	IFMLVTAVV	1.049669	0.289907	-4.573898	1.339576	-3.234321	37488.453048
HLA A*2601	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.357449	1.122935	-3.234514	22774.500699
HLA B*4001	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.373437	1.138874	-3.234564	23628.552096
HLA A*2402	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.569558	1.334657	-3.234901	37115.731210
HLA A*2501	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.220991	0.985844	-3.235147	16633.773195
HLA B*7301	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.604234	1.368126	-3.236108	40200.742091
HLA A*0201	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.236429	1.000164	-3.236265	17235.712508
HLA A*0250	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.483442	1.246912	-3.236531	30439.838725
HLA A*2301	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.257436	1.020870	-3.236566	18089.892533
HLA A*8001	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.398504	1.161468	-3.237036	25032.473515
HLA B*0702	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.309205	1.071973	-3.237232	20380.016880
HLA B*1501	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.284218	1.046875	-3.237343	19240.562582
HLA B*4501	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.606043	1.368668	-3.237375	40368.552164
HLA A*0203	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.251276	1.013420	-3.237856	17835.103632
HLA B*4002	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.360933	1.122935	-3.237998	22957.952378

HLA B*5401	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.399648	1.161468	-3.238180	25098.511425
HLA B*5801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.276103	1.037888	-3.238214	18884.376272
HLA B*4402	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.400038	1.161468	-3.238570	25121.061056
HLA A*2603	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.417697	1.179033	-3.238664	26163.552256
HLA B*0802	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.400200	1.161468	-3.238732	25130.440055
HLA A*0301	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.362009	1.122935	-3.239074	23014.906497
HLA A*2602	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.573914	1.334657	-3.239257	37489.872733
HLA A*3301	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.635656	1.396176	-3.239480	43217.145921
HLA A*0301	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.164457	0.924700	-3.239757	14603.517229
HLA A*3001	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.197003	0.956718	-3.240284	15739.920469
HLA B*7301	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.495491	1.254764	-3.240726	31296.120569
HLA A*2301	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.402249	1.161468	-3.240781	25249.271047
HLA A*0301	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.333550	1.092768	-3.240782	21555.093100
HLA B*3901	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.195447	0.954583	-3.240864	15683.651178
HLA A*0301	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.316671	1.075733	-3.240938	20733.432287
HLA B*1509	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.496090	1.254764	-3.241326	31339.324041

HLA B*3501	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.242087	1.000164	-3.241923	17461.711208
HLA A*2301	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.528273	1.285203	-3.243070	33749.929539
HLA B*3801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.528275	1.285203	-3.243072	33750.112123
HLA B*5401	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.503171	1.260066	-3.243105	31854.513209
HLA A*1101	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.447314	1.203934	-3.243381	28010.077875
HLA A*2603	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.612211	1.368126	-3.244084	40945.914163
HLA A*1101	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.092023	0.847335	-3.244688	12360.124485
HLA B*5701	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.337713	1.092768	-3.244946	21762.720800
HLA A*2501	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.448985	1.203934	-3.245051	28118.024183
HLA B*5701	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.317111	1.071973	-3.245138	20754.417862
HLA B*5701	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.384308	1.138874	-3.245435	24227.476276
HLA A*6901	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.244547	0.999064	-3.245483	17560.897667
HLA B*0801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.321478	1.075247	-3.246231	20964.197817
HLA A*2403	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.284439	1.037888	-3.246550	19250.349466
HLA B*1503	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.156013	0.909340	-3.246674	14322.321499
HLA B*0702	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.000872	0.754093	-3.246779	10020.103895

HLA B*1501	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.285113	1.037888	-3.247225	19280.261508
HLA A*0301	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.246452	0.999064	-3.247388	17638.113968
HLA B*7301	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.507529	1.260066	-3.247463	32175.793602
HLA A*3002	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.582147	1.334657	-3.247490	38207.318751
HLA A*1101	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-3.867210	0.619394	-3.247816	7365.632100
HLA A*3001	1:49-57	9	AYNINISLP	0.584960	0.117828	-3.950631	0.702788	-3.247843	8925.464713
HLA B*4402	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.250425	1.002409	-3.248017	17800.209903
HLA A*2402	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.485092	1.236794	-3.248298	30555.661177
HLA B*4402	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.387299	1.138874	-3.248426	24394.901640
HLA B*5801	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.332455	1.083538	-3.248917	21500.820969
HLA B*1509	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.169908	0.920569	-3.249339	14787.960184
HLA B*3801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.495272	1.245899	-3.249373	31280.378835
HLA B*1509	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.324659	1.075247	-3.249412	21118.324152
HLA A*2301	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.509609	1.260066	-3.249542	32330.212683
HLA A*2602	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-3.938070	0.688457	-3.249613	8671.026041
HLA A*2301	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.462445	1.212549	-3.249896	29003.138712

HLA A*3301	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.634803	1.384894	-3.249909	43132.359811
HLA A*3201	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.584841	1.334657	-3.250185	38445.137709
HLA B*1502	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.429228	1.179033	-3.250195	26867.544739
HLA B*3501	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.227771	0.977336	-3.250435	16895.513248
HLA A*3101	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.249824	0.999064	-3.250760	17775.574892
HLA A*6901	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.326497	1.075733	-3.250764	21207.855175
HLA A*6901	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.389667	1.138874	-3.250794	24528.294519
HLA A*0216	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-3.964826	0.713674	-3.251152	9222.027771
HLA A*0219	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.390128	1.138874	-3.251254	24554.316602
HLA A*6901	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.323459	1.071973	-3.251486	21060.024151
HLA A*0216	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-3.638967	0.387379	-3.251588	4354.787351
HLA A*0216	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.390598	1.138874	-3.251724	24580.898206
HLA B*1503	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.328522	1.075733	-3.252789	21306.985242
HLA A*2602	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.498770	1.245899	-3.252872	31533.370045
HLA A*0203	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.392374	1.138874	-3.253500	24681.636900
HLA A*0250	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.021064	0.767355	-3.253709	10496.963781

HLA A*0250	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.588403	1.334657	-3.253747	38761.737858
HLA A*0219	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.330239	1.076055	-3.254185	21391.413294
HLA B*4002	1:126-134	9	TTTYKAFDW	1.082766	0.285902	-4.622920	1.368668	-3.254251	41968.120896
HLA B*0803	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.433408	1.179033	-3.254375	27127.371475
HLA B*1501	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.268483	1.013420	-3.255063	18555.953064
HLA B*1503	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.338655	1.083538	-3.255117	21809.983343
HLA B*4403	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-3.775538	0.519628	-3.255910	5964.002503
HLA A*2603	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.492899	1.236794	-3.256105	31109.929310
HLA A*0216	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.035974	0.779687	-3.256286	10863.594100
HLA B*1503	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.323854	1.067238	-3.256616	21079.173495
HLA B*1501	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-3.876241	0.619394	-3.256848	7520.408700
HLA B*7301	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.591862	1.334657	-3.257205	39071.643715
HLA B*5801	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.015975	0.758478	-3.257497	10374.680099
HLA A*6802	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.122402	0.864656	-3.257746	13255.670063
HLA B*0802	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.461822	1.203934	-3.257889	28961.589005
HLA B*1517	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.396819	1.138874	-3.257946	24935.563365

HLA A*3002	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.252667	0.994492	-3.258175	17892.314869
HLA B*5301	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.462198	1.203934	-3.258265	28986.668495
HLA A*6901	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-3.796091	0.537766	-3.258325	6253.038632
HLA B*1509	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.296266	1.037888	-3.258378	19781.805410
HLA A*0201	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.397449	1.138874	-3.258575	24971.742419
HLA A*6901	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.296578	1.037888	-3.258690	19796.043843
HLA A*2902	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.244768	0.985844	-3.258923	17569.830174
HLA B*4002	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.495810	1.236794	-3.259016	31319.155003
HLA A*3201	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.306044	1.046875	-3.259170	20232.263944
HLA B*5801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.331294	1.071973	-3.259322	21443.437056
HLA A*2601	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.343162	1.083538	-3.259624	22037.465536
HLA A*3001	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.199780	0.940065	-3.259715	15840.891703
HLA A*6802	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.007972	0.748062	-3.259911	10185.265829
HLA B*7301	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.545215	1.285203	-3.260012	35092.556420
HLA B*1501	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.238466	0.977336	-3.261130	17316.744330
HLA B*4403	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.263592	1.002409	-3.261183	18348.122777

HLA A*6801	1:46-54	9	SDPAYNINI	1.266370	0.129806	-4.657417	1.396176	-3.261241	45437.770389
HLA B*0801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.181971	0.920569	-3.261402	15204.443482
HLA B*1502	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.546843	1.285203	-3.261640	35224.367209
HLA A*0301	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.345457	1.083538	-3.261919	22154.252079
HLA B*3801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.517381	1.254764	-3.262617	32913.999485
HLA B*4002	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.631096	1.368126	-3.262970	42765.714479
HLA A*2301	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.510252	1.246912	-3.263341	32378.171605
HLA B*1501	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.549640	0.286028	-3.263612	3545.190142
HLA B*4501	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.509719	1.245899	-3.263820	32338.434163
HLA A*2601	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.403069	1.138874	-3.264195	25296.987998
HLA B*5701	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.111599	0.847335	-3.264263	12930.006815
HLA B*4801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.403374	1.138874	-3.264501	25314.785263
HLA B*1503	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.622699	0.357949	-3.264750	4194.682736
HLA A*2301	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.204916	0.940065	-3.264851	16029.338459
HLA A*2602	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.501869	1.236794	-3.265076	31759.185653
HLA A*1101	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.388147	1.122935	-3.265212	24442.590703

HLA A*0250	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.265659	1.000164	-3.265495	18435.680983
HLA A*0211	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.222236	0.956718	-3.265518	16681.534675
HLA A*0211	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.337894	1.071973	-3.265922	21771.788199
HLA B*4402	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.389122	1.122935	-3.266187	24497.528508
HLA B*0702	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.405486	1.138874	-3.266613	25438.203354
HLA A*3001	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.267224	1.000164	-3.267060	18502.224292
HLA B*3801	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.498787	1.231508	-3.267279	31534.564212
HLA A*0206	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.286889	1.019585	-3.267305	19359.276862
HLA B*0802	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.343007	1.075247	-3.267759	22029.598404
HLA B*1509	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.429728	1.161468	-3.268261	26898.522227
HLA B*4403	1:4-12	9	KIFMLVTAV	1.048201	0.290033	-4.606915	1.338234	-3.268681	40449.655992
HLA A*3301	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.596939	1.328019	-3.268920	39531.101809
HLA A*3002	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.472905	1.203934	-3.268971	29710.154272
HLA B*0801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.288668	1.019585	-3.269083	19438.721202
HLA A*1101	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.482369	1.212549	-3.269819	30364.674676
HLA A*2402	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.431368	1.161468	-3.269901	27000.285821

HLA A*0250	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.501524	1.231508	-3.270016	31733.939083
HLA A*3002	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.123346	0.852998	-3.270348	13284.529538
HLA B*1801	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.225403	0.954583	-3.270820	16803.629927
HLA B*3501	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.317790	1.046875	-3.270915	20786.891901
HLA B*5701	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.393974	1.122935	-3.271039	24772.735077
HLA A*0212	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.291146	1.019585	-3.271562	19549.983611
HLA A*0212	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.348208	1.076055	-3.272154	22295.044315
HLA A*6802	1:177-185	9	APNAGLDPV	0.672482	0.029184	-3.974121	0.701666	-3.272455	9421.520304
HLA B*5801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.348368	1.075733	-3.272635	22303.247556
HLA A*2301	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.527434	1.254764	-3.272670	33684.810177
HLA B*0801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.411966	1.138874	-3.273093	25820.599081
HLA B*1509	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.533385	1.260066	-3.273319	34149.578671
HLA B*4403	1:79-87	9	SAATSSTPR	0.650358	0.717768	-4.641875	1.368126	-3.273749	43840.466756
HLA A*2403	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.049215	0.775271	-3.273944	11199.927929
HLA B*4601	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.350210	1.076055	-3.274156	22398.044395
HLA B*5101	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.292110	1.017829	-3.274281	19593.394667

HLA A*6801	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.529457	1.254764	-3.274693	33842.077128
HLA A*0211	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.313084	1.037888	-3.275195	20562.860968
HLA A*2501	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.347595	1.071973	-3.275623	22263.586348
HLA B*1517	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.488188	1.212549	-3.275639	30774.308766
HLA B*5101	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.296546	1.020870	-3.275676	19794.544578
HLA A*0216	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.289131	1.013420	-3.275711	19459.449027
HLA A*3002	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.278732	1.002409	-3.276323	18999.042704
HLA B*0802	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.399523	1.122935	-3.276588	25091.316108
HLA A*3201	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.489478	1.212549	-3.276929	30865.845225
HLA B*4002	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.531717	1.254764	-3.276953	34018.661002
HLA A*0301	1:18-26	9	SGVATAAPK	0.424227	0.140104	-3.841751	0.564331	-3.277420	6946.259494
HLA A*6801	1:87-95	9	REAPYELNI	1.162222	0.222672	-4.662316	1.384894	-3.277422	45953.192539
HLA B*0801	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.370437	1.092768	-3.277669	23465.878491
HLA B*5801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.353262	1.075247	-3.278015	22555.999804
HLA B*5701	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.315943	1.037888	-3.278055	20698.690101
HLA B*3801	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.525592	1.246912	-3.278680	33542.243555

HLA A*0203	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.346000	1.067238	-3.278762	22181.955209
HLA A*6801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-3.700575	0.421102	-3.279473	5018.514098
HLA A*0101	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.354963	1.075247	-3.279716	22644.519478
HLA B*0801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.003532	0.723137	-3.280395	10081.655234
HLA A*6801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.021266	0.740601	-3.280665	10501.848635
HLA A*2402	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-3.968459	0.687624	-3.280834	9299.481387
HLA B*2705	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.318953	1.037888	-3.281064	20842.631617
HLA B*3501	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.134201	0.852998	-3.281203	13620.743028
HLA B*0702	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.006807	0.725355	-3.281452	10157.972289
HLA B*5801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.357540	1.076055	-3.281486	22779.306300
HLA B*4002	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.616202	1.334657	-3.281546	41323.999411
HLA A*6801	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.609640	1.328019	-3.281621	40704.294805
HLA A*2402	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.513434	1.231508	-3.281925	32616.212143
HLA A*0202	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.374760	1.092768	-3.281992	23700.628883
HLA A*2603	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.365566	1.083538	-3.282028	23204.185844
HLA B*0803	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.405068	1.122935	-3.282133	25413.719166

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HLA A*0201	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.882693
	0.600517	-3.282176	7632.962505

HLA A*2501	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.303211
	1.020870	-3.282341	20100.691729

HLA A*2402	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.177511
	0.895143	-3.282368	15049.123494

HLA B*4601	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.355238
	1.071973	-3.283265	22658.857023

HLA A*6801	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.529295
	1.245899	-3.283396	33829.446835

HLA B*0803	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.487429
	1.203934	-3.283496	30720.580873

HLA A*2601	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.376491
	1.092768	-3.283724	23795.314016

HLA B*4403	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.611860
	1.328019	-3.283841	40912.922046

HLA A*0212	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.359596
	1.075733	-3.283863	22887.391248

HLA B*1509	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.487841
	1.203934	-3.283907	30749.678759

HLA B*4601	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.376679
	1.092768	-3.283912	23805.614646

HLA B*4403	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.530984
	1.246912	-3.284073	33961.289832

HLA B*0702	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.283158
	0.999064	-3.284094	19193.675525

HLA A*1101	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.297633
	1.013420	-3.284213	19844.187678

HLA A*0101	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.131969
	0.847335	-3.284634	13550.920231

HLA B*5401	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.302795
	1.017829	-3.284966	20081.453517
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HLA B*4601	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.368588	1.083538	-3.285050	23366.182953
HLA A*6901	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.279859	0.994492	-3.285368	19048.442519
HLA A*3101	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.361311	1.075733	-3.285578	22977.957285
HLA A*2601	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.306679	1.020870	-3.285809	20261.838201
HLA A*2603	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.531738	1.245899	-3.285840	34020.317377
HLA B*0801	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.369572	1.083538	-3.286034	23419.208172
HLA A*0219	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.361845	1.075733	-3.286112	23006.192580
HLA B*3801	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.498857	1.212549	-3.286308	31539.682583
HLA B*3501	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.616661	0.330347	-3.286314	4136.765875
HLA A*2402	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.571755	1.285203	-3.286551	37303.947343
HLA B*3801	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.465751	1.179033	-3.286718	29224.744641
HLA A*2902	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.358753	1.071973	-3.286780	22842.983633
HLA B*4501	1:166-174	9	LSKQTGQQV	1.247032	0.080987	-4.615272	1.328019	-3.287253	41235.565102
HLA A*6801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.276030	0.987852	-3.288178	18881.209504
HLA B*3901	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.215719	0.927533	-3.288186	16433.063413
HLA B*4801	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.065220	0.776623	-3.288597	11620.369020

HLA A*0212	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-3.889131	0.600517	-3.288613	7746.949375
HLA A*3201	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.573818	1.285203	-3.288614	37481.558197
HLA A*1101	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.428281	1.138874	-3.289408	26809.032319
HLA A*2301	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.307252	1.017829	-3.289423	20288.601750
HLA B*4402	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.382328	1.092768	-3.289560	24117.237550
HLA A*2501	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.373526	1.083538	-3.289988	23633.410053
HLA B*1502	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.545119	1.254764	-3.290355	35084.773563
HLA A*0301	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.366438	1.076055	-3.290383	23250.805011
HLA A*0250	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.527213	1.236794	-3.290419	33667.684809
HLA B*5301	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.575660	1.285203	-3.290456	37640.868326
HLA B*4001	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.293132	1.002409	-3.290723	19639.558135
HLA B*7301	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.503509	1.212549	-3.290960	31879.338309
HLA A*0203	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.328924	1.037888	-3.291035	21326.705263
HLA A*0212	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.337950	1.046875	-3.291076	21774.615174
HLA A*0101	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.367599	1.075733	-3.291865	23313.025549
HLA A*2403	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.368238	1.076055	-3.292183	23347.355682

HLA A*2402	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.546994	1.254764	-3.292229	35236.565155
HLA A*0101	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.368449	1.076055	-3.292395	23358.726044
HLA A*0101	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.385504	1.092768	-3.292736	24294.281804
HLA A*3001	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.260004	0.967178	-3.292826	18197.175096
HLA B*3901	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.249828	0.956718	-3.293110	17775.767221
HLA A*0203	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-3.973769	0.680076	-3.293692	9413.877998
HLA A*6802	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.432790	1.138874	-3.293916	27088.802073
HLA B*5801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.312071	1.017829	-3.294242	20514.971175
HLA B*4801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.369718	1.075247	-3.294470	23427.064599
HLA A*0201	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.370827	1.076055	-3.294772	23486.961291
HLA A*2601	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.366769	1.071973	-3.294797	23268.547360
HLA A*0201	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.251598	0.956718	-3.294879	17848.327104
HLA A*0101	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.366877	1.071973	-3.294905	23274.338573
HLA B*5401	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.542085	1.246912	-3.295174	34840.589354
HLA B*0702	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.418160	1.122935	-3.295224	26191.450878
HLA A*2501	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.418305	1.122935	-3.295370	26200.237308

HLA A*0219	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.038210	0.742712	-3.295498	10919.688264
HLA B*5801	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.362770	1.067238	-3.295533	23055.282494
HLA A*2902	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.272905	0.977336	-3.295569	18745.843893
HLA B*0801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.342548	1.046875	-3.295674	22006.371010
HLA A*0301	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.309129	1.013420	-3.295710	20376.489069
HLA A*3001	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.283666	0.987852	-3.295814	19216.117136
HLA B*4501	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.630694	1.334657	-3.296037	42726.170594
HLA A*0301	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.143674	0.847335	-3.296339	13921.111856
HLA B*4501	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.253106	0.956718	-3.296388	17910.424776
HLA A*6801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.500664	1.203934	-3.296730	31671.167432
HLA B*1502	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.295803	0.999064	-3.296739	19760.734218
HLA A*3001	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.269343	0.972498	-3.296845	18592.730610
HLA A*0206	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.010651	0.713674	-3.296977	10248.275249
HLA B*1503	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.628018	0.330347	-3.297671	4246.375082
HLA A*0216	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.335754	1.037888	-3.297865	21664.751898
HLA B*4601	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.373785	1.075733	-3.298052	23647.478193

HLA B*5401	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.543972	1.245899	-3.298074	34992.271010
HLA A*6802	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.370113	1.071973	-3.298140	23448.366232
HLA A*0201	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.391115	1.092768	-3.298347	24610.171208
HLA A*0203	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.382036	1.083538	-3.298498	24101.064499
HLA A*0301	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.365775	1.067238	-3.298538	23215.360888
HLA B*1801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.421557	1.122935	-3.298622	26397.142215
HLA A*3001	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.226639	0.927533	-3.299106	16851.514462
HLA A*0203	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.391885	1.092768	-3.299118	24653.879337
HLA A*2403	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.382866	1.083538	-3.299328	24147.134057
HLA A*2902	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.438372	1.138874	-3.299499	27439.246195
HLA A*3301	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.559749	1.260066	-3.299683	36286.820888
HLA B*5701	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.347475	1.046875	-3.300601	22257.444575
HLA B*3801	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.504653	1.203934	-3.300720	31963.438862
HLA B*5301	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.546855	1.245899	-3.300956	35225.320021
HLA B*1501	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.377022	1.076055	-3.300968	23824.424791
HLA B*4403	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.424036	1.122935	-3.301100	26548.232896

HLA B*5701	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.080853	0.779687	-3.301166	12046.292191
HLA B*4501	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.561248	1.260066	-3.301182	36412.281577
HLA A*6901	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.368468	1.067238	-3.301230	23359.737011
HLA B*1517	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.348206	1.046875	-3.301331	22294.923701
HLA A*8001	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.440623	1.138874	-3.301749	27581.824005
HLA A*1101	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.348648	1.046875	-3.301773	22317.610492
HLA A*3101	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.377871	1.076055	-3.301816	23870.998641
HLA A*2601	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.377793	1.075733	-3.302060	23866.737420
HLA A*2902	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.369445	1.067238	-3.302208	23412.367624
HLA A*3101	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.296769	0.994492	-3.302277	19804.720390
HLA A*0101	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.369645	1.067238	-3.302407	23423.136056
HLA B*0802	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.378545	1.076055	-3.302490	23908.090453
HLA B*4001	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.378994	1.076055	-3.302939	23932.807183
HLA A*0216	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.079636	0.776623	-3.303014	12012.581850
HLA B*4801	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.395839	1.092768	-3.303072	24879.374038
HLA B*1502	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.550292	1.246912	-3.303381	35505.222936

HLA A*0201	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.083381	0.779687	-3.303694	12116.618636
HLA A*0216	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-3.344393	0.040514	-3.303879	2210.004827
HLA A*1101	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.387518	1.083538	-3.303980	24407.178283
HLA A*2902	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.379318	1.075247	-3.304070	23950.681243
HLA B*2705	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.442968	1.138874	-3.304094	27731.142915
HLA B*4403	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.639079	1.334657	-3.304423	43559.138533
HLA B*3901	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.306862	1.002409	-3.304454	20270.389920
HLA B*4001	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.388326	1.083538	-3.304788	24452.642379
HLA A*0202	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.259294	0.954256	-3.305039	18167.469070
HLA A*8001	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.381942	1.076055	-3.305888	24095.849699
HLA B*3801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.467494	1.161468	-3.306026	29342.292560
HLA B*1509	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.262840	0.956718	-3.306121	18316.386635
HLA B*5801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.261158	0.954978	-3.306180	18245.575698
HLA A*3002	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.283957	0.977336	-3.306621	19229.012137
HLA B*3801	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.373874	1.067238	-3.306636	23652.340041
HLA A*2403	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.379097	1.071973	-3.307124	23938.504710

HLA B*1501	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.194061	0.886699	-3.307362	15633.671364
HLA A*2403	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.328423	1.020870	-3.307554	21302.144518
HLA B*1517	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.327512	1.019585	-3.307927	21257.477424
HLA A*3101	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.327735	1.019585	-3.308150	21268.405289
HLA A*2601	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.384266	1.076055	-3.308211	24225.117167
HLA B*0801	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.262988	0.954583	-3.308405	18322.630346
HLA B*0801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.204140	0.895143	-3.308997	16000.747396
HLA A*0101	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.392973	1.083538	-3.309435	24715.709251
HLA A*0201	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.196749	0.886699	-3.310050	15730.726823
HLA A*2601	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.348086	1.037888	-3.310198	22288.773283
HLA B*4402	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.266954	0.956718	-3.310235	18490.716949
HLA A*3301	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.403118	1.092768	-3.310351	25299.862093
HLA B*3501	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.331236	1.020870	-3.310366	21440.537086
HLA A*3201	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.433518	1.122935	-3.310583	27134.269887
HLA A*2603	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.595987	1.285203	-3.310784	39444.583779
HLA A*2902	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.309865	0.999064	-3.310801	20411.021711

HLA A*2603	1:212-220	9	GPTQVLVPR	0.849469	0.485188	-4.645580	1.334657	-3.310924	44216.087107
HLA B*1801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.387306	1.076055	-3.311252	24395.297564
HLA B*3901	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.386674	1.075247	-3.311427	24359.821878
HLA A*0250	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.383444	1.071973	-3.311471	24179.291246
HLA B*4801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.383834	1.071973	-3.311861	24201.015009
HLA B*5401	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.548899	1.236794	-3.312105	35391.502408
HLA A*3101	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.252225	0.940065	-3.312160	17874.126578
HLA B*4402	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.395724	1.083538	-3.312186	24872.779774
HLA A*6801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.359082	1.046875	-3.312207	22860.291108
HLA B*1501	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-3.405052	0.091985	-3.313067	2541.278288
HLA A*2501	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.451985	1.138874	-3.313112	28312.948074
HLA A*0101	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.199883	0.886699	-3.313184	15844.662840
HLA A*3002	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.544799	1.231508	-3.313291	35058.969613
HLA A*2501	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.389454	1.076055	-3.313399	24516.222214
HLA A*0201	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.397061	1.083538	-3.313523	24949.461796
HLA B*0802	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.406859	1.092768	-3.314091	25518.699276

HLA B*5301	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.574412	1.260066	-3.314346	37532.894403
HLA B*4403	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.527145	1.212549	-3.314596	33662.403209
HLA A*3001	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.269216	0.954256	-3.314961	18587.299834
HLA A*0201	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.390264	1.075247	-3.315017	24562.022307
HLA A*3002	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.408080	1.092768	-3.315313	25590.588079
HLA B*4402	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.382793	1.067238	-3.315555	24143.084763
HLA A*0201	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.383166	1.067238	-3.315929	24163.860912
HLA B*4001	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.408905	1.092768	-3.316137	25639.227472
HLA B*1503	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.059717	0.742712	-3.317005	11474.068175
HLA B*7301	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.563012	1.245899	-3.317114	36560.519296
HLA B*3801	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.577182	1.260066	-3.317116	37773.054022
HLA B*0702	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.392548	1.075247	-3.317300	24691.519723
HLA B*4001	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.393166	1.075733	-3.317433	24726.675842
HLA B*2705	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.364493	1.046875	-3.317618	23146.888544
HLA B*1503	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.024630	0.706847	-3.317783	10583.522001
HLA A*2902	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.393713	1.075733	-3.317980	24757.863572

HLA B*1503	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.273551	0.954978	-3.318573	18773.753207
HLA B*1501	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.394185	1.075247	-3.318938	24784.799611
HLA A*0250	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.457838	1.138874	-3.318964	28697.076773
HLA B*5101	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.366090	1.046875	-3.319216	23232.196389
HLA A*2601	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.332744	1.013420	-3.319324	21515.132729
HLA B*4601	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.395179	1.075247	-3.319932	24841.581672
HLA A*1101	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.244850	0.924700	-3.320150	17573.157268
HLA B*5401	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.499313	1.179033	-3.320280	31572.801439
HLA A*3101	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.387527	1.067238	-3.320289	24407.706449
HLA A*2602	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.524330	1.203934	-3.320397	33444.941037
HLA A*2902	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.320623	1.000164	-3.320459	20922.955747
HLA A*8001	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.338359	1.017829	-3.320530	21795.121720
HLA B*5401	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.367429	1.046875	-3.320555	23303.946614
HLA A*6901	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.168080	0.847335	-3.320745	14725.850030
HLA A*3001	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.079242	0.758478	-3.320764	12001.669038
HLA B*4001	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.358675	1.037888	-3.320787	22838.905923

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HLA B*4801	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.404704
	1.083538	-3.321166	25392.417861

HLA A*6801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.017831
	0.696230	-3.321600	10419.114420

HLA A*0250	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.500657
	1.179033	-3.321624	31670.653424

HLA A*2402	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.388911
	1.067238	-3.321673	24485.603809

HLA A*8001	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.405451
	1.083538	-3.321913	25436.139170

HLA B*2705	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.397801
	1.075733	-3.322068	24992.014797

HLA B*1503	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.369088
	1.046875	-3.322213	23393.123474

HLA B*4403	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.553791
	1.231508	-3.322283	35792.384079

HLA A*3002	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.461214
	1.138874	-3.322340	28921.037564

HLA B*4501	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.501562
	1.179033	-3.322529	31736.686035

HLA A*2601	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.390311
	1.067238	-3.323073	24564.680007

HLA A*3001	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-3.758015
	0.434427	-3.323588	5728.162870

HLA B*1501	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.318130
	0.994492	-3.323638	20803.204242

HLA A*0250	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.536362
	1.212549	-3.323813	34384.455178

HLA B*0801	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.391394
	1.067238	-3.324157	24626.019767

HLA A*3101	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.312151
	0.987852	-3.324299	20518.744969
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HLA A*0250	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.407902	1.083538	-3.324364	25580.068631
HLA A*0101	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.301919	0.977336	-3.324583	20040.972237
HLA A*3002	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.362514	1.037888	-3.324626	23041.691311
HLA A*3001	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.279331	0.954583	-3.324748	19025.270383
HLA A*0206	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.417654	1.092768	-3.324887	26161.004626
HLA A*2301	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.325148	1.000164	-3.324984	21142.101068
HLA A*2602	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.115583	0.790540	-3.325044	13049.187768
HLA B*4001	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.400578	1.075247	-3.325331	25152.338006
HLA A*0212	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.397491	1.071973	-3.325519	24974.174236
HLA B*1502	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.409217	1.083538	-3.325679	25657.681926
HLA A*0219	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.339287	1.013420	-3.325867	21841.745649
HLA B*3801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.402150	1.076055	-3.326096	25243.534677
HLA B*7301	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.393614	1.067238	-3.326377	24752.238844
HLA B*1801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.465340	1.138874	-3.326466	29197.089774
HLA A*1101	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.419238	1.092768	-3.326470	26256.568709
HLA A*0101	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.346185	1.019585	-3.326601	22191.437387

HLA A*6901	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.130700	0.804086	-3.326614	13511.391151
HLA A*0202	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.321502	0.994492	-3.327010	20965.331988
HLA B*2705	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.103662	0.776623	-3.327039	12695.862010
HLA B*0802	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.411095	1.083538	-3.327557	25768.827333
HLA B*4001	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.399538	1.071973	-3.327565	25092.130568
HLA A*0203	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.075793	0.748062	-3.327731	11906.732654
HLA A*6901	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.255272	0.927533	-3.327739	17999.983672
HLA B*1501	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-3.729450	0.401614	-3.327836	5363.525123
HLA B*1517	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.323487	0.994492	-3.328995	21061.391385
HLA B*5301	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.421782	1.092768	-3.329015	26410.855114
HLA B*5301	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.583951	1.254764	-3.329187	38366.392554
HLA B*0702	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.367415	1.037888	-3.329527	23303.190195
HLA A*0203	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.043215	0.713674	-3.329540	11046.244285
HLA B*1517	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.405618	1.075733	-3.329885	25445.911122
HLA A*3002	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-3.978505	0.648415	-3.330090	9517.110842
HLA A*3201	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.397750	1.067238	-3.330512	24989.040486

HLA B*5701	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.407014	1.075733	-3.331280	25527.812423
HLA B*0702	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.349573	1.017829	-3.331744	22365.231131
HLA A*2601	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.407150	1.075247	-3.331902	25535.823633
HLA B*2705	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.352832	1.020870	-3.331962	22533.680195
HLA B*5701	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.407486	1.075247	-3.332238	25555.586150
HLA B*4501	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.309804	0.977336	-3.332468	20408.150958
HLA B*3501	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.455528	1.122935	-3.332593	28544.873048
HLA B*0802	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.370545	1.037888	-3.332657	23471.718816
HLA A*0202	1:53-61	9	NISLPSYYP	0.515820	0.118220	-3.967101	0.634040	-3.333061	9270.448107
HLA A*3301	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.579088	1.245899	-3.333189	37939.144366
HLA A*0203	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.408651	1.075247	-3.333404	25624.251667
HLA B*4002	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.546550	1.212549	-3.334000	35200.555271
HLA A*3101	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.336574	1.002409	-3.334165	21705.694700
HLA B*4601	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.381160	1.046875	-3.334285	24052.480269
HLA B*1517	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.457297	1.122935	-3.334362	28661.391938
HLA A*0212	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.401640	1.067238	-3.334403	25213.917520

HLA B*4402	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.410460	1.076055	-3.334406	25731.215054
HLA A*8001	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.427466	1.092768	-3.334698	26758.752766
HLA B*4403	1:108-116	9	GTQAVVLKV	1.154603	0.091296	-4.580671	1.245899	-3.334773	38077.733062
HLA B*1509	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.355675	1.020870	-3.334805	22681.668732
HLA A*2402	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.088931	0.754093	-3.334838	12272.440141
HLA B*5401	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.547875	1.212549	-3.335325	35308.122432
HLA B*5701	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.312792	0.977336	-3.335456	20549.071487
HLA B*1502	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.595543	1.260066	-3.335477	39404.273524
HLA A*0219	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.402839	1.067238	-3.335601	25283.579871
HLA B*1509	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.474853	1.138874	-3.335979	29843.697549
HLA B*5701	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.412283	1.076055	-3.336229	25839.463657
HLA B*0801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.357111	1.020870	-3.336241	22756.765725
HLA A*3001	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.201030	0.864656	-3.336374	15886.548426
HLA B*5301	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.549031	1.212549	-3.336481	35402.226022
HLA B*2705	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-3.929438	0.592876	-3.336563	8500.382776
HLA A*0212	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.293806	0.956718	-3.337088	19670.074947

HLA B*1502	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.568675	1.231508	-3.337167	37040.310155
HLA A*0216	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.331663	0.994492	-3.337171	21461.657831
HLA A*3002	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.223961	0.886699	-3.337262	16747.906380
HLA B*4601	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.404525	1.067238	-3.337288	25381.979874
HLA B*5101	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.476197	1.138874	-3.337323	29936.190609
HLA A*6901	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.291955	0.954583	-3.337372	19586.400042
HLA A*6802	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.375263	1.037888	-3.337374	23728.083376
HLA B*3501	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.413197	1.075733	-3.337464	25893.898694
HLA B*2705	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.184851	0.847335	-3.337516	15305.622485
HLA A*6801	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.499059	1.161468	-3.337592	31554.359849
HLA B*7301	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-3.722129	0.384238	-3.337892	5273.868830
HLA A*2603	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.461064	1.122935	-3.338128	28911.025882
HLA B*5101	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.061729	0.723137	-3.338592	11527.326257
HLA B*1509	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.414699	1.076055	-3.338644	25983.566707
HLA B*1517	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-3.905220	0.566374	-3.338846	8039.332502
HLA B*4601	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.376804	1.037888	-3.338916	23812.441269

HLA A*2902	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.192040	0.852998	-3.339043	15561.104575
HLA B*1503	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.234296	0.895143	-3.339153	17151.255202
HLA A*0101	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.377293	1.037888	-3.339404	23839.251465
HLA A*0212	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.414743	1.075247	-3.339496	25986.237640
HLA A*3101	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.234961	0.895143	-3.339818	17177.533861
HLA A*2501	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.415655	1.075733	-3.339922	26040.841001
HLA B*0702	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.432701	1.092768	-3.339933	27083.233843
HLA B*5701	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.353405	1.013420	-3.339986	22563.444586
HLA A*3001	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.249880	0.909340	-3.340540	17777.882975
HLA A*2403	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.387701	1.046875	-3.340826	24417.479586
HLA B*4001	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.387713	1.046875	-3.340838	24418.140075
HLA B*5801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.360498	1.019585	-3.340914	22934.986876
HLA A*2402	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.361901	1.020870	-3.341031	23009.179837
HLA B*4801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.194564	0.853458	-3.341106	15651.781201
HLA A*6802	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.262006	0.920569	-3.341437	18281.243577
HLA A*0301	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.361321	1.019585	-3.341736	22978.454523

HLA B*4001	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.408980	1.067238	-3.341742	25643.666429
HLA B*5301	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.464712	1.122935	-3.341777	29154.946761
HLA A*0216	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.413942	1.071973	-3.341970	25938.343142
HLA A*2902	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.336689	0.994492	-3.342197	21711.449307
HLA A*0202	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.481356	1.138874	-3.342482	30293.956988
HLA B*4801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.299294	0.956718	-3.342576	19920.232896
HLA A*3301	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.096759	0.754093	-3.342667	12495.665948
HLA B*3501	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.263303	0.920569	-3.342734	18335.917697
HLA B*3901	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.481777	1.138874	-3.342903	30323.306961
HLA B*0803	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.380984	1.037888	-3.343095	24042.723155
HLA A*6901	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.300039	0.956718	-3.343321	19954.424108
HLA B*4402	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.418604	1.075247	-3.343356	26218.244521
HLA A*2403	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.437061	1.092768	-3.344294	27356.539741
HLA A*0201	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.382339	1.037888	-3.344451	24117.889916
HLA B*4403	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.548643	1.203934	-3.344709	35370.638973
HLA A*2403	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.239857	0.895143	-3.344714	17372.292781

HLA A*3001	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.265403	0.920569	-3.344834	18424.813074
HLA A*0101	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.362796	1.017829	-3.344967	23056.654526
HLA A*3101	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.330839	0.985844	-3.344994	21420.943578
HLA B*0702	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.300044	0.954583	-3.345461	19954.640011
HLA B*0803	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.484796	1.138874	-3.345922	30534.840129
HLA B*4801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.383923	1.037888	-3.346035	24205.990663
HLA A*3001	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.241438	0.895143	-3.346295	17435.658069
HLA B*0801	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.202416	0.856017	-3.346399	15937.336671
HLA B*5701	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.413698	1.067238	-3.346460	25923.753596
HLA B*2705	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.439234	1.092768	-3.346467	27493.778996
HLA B*3801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.469451	1.122935	-3.346516	29474.820162
HLA B*5801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.348995	1.002409	-3.346587	22335.486546
HLA B*4801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.422880	1.076055	-3.346825	26477.664338
HLA A*2902	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.360329	1.013420	-3.346909	22926.055163
HLA A*2602	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.593925	1.246912	-3.347013	39257.670892
HLA A*3201	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.578552	1.231508	-3.347044	37892.376997

HLA A*0216	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.430664	1.083538	-3.347126	26956.500795
HLA A*0219	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.440106	1.092768	-3.347339	27549.016318
HLA A*0202	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.054187	0.706847	-3.347340	11328.873783
HLA A*0212	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.440308	1.092768	-3.347541	27561.836493
HLA B*5801	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.347731	1.000164	-3.347567	22270.573169
HLA A*0301	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.350041	1.002409	-3.347632	22389.321787
HLA A*2501	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.414934	1.067238	-3.347696	25997.627331
HLA A*1101	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.365540	1.017829	-3.347712	23202.805032
HLA B*4601	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.346883	0.999064	-3.347820	22227.121852
HLA B*2705	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.423068	1.075247	-3.347820	26489.126117
HLA B*1501	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.415533	1.067238	-3.348295	26033.516372
HLA A*6802	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.423606	1.075247	-3.348358	26521.962894
HLA A*3002	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.928132	0.579719	-3.348413	8474.852903
HLA B*5801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.343009	0.994492	-3.348517	22029.717582
HLA A*3101	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.303150	0.954583	-3.348567	20097.864623
HLA A*2902	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.366530	1.017829	-3.348701	23255.711116

HLA A*0201	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.362131	1.013420	-3.348712	23021.381828
HLA B*5801	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.157780	0.809025	-3.348756	14380.706774
HLA B*4601	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.343251	0.994492	-3.348759	22041.996371
HLA B*3901	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.303129	0.954256	-3.348873	20096.886102
HLA A*0216	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.416179	1.067238	-3.348941	26072.275767
HLA B*4801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.425079	1.075733	-3.349346	26612.078154
HLA A*2403	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.316544	0.967178	-3.349366	20727.376231
HLA A*3201	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.586270	1.236794	-3.349476	38571.800136
HLA A*2501	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.424839	1.075247	-3.349592	26597.397429
HLA A*2902	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.425746	1.076055	-3.349692	26652.996603
HLA B*0802	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.488578	1.138874	-3.349705	30801.957789
HLA B*4601	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.369513	1.019585	-3.349929	23416.041003
HLA A*0206	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.433852	1.083538	-3.350314	27155.122557
HLA A*0101	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.363781	1.013420	-3.350361	23108.977328
HLA B*1502	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.489577	1.138874	-3.350703	30872.859216
HLA A*2402	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.368555	1.017829	-3.350726	23364.413301

HLA B*4002	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.530004	1.179033	-3.350972	33884.762104
HLA A*3301	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.636279	1.285203	-3.351075	43279.147345
HLA B*5801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.350372	0.999064	-3.351309	22406.406751
HLA A*0301	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.324314	0.972498	-3.351816	21101.536403
HLA A*1101	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.346359	0.994492	-3.351867	22200.323103
HLA B*3501	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.292225	0.940065	-3.352160	19598.589262
HLA B*7301	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.599286	1.246912	-3.352374	39745.325190
HLA B*4601	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.330026	0.977336	-3.352690	21380.884895
HLA A*6901	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.161793	0.809025	-3.352769	14514.201610
HLA A*2501	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.445679	1.092768	-3.352912	27904.810315
HLA A*2403	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.428319	1.075247	-3.353071	26811.352962
HLA B*0702	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.374029	1.020870	-3.353159	23660.786681
HLA B*1801	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.446062	1.092768	-3.353294	27929.427962
HLA B*5101	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.446144	1.092768	-3.353377	27934.716791
HLA A*2601	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.371748	1.017829	-3.353919	23536.822390
HLA A*2603	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.614102	1.260066	-3.354036	41124.620860

HLA B*1801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.400921	1.046875	-3.354047	25172.212273
HLA A*2601	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.354312	1.000164	-3.354148	22610.611189
HLA B*4402	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.375216	1.020870	-3.354346	23725.516188
HLA A*3101	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.208130	0.852998	-3.355132	16148.407293
HLA A*2402	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.431761	1.076055	-3.355706	27024.690292
HLA A*0216	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.448562	1.092768	-3.355794	28090.656739
HLA B*3901	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.439460	1.083538	-3.355922	27508.061581
HLA A*6802	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.310370	0.954256	-3.356114	20434.776117
HLA B*0802	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.428138	1.071973	-3.356165	26800.186711
HLA A*0250	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.350802	0.994492	-3.356310	22428.600295
HLA A*0101	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.356657	1.000164	-3.356493	22733.017590
HLA A*2603	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.165754	0.809025	-3.356730	14647.192291
HLA B*1503	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-3.741000	0.384238	-3.356763	5508.081879
HLA B*1501	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.357073	1.000164	-3.356909	22754.796025
HLA A*3002	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.604279	1.246912	-3.357367	40204.874453
HLA B*1509	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.440945	1.083538	-3.357407	27602.273984

HLA A*1101	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.433436	1.075733	-3.357703	27129.132605
HLA B*0801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.222396	0.864656	-3.357740	16687.672481
HLA B*4001	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.378676	1.020870	-3.357807	23915.334597
HLA A*0203	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.028906	0.671022	-3.357884	10688.242031
HLA A*2603	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.344026	0.985844	-3.358182	22081.382287
HLA A*2902	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.283005	0.924700	-3.358305	19186.927394
HLA A*0212	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.371830	1.013420	-3.358410	23541.279418
HLA B*4402	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.358588	1.000164	-3.358424	22834.334810
HLA A*3201	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.245219	0.886699	-3.358520	17588.089415
HLA B*1801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.430579	1.071973	-3.358606	26951.251366
HLA B*4002	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.619193	1.260066	-3.359127	41609.571278
HLA A*0301	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.353967	0.994492	-3.359475	22592.637164
HLA A*0202	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.397430	1.037888	-3.359542	24970.661688
HLA B*0801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.113727	0.754093	-3.359635	12993.536993
HLA A*2403	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.337046	0.977336	-3.359710	21729.310043
HLA B*0803	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.377617	1.017829	-3.359788	23857.055654

HLA B*5101	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.215831	0.856017	-3.359814	16437.331218
HLA B*5101	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.195189	0.835252	-3.359937	15674.320805
HLA B*7301	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.521450	1.161468	-3.359982	33223.850665
HLA B*4402	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.435776	1.075733	-3.360043	27275.705674
HLA A*3002	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.255559	0.895143	-3.360416	18011.867700
HLA B*4601	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.378298	1.017829	-3.360469	23894.513597
HLA B*3901	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.360682	1.000164	-3.360517	22944.666826
HLA B*0801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.363215	1.002409	-3.360806	23078.867862
HLA B*4801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.381902	1.020870	-3.361033	24093.633751
HLA A*3301	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.597909	1.236794	-3.361115	39619.524269
HLA A*2403	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.380836	1.019585	-3.361251	24034.530238
HLA A*0219	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.436716	1.075247	-3.361468	27334.793000
HLA A*2902	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.363882	1.002409	-3.361473	23114.353685
HLA A*8001	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.399702	1.037888	-3.361814	25101.634563
HLA A*2403	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.375272	1.013420	-3.361852	23728.596846
HLA A*0212	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.445435	1.083538	-3.361897	27889.114690

HLA A*0212	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.399918	1.037888	-3.362030	25114.131002
HLA A*8001	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.429378	1.067238	-3.362141	26876.848778
HLA A*3201	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.400233	1.037888	-3.362345	25132.343468
HLA A*0101	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.361619	0.999064	-3.362556	22994.247431
HLA B*3501	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.434535	1.071973	-3.362563	27197.905930
HLA A*0216	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.249340	0.886699	-3.362641	17755.776165
HLA B*0702	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.376346	1.013420	-3.362926	23787.334094
HLA B*4501	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.609868	1.246912	-3.362957	40725.660366
HLA A*0203	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.317240	0.954256	-3.362984	20760.594131
HLA A*2402	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.363215	1.000164	-3.363050	23078.867862
HLA A*0301	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.363792	1.000164	-3.363628	23109.602422
HLA A*6801	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.610705	1.246912	-3.363793	40804.170329
HLA B*5401	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.456581	1.092768	-3.363813	28614.139172
HLA A*8001	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.439751	1.075247	-3.364504	27526.520902
HLA A*3301	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.568672	1.203934	-3.364739	37040.109772
HLA A*3101	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.229428	0.864656	-3.364772	16960.075301

HLA B*4402	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.402914	1.037888	-3.365025	25287.957253
HLA A*3301	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.544510	1.179033	-3.365477	35035.648561
HLA A*2403	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.367895	1.002409	-3.365486	23328.922198
HLA A*3001	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.945457	0.579719	-3.365738	8819.770234
HLA B*5801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.353737	0.987852	-3.365885	22580.662420
HLA B*4403	1:9-17	9	VTAVVLLCC	1.208701	0.051365	-4.626091	1.260066	-3.366025	42275.750783
HLA A*0202	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.433330	1.067238	-3.366093	27122.528957
HLA B*4001	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.366318	1.000164	-3.366154	23244.390898
HLA A*0301	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.343599	0.977336	-3.366263	22059.651662
HLA B*1801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.386007	1.019585	-3.366422	24322.423977
HLA A*1101	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.343808	0.977336	-3.366472	22070.275503
HLA B*5801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.352414	0.985844	-3.366570	22511.991601
HLA A*1101	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.433824	1.067238	-3.366586	27153.359740
HLA B*4002	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.438640	1.071973	-3.366667	27456.173948
HLA B*1517	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.365888	0.999064	-3.366825	23221.390113
HLA B*5701	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.384675	1.017829	-3.366846	24247.931508

HLA A*8001 1:141-149 9 PITYDTLWQ 1.144380 -0.171882 -4.339454
0.972498 -3.366956 21850.136721

HLA A*3201 1:149-157 9 QADTDPLPV 0.679726 0.062986 -4.109714
0.742712 -3.367002 12874.028518

HLA B*7301 1:37-45 9 TGQACQIQM 1.304282 -0.067488 -4.604067
1.236794 -3.367273 40185.303866

HLA B*4801 1:123-131 9 THPTTTYKA 1.324444 -0.257206 -4.434526
1.067238 -3.367288 27197.317386

HLA B*3501 1:123-131 9 THPTTTYKA 1.324444 -0.257206 -4.434597
1.067238 -3.367359 27201.731778

HLA B*2705 1:210-218 9 AAGPTQVLV 0.899889 0.077447 -4.344907
0.977336 -3.367571 22126.224444

HLA B*3901 1:110-118 9 QAVVLKVYQ 1.073710 0.019058 -4.460638
1.092768 -3.367871 28882.730352

HLA A*0250 1:122-130 9 GTHPTTTYK 0.923012 0.114876 -4.406184
1.037888 -3.368296 25479.108712

HLA A*0211 1:185-193 9 VNYQNFAVT 1.248328 -0.327759 -4.289081
0.920569 -3.368512 19457.238410

HLA A*0301 1:25-33 9 PKTYCEELK 0.921220 0.066632 -4.356375
0.987852 -3.368523 22718.264407

HLA A*6801 1:62-70 9 DQKSLENYI 1.150042 0.062507 -4.581181
1.212549 -3.368632 38122.460511

HLA B*1501 1:116-124 9 VYQNAGGTH 1.000005 -0.059940 -4.308845
0.940065 -3.368780 20363.155054

HLA A*2603 1:35-43 9 TDTGQACQI 1.187370 0.059542 -4.617086
1.246912 -3.370174 41408.142865

HLA B*4402 1:180-188 9 AGLDPVNYQ 1.025360 -0.030868 -4.364951
0.994492 -3.370459 23171.319738

HLA A*3002 1:189-197 9 NFAVTNDGV 0.789539 0.210625 -4.370651
1.000164 -3.370486 23477.433585

HLA A*0211 1:153-161 9 DPLPVVFPI 0.780193 -0.026100 -4.124751
0.754093 -3.370658 13327.576095

HLA B*2705	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.224228	0.853458	-3.370771	16758.238458
HLA A*8001	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.370153	0.999064	-3.371089	23450.522833
HLA B*1501	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.338272	0.967178	-3.371094	21790.759516
HLA A*2603	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.295906	0.924700	-3.371206	19765.438527
HLA B*4801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.418122	1.046875	-3.371247	26189.183891
HLA B*4501	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.258012	0.886699	-3.371313	18113.885187
HLA B*4402	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.444450	1.071973	-3.372478	27825.968814
HLA B*0801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.326779	0.954256	-3.372523	21221.627502
HLA A*8001	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.448388	1.075733	-3.372655	28079.413406
HLA A*0211	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.456195	1.083538	-3.372657	28588.763342
HLA B*1502	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.113276	0.740601	-3.372675	12980.047630
HLA B*4403	1:72-80	9	QTRDKFLSA	1.401913	-0.147149	-4.627649	1.254764	-3.372885	42427.655867
HLA B*1801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.448181	1.075247	-3.372934	28066.048815
HLA A*3101	1:18-26	9	SGVATAAPK	0.424227	0.140104	-3.937300	0.564331	-3.372969	8655.653437
HLA B*0702	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.440679	1.067238	-3.373442	27585.405388
HLA B*4801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.362608	0.987852	-3.374757	23046.677970

HLA B*3501	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.392830	1.017829	-3.375001	24707.554333
HLA B*4001	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.393109	1.017829	-3.375280	24723.465604
HLA B*1517	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.451370	1.076055	-3.375315	28272.845984
HLA B*4402	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.422412	1.046875	-3.375537	26449.174672
HLA B*0801	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.389129	1.013420	-3.375709	24497.926098
HLA A*0202	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.452143	1.076055	-3.376088	28323.212318
HLA B*4402	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.389804	1.013420	-3.376384	24535.992057
HLA B*7301	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.333129	0.956718	-3.376411	21534.229894
HLA B*3501	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.024950	0.648272	-3.376677	10591.311639
HLA B*4601	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.390102	1.013420	-3.376682	24552.855448
HLA A*0211	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.039601	0.662917	-3.376684	10954.716313
HLA A*2601	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.379236	1.002409	-3.376827	23946.146704
HLA B*5401	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.444067	1.067238	-3.376830	27801.442358
HLA A*0219	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.460495	1.083538	-3.376957	28873.200530
HLA B*5101	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.444246	1.067238	-3.377008	27812.875315
HLA B*5401	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.297673	0.920569	-3.377104	19846.012794

HLA A*2602	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.608632	1.231508	-3.377124	40609.936089
HLA A*3002	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.390553	1.013420	-3.377133	24578.371717
HLA B*1509	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.469952	1.092768	-3.377184	29508.803761
HLA A*0206	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.040118	0.662917	-3.377201	10967.762111
HLA A*3201	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.956984	0.579719	-3.377265	9056.989094
HLA B*2705	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.453569	1.076055	-3.377514	28416.373036
HLA A*6901	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.298183	0.920569	-3.377614	19869.324621
HLA A*2902	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.397282	1.019585	-3.377698	24962.152562
HLA B*4001	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.391270	1.013420	-3.377850	24618.959905
HLA A*0219	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.449882	1.071973	-3.377910	28176.192347
HLA B*2705	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.366316	0.987852	-3.378464	23244.265149
HLA B*3801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.416759	1.037888	-3.378871	26107.137940
HLA A*0101	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.381421	1.002409	-3.379012	24066.928066
HLA A*0206	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.133167	0.754093	-3.379074	13588.359433
HLA A*6801	1:150-158	9	ADTDPLPVV	1.257750	0.027453	-4.664374	1.285203	-3.379171	46171.484449
HLA A*0101	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.347146	0.967178	-3.379968	22240.593514

HLA A*6801	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.617227	1.236794	-3.380433	41421.585854
HLA A*2501	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.418552	1.037888	-3.380664	26215.124275
HLA A*2603	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.612220	1.231508	-3.380712	40946.800224
HLA A*2602	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.400553	1.019585	-3.380968	25150.841266
HLA A*2602	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.237228	0.856017	-3.381211	17267.444403
HLA A*2601	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.400797	1.019585	-3.381212	25164.995827
HLA B*4601	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.301825	0.920569	-3.381256	20036.635928
HLA B*5301	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.402145	1.020870	-3.381276	25243.261549
HLA A*3101	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.189536	0.808230	-3.381306	15471.622856
HLA A*6801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-3.725992	0.344471	-3.381521	5320.983072
HLA A*3002	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.061719	0.680076	-3.381643	11527.076814
HLA A*3001	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-3.834782	0.452621	-3.382161	6835.691128
HLA B*5301	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.429125	1.046875	-3.382250	26861.150081
HLA B*4001	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.401856	1.019585	-3.382272	25226.469857
HLA B*7301	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.561516	1.179033	-3.382483	36434.744953
HLA B*0801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.339661	0.956718	-3.382943	21860.541397

HLA B*0702	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.360322	0.977336	-3.382986	22925.683083
HLA B*4402	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.400992	1.017829	-3.383163	25176.297970
HLA B*1517	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.173832	0.790540	-3.383292	14922.167566
HLA A*0203	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.377948	0.994492	-3.383456	23875.260624
HLA A*1101	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.459612	1.076055	-3.383557	28814.528717
HLA B*4402	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.237085	0.853458	-3.383627	17261.747030
HLA B*4402	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.360997	0.977336	-3.383660	22961.306022
HLA B*5801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.356227	0.972498	-3.383729	22710.522819
HLA B*5101	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.467320	1.083538	-3.383782	29330.548258
HLA B*0803	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.476826	1.092768	-3.384059	29979.625083
HLA B*2705	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.338561	0.954256	-3.384306	21805.264270
HLA B*0801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.361692	0.977336	-3.384356	22998.104040
HLA A*0211	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.452406	1.067238	-3.385168	28340.378767
HLA A*0202	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.127923	0.742712	-3.385211	13425.268358
HLA B*1501	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.340523	0.954978	-3.385545	21903.987072
HLA B*3501	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.387990	1.002409	-3.385581	24433.732784

HLA B*1501	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.371494	0.985844	-3.385650	23523.074594
HLA B*1509	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.363118	0.977336	-3.385782	23073.749411
HLA B*1801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.342508	0.956718	-3.385790	22004.347218
HLA A*3001	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.176445	0.790540	-3.385905	15012.206851
HLA B*2705	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.403795	1.017829	-3.385966	25339.311219
HLA A*0206	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.453226	1.067238	-3.385988	28393.937401
HLA B*0802	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.461754	1.075733	-3.386021	28957.045671
HLA A*3201	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.461773	1.075733	-3.386040	28958.298933
HLA B*2705	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.453327	1.067238	-3.386089	28400.543316
HLA A*2603	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.424313	1.037888	-3.386425	26565.185820
HLA A*0219	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.381510	0.994492	-3.387018	24071.876152
HLA A*0201	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.381576	0.994492	-3.387084	24075.522761
HLA A*2902	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.341672	0.954583	-3.387089	21962.009377
HLA A*8001	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.387550	1.000164	-3.387386	24409.026915
HLA A*3301	1:35-43	9	TDTGQACQI	1.187370	0.059542	-4.634653	1.246912	-3.387741	43117.428553
HLA B*5701	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.407552	1.019585	-3.387967	25559.457525

HLA A*0101	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.373815	0.985844	-3.387971	23649.141344
HLA A*2301	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.526866	1.138874	-3.387992	33640.739108
HLA A*2601	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.374100	0.985844	-3.388255	23664.627059
HLA A*2602	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.401725	1.013420	-3.388305	25218.828560
HLA A*3002	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.309052	0.920569	-3.388483	20372.851654
HLA A*0203	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.361119	0.972498	-3.388621	22967.766273
HLA A*2403	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.387731	0.999064	-3.388668	24419.196893
HLA B*4001	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.387966	0.999064	-3.388903	24432.410982
HLA B*1517	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.464271	1.075247	-3.389023	29125.309530
HLA B*4001	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.375061	0.985844	-3.389216	23717.046441
HLA A*0216	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.464494	1.075247	-3.389246	29140.282023
HLA B*3901	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.366920	0.977336	-3.389584	23276.605092
HLA A*3101	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.389996	1.000164	-3.389832	24546.878906
HLA B*1502	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.465800	1.075733	-3.390067	29228.064984
HLA B*4001	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.243630	0.853458	-3.390173	17523.885747
HLA B*4001	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.367568	0.977336	-3.390232	23311.386035

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HLA B*4601	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.330550
	0.940065	-3.390485	21406.694473

HLA A*3301	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.474049
	1.083538	-3.390511	29788.532323

HLA A*0212	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.385018
	0.994492	-3.390526	24267.091152

HLA B*4601	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.390835
	1.000164	-3.390671	24594.332850

HLA B*4601	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.393380
	1.002409	-3.390971	24738.851779

HLA B*0802	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.318687
	0.927533	-3.391154	20829.894046

HLA A*0101	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.385753
	0.994492	-3.391261	24308.217313

HLA B*0801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.429204
	1.037888	-3.391316	26866.091274

HLA B*4501	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.628281
	1.236794	-3.391487	42489.444093

HLA A*3201	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.530369
	1.138874	-3.391495	33913.187505

HLA A*0219	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.429505
	1.037888	-3.391617	26884.701566

HLA B*4601	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.319230
	0.927533	-3.391697	20855.941111

HLA B*1503	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.331870
	0.940065	-3.391805	21471.877521

HLA A*0201	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.239190
	0.847335	-3.391855	17345.622336

HLA A*0101	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.346841
	0.954978	-3.391863	22224.957525

HLA A*2301	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.459621
	1.067238	-3.392383	28815.152258
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HLA A*1101	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.279089	0.886699	-3.392390	19014.672102
HLA B*4501	1:132-140	9	FDWDQAYRK	1.061895	0.169613	-4.624111	1.231508	-3.392603	42083.389645
HLA B*5401	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.063815	0.671022	-3.392793	11582.836548
HLA B*0702	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.412410	1.019585	-3.392826	25847.013346
HLA A*3002	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.201871	0.809025	-3.392846	15917.346358
HLA B*4501	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.515792	1.122935	-3.392857	32793.850021
HLA B*1502	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.596939	1.203934	-3.393005	39531.101809
HLA A*3101	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.349811	0.956718	-3.393092	22377.454805
HLA B*3901	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.465354	1.071973	-3.393381	29198.037507
HLA A*2403	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.348427	0.954978	-3.393449	22306.264213
HLA B*1503	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.379410	0.985844	-3.393565	23955.735027
HLA B*4002	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.350311	0.956718	-3.393593	22403.255352
HLA B*5801	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.348234	0.954583	-3.393651	22296.371105
HLA B*0803	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.469865	1.076055	-3.393810	29502.897696
HLA A*2301	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.469482	1.075247	-3.394234	29476.893156
HLA B*1801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.412178	1.017829	-3.394349	25833.173935

HLA B*1501	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.248139	0.853458	-3.394681	17706.758934
HLA B*0801	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.394991	1.000164	-3.394827	24830.832782
HLA B*5801	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.362059	0.967178	-3.394881	23017.521315
HLA A*2601	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.367387	0.972498	-3.394889	23301.677432
HLA B*1503	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.247942	0.852998	-3.394944	17698.714268
HLA B*1801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.230283	0.835252	-3.395031	16993.505980
HLA B*5401	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.533935	1.138874	-3.395062	34192.836478
HLA A*6901	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.381449	0.985844	-3.395605	24068.490510
HLA B*4501	1:62-70	9	DQKSLENYI	1.150042	0.062507	-4.608205	1.212549	-3.395655	40569.971231
HLA A*0216	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.143951	0.748062	-3.395889	13930.001471
HLA B*0702	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.443048	1.046875	-3.396173	27736.244146
HLA A*0211	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.488950	1.092768	-3.396182	30828.297402
HLA B*1501	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.305654	0.909340	-3.396315	20214.102686
HLA B*5801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.353342	0.956718	-3.396624	22560.149051
HLA B*4801	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.103747	0.706847	-3.396900	12698.334846
HLA A*0206	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.016402	0.619394	-3.397009	10384.900037

HLA A*2603	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.137673	0.740601	-3.397072	13730.088556
HLA A*3101	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.244439	0.847335	-3.397103	17556.528095
HLA B*1801	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.480731	1.083538	-3.397193	30250.394411
HLA A*2601	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.396269	0.999064	-3.397206	24904.017056
HLA B*5801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.351498	0.954256	-3.397242	22464.544594
HLA A*0206	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.435149	1.037888	-3.397260	27236.335983
HLA A*0301	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.364457	0.967178	-3.397279	23145.010289
HLA A*3002	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.464780	1.067238	-3.397543	29159.521146
HLA B*5301	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.123045	0.725355	-3.397691	13275.333640
HLA A*6901	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-3.978049	0.579719	-3.398331	9507.127698
HLA B*4001	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.355059	0.956718	-3.398341	22649.542713
HLA B*4501	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.470367	1.071973	-3.398395	29537.073460
HLA B*5701	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.398804	1.000164	-3.398640	25049.813650
HLA A*0216	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.150591	0.751912	-3.398679	14144.604445
HLA A*0301	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.355480	0.956718	-3.398762	22671.486477
HLA A*8001	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.401643	1.002409	-3.399234	25214.053925

HLA A*3201	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.417109	1.017829	-3.399280	26128.190695
HLA A*2501	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.356645	0.956718	-3.399927	22732.402683
HLA B*0803	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.475290	1.075247	-3.400042	29873.742566
HLA A*0211	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.148124	0.748062	-3.400062	14064.485435
HLA A*0202	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.320766	0.920569	-3.400198	20929.861529
HLA B*4403	1:37-45	9	TGQACQIQM	1.304282	-0.067488	-4.637251	1.236794	-3.400458	43376.188026
HLA A*2601	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.377880	0.977336	-3.400544	23871.515205
HLA B*5401	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.484091	1.083538	-3.400553	30485.323292
HLA A*2501	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.418425	1.017829	-3.400596	26207.467065
HLA B*4801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.418933	1.017829	-3.401104	26238.109335
HLA A*2601	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.395976	0.994492	-3.401484	24887.181753
HLA B*1517	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-3.874103	0.472542	-3.401561	7483.476718
HLA B*0702	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.387428	0.985844	-3.401584	24402.161274
HLA A*0203	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.322578	0.920569	-3.402009	21017.342812
HLA A*0101	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.255016	0.852998	-3.402018	17989.372608
HLA A*2602	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.104926	0.702905	-3.402021	12732.867401

HLA B*4801 1:21-29 9 ATAAPKTYC 0.926919 0.086501 -4.415533 1.013420 -3.402113 26033.516372

HLA A*6802 1:180-188 9 AGLDPVNYQ 1.025360 -0.030868 -4.396852 0.994492 -3.402360 24937.452017

HLA A*6801 1:21-29 9 ATAAPKTYC 0.926919 0.086501 -4.415930 1.013420 -3.402510 26057.328952

HLA A*1101 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.211569 0.809025 -3.402545 16276.811749

HLA B*1501 1:155-163 9 LPVVFPIVQ 1.161225 -0.206642 -4.357132 0.954583 -3.402549 22757.873756

HLA A*0301 1:155-163 9 LPVVFPIVQ 1.161225 -0.206642 -4.357355 0.954583 -3.402772 22769.572932

HLA B*0803 1:142-150 9 ITYDTLWQA 1.233555 -0.212685 -4.423669 1.020870 -3.402799 26525.837161

HLA B*1517 1:123-131 9 THPTTTYKA 1.324444 -0.257206 -4.470111 1.067238 -3.402874 29519.661234

HLA A*6901 1:169-177 9 QTGQQVSIA 0.950594 -0.262137 -4.091492 0.688457 -3.403035 12345.021799

HLA A*3002 1:15-23 9 LCCSGVATA 1.215808 -0.196223 -4.422788 1.019585 -3.403204 26472.078520

HLA A*0101 1:25-33 9 PKTYCEELK 0.921220 0.066632 -4.391204 0.987852 -3.403352 24615.230984

HLA A*3201 1:21-29 9 ATAAPKTYC 0.926919 0.086501 -4.416881 1.013420 -3.403462 26114.483282

HLA B*2705 1:102-110 9 SAIPPRGTQ 1.076283 0.007255 -4.487084 1.083538 -3.403546 30696.159929

HLA A*0301 1:116-124 9 VYQNAGGTH 1.000005 -0.059940 -4.343676 0.940065 -3.403612 22063.590243

HLA A*2602 1:110-118 9 QAVVLKVYQ 1.073710 0.019058 -4.496421 1.092768 -3.403653 31363.238620

HLA B*1509 1:218-226 9 VPRSAIDSM 0.858689 0.068844 -4.331677 0.927533 -3.404144 21462.354474

HLA B*0803	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.488177	1.083538	-3.404639	30773.476349
HLA B*1509	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.156577	0.751912	-3.404665	14340.929297
HLA A*3101	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.325555	0.920569	-3.404986	21161.897452
HLA B*3501	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.005801	0.600517	-3.405284	10134.479398
HLA B*0803	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.404392	0.999064	-3.405328	25374.154200
HLA B*0801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.391324	0.985844	-3.405480	24622.023370
HLA A*2501	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.452807	1.046875	-3.405933	28366.608328
HLA B*5101	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.408517	1.002409	-3.406109	25616.351297
HLA A*0203	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.158556	0.751912	-3.406643	14406.403054
HLA B*5101	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.482535	1.075733	-3.406802	30376.340053
HLA B*0801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.379311	0.972498	-3.406813	23950.292535
HLA B*1517	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.424884	1.017829	-3.407055	26600.131460
HLA B*4402	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.426827	1.019585	-3.407242	26719.406489
HLA A*6801	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.530282	1.122935	-3.407347	33906.399921
HLA A*0101	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.379877	0.972498	-3.407379	23981.538891
HLA A*2603	1:3-11	9	IKIFMLVTA	1.316552	-0.112618	-4.611482	1.203934	-3.407549	40877.302726

HLA A*0201	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.395471	0.987852	-3.407619	24858.251648
HLA A*2603	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.428765	1.020870	-3.407895	26838.925955
HLA B*0803	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.484044	1.075733	-3.408311	30482.025026
HLA B*3801	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.501136	1.092768	-3.408369	31705.625002
HLA A*2403	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.402933	0.994492	-3.408441	25289.051717
HLA A*8001	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.348601	0.940065	-3.408536	22315.195907
HLA A*3001	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.097098	0.688457	-3.408641	12505.404165
HLA A*8001	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.428810	1.019585	-3.409225	26841.684814
HLA B*1801	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.476483	1.067238	-3.409246	29955.955211
HLA B*5301	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.386641	0.977336	-3.409305	24357.976973
HLA A*3301	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.484645	1.075247	-3.409398	30524.269793
HLA B*4001	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.364389	0.954978	-3.409411	23141.379428
HLA B*0802	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.476810	1.067238	-3.409572	29978.489800
HLA A*0201	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.363910	0.954256	-3.409654	23115.854287
HLA B*5801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.349750	0.940065	-3.409685	22374.307478
HLA A*6901	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.382304	0.972498	-3.409806	24115.932869

HLA B*5701	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.404474	0.994492	-3.409982	25378.959152
HLA A*6901	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.319437	0.909340	-3.410097	20865.872368
HLA B*3901	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.448000	1.037888	-3.410112	28054.360015
HLA A*8001	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.219022	0.808230	-3.410792	16558.534874
HLA A*2601	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.398997	0.987852	-3.411145	25060.928486
HLA B*2705	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.410235	0.999064	-3.411171	25717.855034
HLA A*0219	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.298023	0.886699	-3.411325	19862.016588
HLA A*8001	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.388690	0.977336	-3.411354	24473.155321
HLA B*4501	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-3.931252	0.519628	-3.411624	8535.958304
HLA B*2705	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-3.796035	0.384238	-3.411797	6252.226807
HLA A*0301	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.366400	0.954256	-3.412145	23248.792550
HLA B*4801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.398107	0.985844	-3.412262	25009.597503
HLA B*0801	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.379792	0.967178	-3.412615	23976.868797
HLA B*3801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.551498	1.138874	-3.412624	35603.896487
HLA A*3001	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.266110	0.853458	-3.412653	18454.840050
HLA B*1501	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.101172	0.688457	-3.412715	12623.266160

HLA B*1503	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.120339	0.707433	-3.412905	13192.856482
HLA A*6901	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-3.979445	0.566374	-3.413071	9537.727747
HLA B*3901	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.488903	1.075733	-3.413169	30824.962029
HLA A*0212	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.299877	0.886699	-3.413178	19946.976863
HLA B*5101	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.413693	1.000164	-3.413529	25923.473109
HLA A*0212	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.193413	0.779687	-3.413725	15610.345688
HLA B*1503	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.413938	1.000164	-3.413773	25938.062496
HLA B*4801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.433380	1.019585	-3.413795	27125.610459
HLA B*0801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.217951	0.804086	-3.413865	16517.736811
HLA B*4402	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.368454	0.954256	-3.414198	23358.978782
HLA A*3301	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.537394	1.122935	-3.414458	34466.213289
HLA A*0206	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.700693	0.286028	-3.414665	5019.871762
HLA A*3101	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.387231	0.972498	-3.414733	24391.074702
HLA A*0101	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.371503	0.956718	-3.414785	23523.583628
HLA B*4801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.370077	0.954978	-3.415099	23446.463513
HLA A*2501	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.428873	1.013420	-3.415453	26845.605785

HLA B*1501 1:184-192 9 PVNYQNFAV 0.967153 -0.114155 -4.269378 0.852998 -3.416381 18594.239440

HLA A*0201 1:160-168 9 PIVQGELSK 0.947962 0.037882 -4.402310 0.985844 -3.416466 25252.822787

HLA A*2402 1:8-16 9 LVTAVVLLC 0.979168 0.067707 -4.463361 1.046875 -3.416487 29064.395780

HLA B*0801 1:95-103 9 ITSATYQSA 0.951011 -0.171324 -4.196288 0.779687 -3.416601 15714.055771

HLA B*4601 1:160-168 9 PIVQGELSK 0.947962 0.037882 -4.402456 0.985844 -3.416611 25261.294335

HLA A*6901 1:63-71 9 QKSLENYIA 1.220826 -0.266570 -4.370893 0.954256 -3.416637 23490.519293

HLA A*3002 1:104-112 9 IPPRGTQAV 1.002370 0.073685 -4.492725 1.076055 -3.416671 31097.477509

HLA A*2301 1:122-130 9 GTHPTTTYK 0.923012 0.114876 -4.454574 1.037888 -3.416686 28482.245464

HLA B*5701 1:13-21 9 VLLCCSGVA 1.166577 -0.167513 -4.415841 0.999064 -3.416777 26051.972747

HLA B*5701 1:172-180 9 QQVSIAPNA 1.175074 -0.172665 -4.419236 1.002409 -3.416827 26256.426664

HLA B*1801 1:189-197 9 NFAVTNDGV 0.789539 0.210625 -4.417020 1.000164 -3.416856 26122.819924

HLA B*3801 1:102-110 9 SAIPPRGTQ 1.076283 0.007255 -4.500615 1.083538 -3.417077 31667.569549

HLA A*3201 1:111-119 9 AVVLKVYQN 1.224563 -0.434023 -4.207735 0.790540 -3.417195 16133.737297

HLA A*6901 1:25-33 9 PKTYCEELK 0.921220 0.066632 -4.405106 0.987852 -3.417254 25415.919028

HLA B*0802 1:142-150 9 ITYDTLWQA 1.233555 -0.212685 -4.438130 1.020870 -3.417260 27423.960796

HLA B*3501 1:122-130 9 GTHPTTTYK 0.923012 0.114876 -4.455159 1.037888 -3.417271 28520.638679

HLA B*5701	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.372347	0.954978	-3.417369	23569.314354
HLA B*1501	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-3.864132	0.446632	-3.417500	7313.616731
HLA A*0216	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.119559	0.701666	-3.417893	13169.182281
HLA A*0206	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.304686	0.886699	-3.417988	20169.098165
HLA B*5801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.338599	0.920569	-3.418030	21807.151776
HLA A*0216	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.172178	0.754093	-3.418085	14865.443654
HLA B*7301	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.372462	0.954256	-3.418206	23575.563044
HLA A*3201	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.420697	1.002409	-3.418288	26344.927071
HLA B*1517	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.373268	0.954978	-3.418290	23619.350283
HLA A*0216	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.391432	0.972498	-3.418934	24628.151443
HLA B*1501	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.205573	0.786460	-3.419114	16053.637602
HLA B*1509	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.495124	1.075733	-3.419391	31269.719578
HLA B*3901	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.466336	1.046875	-3.419461	29264.138722
HLA A*0101	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.373862	0.954256	-3.419607	23651.700267
HLA A*2301	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.495808	1.076055	-3.419753	31318.985571
HLA B*0803	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.487155	1.067238	-3.419917	30701.142218

HLA B*0802	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.466928	1.046875	-3.420053	29304.061497
HLA B*4801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.397679	0.977336	-3.420343	24984.985176
HLA A*2403	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.267734	0.847335	-3.420399	18523.957658
HLA A*0101	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.375531	0.954583	-3.420948	23742.721647
HLA B*0803	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.468084	1.046875	-3.421209	29382.163000
HLA A*0250	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.393744	0.972498	-3.421246	24759.604818
HLA B*4403	1:96-104	9	TSATYQSAI	0.928477	0.250556	-4.600644	1.179033	-3.421611	39869.799990
HLA B*1801	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.277942	0.856017	-3.421925	18964.539080
HLA B*7301	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.014894	0.592876	-3.422018	10348.894297
HLA A*0206	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.342610	0.920569	-3.422041	22009.466580
HLA A*6901	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.377029	0.954978	-3.422052	23824.811457
HLA B*4402	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.309355	0.886699	-3.422656	20387.074334
HLA A*0206	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.497908	1.075247	-3.422661	31470.824878
HLA B*1801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.425365	1.002409	-3.422957	26629.648096
HLA B*1501	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.377236	0.954256	-3.422980	23836.156441
HLA A*1101	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.422283	0.999064	-3.423219	26441.306052

HLA B*5101	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.443066	1.019585	-3.423482	27737.444572
HLA A*0250	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.310877	0.886699	-3.424179	20458.668846
HLA B*4002	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.426745	1.002409	-3.424336	26714.347752
HLA B*0802	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.424583	1.000164	-3.424419	26581.718154
HLA A*0250	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.517327	1.092768	-3.424559	32909.904334
HLA A*8001	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.438168	1.013420	-3.424748	27426.334668
HLA A*3101	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.215455	0.790540	-3.424915	16423.109512
HLA B*1501	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.397543	0.972498	-3.425045	24977.146778
HLA B*1801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.500923	1.075733	-3.425189	31690.020167
HLA B*3801	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.500481	1.075247	-3.425233	31657.805926
HLA B*3501	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.148425	0.723137	-3.425288	14074.227983
HLA A*3101	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.392576	0.967178	-3.425398	24693.122715
HLA A*0201	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.398043	0.972498	-3.425545	25005.944693
HLA B*1517	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.168297	0.742712	-3.425584	14733.181054
HLA A*0219	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.290279	0.864656	-3.425624	19510.995902
HLA A*0301	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.290808	0.864656	-3.426152	19534.759635

HLA B*0702	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.398668	0.972498	-3.426170	25041.954914
HLA B*4801	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.426348	1.000164	-3.426183	26689.934754
HLA A*8001	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.412098	0.985844	-3.426254	25828.422715
HLA B*0801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.420814	0.994492	-3.426323	26352.054192
HLA A*0216	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.383131	0.956718	-3.426413	24161.900135
HLA B*3801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.502208	1.075733	-3.426474	31783.936461
HLA B*4801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.425727	0.999064	-3.426664	26651.843110
HLA B*5801	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.351394	0.924700	-3.426694	22459.197880
HLA A*2601	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.393880	0.967178	-3.426702	24767.374947
HLA A*6901	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.280289	0.853458	-3.426832	19067.310000
HLA A*6802	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.280334	0.853458	-3.426876	19069.269989
HLA A*2603	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.519657	1.092768	-3.426890	33086.993717
HLA B*5801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.354575	0.927533	-3.427042	22624.315281
HLA A*0301	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.313922	0.886699	-3.427223	20602.613022
HLA B*5301	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.446941	1.019585	-3.427356	27985.994739
HLA A*6901	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.394688	0.967178	-3.427510	24813.509993

HLA A*0203	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.194893	0.767355	-3.427538	15663.640107
HLA B*3501	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.381938	0.954256	-3.427682	24095.588989
HLA B*5701	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.355529	0.927533	-3.427996	22674.062279
HLA A*0219	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.207744	0.779687	-3.428057	16134.086427
HLA B*2705	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.447730	1.019585	-3.428146	28036.911781
HLA A*2601	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.384914	0.956718	-3.428196	24261.315420
HLA B*5301	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.281340	0.852998	-3.428342	19113.474755
HLA A*0201	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.395619	0.967178	-3.428441	24866.725357
HLA B*4801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.422950	0.994492	-3.428458	26481.961924
HLA B*4601	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.383171	0.954583	-3.428588	24164.122361
HLA B*3501	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.414541	0.985844	-3.428697	25974.150343
HLA B*2705	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.369521	0.940065	-3.429456	23416.421041
HLA A*2601	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.324629	0.895143	-3.429486	21116.838983
HLA A*2301	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.324866	0.895143	-3.429723	21128.380352
HLA B*3501	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.239047	0.809025	-3.430022	17339.899169
HLA B*1501	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.239166	0.809025	-3.430142	17344.683983

HLA B*0702	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.386972	0.956718	-3.430254	24376.564189
HLA B*0802	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.407624	0.977336	-3.430288	25563.744373
HLA B*5101	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.502546	1.071973	-3.430573	31808.706559
HLA A*0203	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-3.660004	0.229395	-3.430609	4570.926538
HLA B*4002	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.592099	1.161468	-3.430631	39092.998248
HLA B*1801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.182595	0.751912	-3.430683	15226.338890
HLA A*2301	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.523501	1.092768	-3.430733	33381.132486
HLA B*1509	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.317454	0.886699	-3.430755	20770.817086
HLA B*4601	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.387614	0.956718	-3.430896	24412.592529
HLA A*0216	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.416877	0.985844	-3.431033	26114.200731
HLA B*7301	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.449027	1.017829	-3.431198	28120.762393
HLA A*0101	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.352026	0.920569	-3.431457	22491.905650
HLA B*0802	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.444901	1.013420	-3.431482	27854.886627
HLA B*4601	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.398920	0.967178	-3.431742	25056.454850
HLA A*3201	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.409239	0.977336	-3.431902	25658.931203
HLA B*3901	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.451635	1.019585	-3.432051	28290.134953

HLA B*5701	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.386752	0.954583	-3.432169	24364.171136
HLA B*0702	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.426782	0.994492	-3.432290	26716.660199
HLA A*3002	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.450249	1.017829	-3.432420	28199.981476
HLA A*0101	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.341886	0.909340	-3.432546	21972.823934
HLA A*2402	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.507821	1.075247	-3.432573	32197.385210
HLA A*0219	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.389404	0.956718	-3.432686	24513.437141
HLA A*3001	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.270682	0.837899	-3.432783	18650.152326
HLA B*2705	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.419034	0.985844	-3.433189	26244.213691
HLA B*5401	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.297958	0.864656	-3.433302	19859.008179
HLA B*5701	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.421169	0.987852	-3.433318	26373.589802
HLA B*5701	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.390111	0.956718	-3.433393	24553.386767
HLA B*4601	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.421571	0.987852	-3.433719	26397.999062
HLA B*4601	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.406252	0.972498	-3.433754	25483.106361
HLA A*2902	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.281363	0.847335	-3.434028	19114.508800
HLA A*0203	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.287575	0.853458	-3.434117	19389.882640
HLA A*0212	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.388605	0.954256	-3.434350	24468.389491

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HLA A*0201	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.389353
	0.954978	-3.434375	24510.519785

HLA A*6801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.407343
	0.972498	-3.434845	25547.154116

HLA A*2601	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.175857
	0.740601	-3.435256	14991.916981

HLA B*4001	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.429853
	0.994492	-3.435361	26906.235788

HLA A*2501	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.437921
	1.002409	-3.435513	27410.759882

HLA B*0702	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.375664
	0.940065	-3.435600	23750.044169

HLA B*4801	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.390288
	0.954583	-3.435705	24563.351121

HLA A*2501	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.408369
	0.972498	-3.435871	25607.622142

HLA A*6901	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.376123
	0.940065	-3.436058	23775.111985

HLA B*3801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.438494
	1.002409	-3.436086	27446.966331

HLA A*3101	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.345436
	0.909340	-3.436096	22153.173437

HLA A*0301	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.331269
	0.895143	-3.436126	21442.161021

HLA B*4402	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.435229
	0.999064	-3.436165	27241.346193

HLA A*0301	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.357059
	0.920569	-3.436490	22754.057431

HLA A*3201	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.190598
	0.754093	-3.436505	15509.501442

HLA B*1503	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.403684
	0.967178	-3.436506	25332.869143
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HLA B*3501	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.284446	0.847335	-3.437110	19250.661895
HLA A*2402	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.509219	1.071973	-3.437246	32301.191841
HLA A*0250	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.439655	1.002409	-3.437246	27520.416046
HLA B*1501	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.425102	0.987852	-3.437251	26613.517877
HLA B*4402	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.425325	0.987852	-3.437474	26627.199130
HLA B*3501	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.450930	1.013420	-3.437510	28244.258243
HLA A*0301	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.365174	0.927533	-3.437641	23183.231455
HLA B*1503	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.139388	0.701666	-3.437723	13784.418894
HLA B*4001	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.425626	0.987852	-3.437774	26645.643940
HLA B*5801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.324728	0.886699	-3.438029	21121.637598
HLA A*0201	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.393058	0.954583	-3.438475	24720.523253
HLA A*0212	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-3.826136	0.387379	-3.438758	6700.949207
HLA B*0802	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.424729	0.985844	-3.438885	26590.635507
HLA A*6901	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.303636	0.864656	-3.438981	20120.383764
HLA B*0702	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.426975	0.987852	-3.439123	26728.514630
HLA B*5801	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.348469	0.909340	-3.439130	22308.436458

HLA A*3101	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.325923	0.886699	-3.439225	21179.879000
HLA A*2601	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.394399	0.954978	-3.439421	24797.004169
HLA A*3001	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.295561	0.856017	-3.439544	19749.726237
HLA B*4002	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.191524	0.751912	-3.439611	15542.595145
HLA B*5701	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.425734	0.985844	-3.439890	26652.275664
HLA A*2501	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.438995	0.999064	-3.439931	27478.611875
HLA B*5301	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.163170	0.723137	-3.440033	14560.287472
HLA A*2403	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.425892	0.985844	-3.440048	26661.937868
HLA A*3001	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.207552	0.767355	-3.440197	16126.930758
HLA B*0702	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.442667	1.002409	-3.440258	27711.946694
HLA A*6802	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.244676	0.804086	-3.440590	17566.123582
HLA A*6901	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.365374	0.924700	-3.440674	23193.894497
HLA A*2501	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.250000	0.809025	-3.440975	17782.788647
HLA A*3001	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.245376	0.804086	-3.441290	17594.465595
HLA B*4001	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.381738	0.940065	-3.441673	24084.511407
HLA B*0702	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.362256	0.920569	-3.441687	23027.983560

HLA A*0206	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.295209	0.853458	-3.441751	19733.706163
HLA B*1517	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.444413	1.002409	-3.442004	27823.560351
HLA A*6802	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.414769	0.972498	-3.442271	25987.784095
HLA A*2601	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.396876	0.954583	-3.442293	24938.801142
HLA A*2601	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.396791	0.954256	-3.442535	24933.944634
HLA A*3002	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.145328	0.702788	-3.442540	13974.232365
HLA A*3001	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.156258	0.713674	-3.442584	14330.381912
HLA A*1101	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.444995	1.002409	-3.442587	27860.914954
HLA A*0301	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.251818	0.809025	-3.442794	17857.405815
HLA A*3201	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.290143	0.847335	-3.442808	19504.874827
HLA B*3801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.370552	0.927533	-3.443019	23472.099758
HLA A*2602	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.519126	1.076055	-3.443072	33046.565122
HLA B*2705	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.456581	1.013420	-3.443161	28614.139172
HLA B*4001	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.370827	0.927533	-3.443294	23486.961291
HLA B*4001	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.415871	0.972498	-3.443373	26053.805009
HLA B*3901	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.464308	1.020870	-3.443438	29127.830674

HLA B*0801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.398469	0.954978	-3.443491	25030.442254
HLA A*0206	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.398107	0.954256	-3.443851	25009.597503
HLA A*2602	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.516253	1.071973	-3.444280	32828.641037
HLA A*0301	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.354338	0.909340	-3.444999	22611.956759
HLA A*2902	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.432872	0.987852	-3.445020	27093.931718
HLA A*0202	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-3.832485	0.387379	-3.445106	6799.619873
HLA B*1509	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.458550	1.013420	-3.445130	28744.155494
HLA A*0101	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.372859	0.927533	-3.445326	23597.127360
HLA A*2601	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.385483	0.940065	-3.445418	24293.098969
HLA A*6802	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.400057	0.954583	-3.445474	25122.148297
HLA B*1517	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.366635	0.920569	-3.446067	23261.373292
HLA A*0219	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.431930	0.985844	-3.446086	27035.218784
HLA A*2301	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.529760	1.083538	-3.446222	33865.702934
HLA A*3001	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.281537	0.835252	-3.446285	19122.162478
HLA B*5101	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.484330	1.037888	-3.446442	30502.150001
HLA B*4501	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.607935	1.161468	-3.446467	40544.738990

HLA B*4001	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.223190	0.776623	-3.446567	16718.214515
HLA B*3501	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.403308	0.956718	-3.446590	25310.950948
HLA B*3501	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.205108	0.758478	-3.446630	16036.450826
HLA B*4601	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.401650	0.954978	-3.446672	25214.463144
HLA A*2501	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.447364	1.000164	-3.447199	28013.260215
HLA A*2603	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.441748	0.994492	-3.447256	27653.390490
HLA B*3901	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.446346	0.999064	-3.447283	27947.716455
HLA B*0702	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.300749	0.853458	-3.447291	19987.052023
HLA A*6901	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.066799	0.619394	-3.447405	11662.691121
HLA A*2602	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.285397	0.837899	-3.447498	19292.886433
HLA A*1101	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.435372	0.987852	-3.447520	27250.337409
HLA A*2603	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.136118	0.688457	-3.447661	13681.004296
HLA A*2501	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.442559	0.994492	-3.448067	27705.051298
HLA A*8001	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.404814	0.956718	-3.448096	25398.875079
HLA B*0802	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.403085	0.954978	-3.448107	25297.945994
HLA A*2301	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.403454	0.954978	-3.448476	25319.441997

HLA A*0203	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.415695	0.967178	-3.448517	26043.236038
HLA B*1509	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.402850	0.954256	-3.448595	25284.263787
HLA A*2402	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.587633	1.138874	-3.448759	38693.018326
HLA A*0206	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.129262	0.680076	-3.449186	13466.730905
HLA A*0219	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.403445	0.954256	-3.449189	25318.894102
HLA A*1101	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.358645	0.909340	-3.449305	22837.299752
HLA A*2402	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.487279	1.037888	-3.449391	30709.946238
HLA B*5701	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.422316	0.972498	-3.449818	26443.308752
HLA A*3201	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.526055	1.076055	-3.450000	33578.010195
HLA B*3501	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.405197	0.954978	-3.450219	25421.281988
HLA B*0801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.438205	0.987852	-3.450354	27428.708746
HLA A*8001	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.405066	0.954583	-3.450483	25413.581681
HLA A*2602	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.573554	1.122935	-3.450619	37458.854716
HLA A*8001	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.445341	0.994492	-3.450849	27883.080262
HLA B*7301	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.589843	1.138874	-3.450970	38890.495317
HLA B*0802	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.470746	1.019585	-3.451161	29562.811226

HLA B*0702	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.451339	1.000164	-3.451175	28270.857666
HLA B*4001	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.418585	0.967178	-3.451407	26217.109844
HLA A*2603	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.527634	1.076055	-3.451579	33700.303381
HLA A*3101	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.405898	0.954256	-3.451642	25462.297884
HLA B*4402	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.437688	0.985844	-3.451844	27396.083184
HLA A*0201	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.131931	0.680076	-3.451855	13549.747338
HLA A*2501	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.219243	0.767355	-3.451888	16566.957520
HLA A*3201	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.139544	0.687624	-3.451919	13789.341537
HLA B*1502	1:1-9	9	VRIKIFMLV	0.881917	0.241018	-4.575021	1.122935	-3.452085	37585.520902
HLA A*0203	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.440031	0.987852	-3.452179	27544.247543
HLA A*0212	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.228857	0.776623	-3.452234	16937.794182
HLA A*3001	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.238715	0.786460	-3.452256	17326.677435
HLA A*1101	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.242820	0.790540	-3.452280	17491.209464
HLA A*0201	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.372911	0.920569	-3.452342	23599.936000
HLA B*4001	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.406598	0.954256	-3.452342	25503.379956
HLA B*5401	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.454802	1.002409	-3.452394	28497.195708

HLA A*2501	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.472350	1.019585	-3.452766	29672.246517
HLA A*0203	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.439108	0.985844	-3.453263	27485.748301
HLA A*0216	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.373862	0.920569	-3.453294	23651.700267
HLA A*8001	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.378084	0.924700	-3.453384	23882.753225
HLA A*2403	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.407765	0.954256	-3.453510	25572.043541
HLA A*3101	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.233337	0.779687	-3.453650	17113.440104
HLA A*2402	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.431145	0.977336	-3.453809	26986.412874
HLA B*0803	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.456325	1.002409	-3.453916	28597.271020
HLA B*3501	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.448459	0.994492	-3.453967	28083.970972
HLA B*4402	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.408696	0.954583	-3.454113	25626.885665
HLA A*0202	1:94-102	9	NITSATYQS	1.243610	-0.899139	-3.798605	0.344471	-3.454134	6289.339820
HLA A*0202	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-3.855853	0.401614	-3.454238	7175.507329
HLA A*6802	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.442108	0.987852	-3.454256	27676.289037
HLA B*5101	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.453369	0.999064	-3.454305	28403.309039
HLA A*3101	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.381928	0.927533	-3.454395	24095.067577
HLA B*5701	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.408825	0.954256	-3.454569	25634.511923

HLA A*2403	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.382201	0.927533	-3.454668	24110.193113
HLA B*1501	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.349902	0.895143	-3.454759	22382.176626
HLA B*5701	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.422015	0.967178	-3.454837	26425.004003
HLA B*1801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.454135	0.999064	-3.455071	28453.445991
HLA B*3801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.527265	1.071973	-3.455292	33671.692094
HLA B*1509	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.380695	0.924700	-3.455995	24026.730055
HLA A*0206	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.383949	0.927533	-3.456416	24207.431175
HLA B*2705	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.456719	1.000164	-3.456555	28623.273789
HLA A*0212	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.444455	0.987852	-3.456603	27826.269886
HLA B*4001	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.377241	0.920569	-3.456672	23836.414344
HLA A*0211	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.531924	1.075247	-3.456676	34034.860130
HLA A*2301	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.455754	0.999064	-3.456690	28559.701659
HLA B*4801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.429247	0.972498	-3.456749	26868.707568
HLA B*4801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.411012	0.954256	-3.456757	25763.948567
HLA B*4001	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.366144	0.909340	-3.456805	23235.087292
HLA A*3001	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.232116	0.775271	-3.456845	17065.365213

HLA B*1501	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.197637	0.740601	-3.457036	15762.928099
HLA B*0702	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.344132	0.886699	-3.457433	22086.758544
HLA B*4402	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.429952	0.972498	-3.457454	26912.349992
HLA A*2902	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.344466	0.886699	-3.457767	22103.732205
HLA B*4601	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.412126	0.954256	-3.457870	25830.099516
HLA A*8001	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.445775	0.987852	-3.457924	27911.000440
HLA A*0203	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.385537	0.927533	-3.458004	24296.121885
HLA A*0250	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.039451	0.581216	-3.458234	10950.924086
HLA B*1503	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.383072	0.924700	-3.458372	24158.632526
HLA B*0803	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.444349	0.985844	-3.458505	27819.496544
HLA A*0219	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.386096	0.927533	-3.458563	24327.424593
HLA A*2601	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.386110	0.927533	-3.458577	24328.214257
HLA B*1509	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.478252	1.019585	-3.458668	30078.234075
HLA A*1101	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.426094	0.967178	-3.458916	26674.345233
HLA A*2501	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.199596	0.740601	-3.458996	15834.208710
HLA A*0201	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.399476	0.940065	-3.459412	25088.601430

HLA A*0101	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.354714	0.895143	-3.459571	22631.537741
HLA A*0101	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.399690	0.940065	-3.459626	25100.955587
HLA A*1101	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.479465	1.019585	-3.459880	30162.314851
HLA B*5301	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.202669	0.742712	-3.459957	15946.651068
HLA B*0801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.346756	0.886699	-3.460058	22220.629502
HLA B*4001	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.384825	0.924700	-3.460125	24256.328393
HLA B*5301	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.599152	1.138874	-3.460279	39733.071065
HLA B*5101	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.473845	1.013420	-3.460425	29774.515340
HLA B*0801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.313434	0.852998	-3.460436	20579.442827
HLA A*0212	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.415115	0.954583	-3.460532	26008.459197
HLA A*0212	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.269780	0.809025	-3.460756	18611.448763
HLA B*5801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.355931	0.895143	-3.460788	22695.047556
HLA B*1502	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.463803	1.002409	-3.461394	29093.971027
HLA B*5101	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.356558	0.895143	-3.461416	22727.852886
HLA B*1509	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.464320	1.002409	-3.461911	29128.618576
HLA A*2402	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.545556	1.083538	-3.462018	35120.095012

HLA A*0203	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.417753	0.954978	-3.462775	26166.949483
HLA A*3002	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.509651	1.046875	-3.462776	32333.361088
HLA A*0211	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.214826	0.751912	-3.462914	16399.315714
HLA A*2301	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.535206	1.071973	-3.463234	34293.056951
HLA B*1503	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.215324	0.751912	-3.463412	16418.134822
HLA B*4801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.384113	0.920569	-3.463544	24216.600077
HLA A*6802	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.449464	0.985844	-3.463620	28149.072853
HLA B*0802	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.451776	0.987852	-3.463924	28299.319233
HLA B*1501	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.268288	0.804086	-3.464203	18547.622925
HLA A*0202	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.177920	0.713674	-3.464246	15063.296215
HLA A*6802	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.431547	0.967178	-3.464369	27011.389313
HLA A*2403	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.452709	0.987852	-3.464857	28360.163732
HLA B*1517	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.419579	0.954583	-3.464996	26277.173333
HLA B*0803	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.478443	1.013420	-3.465023	30091.417276
HLA A*0101	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.244906	0.779687	-3.465219	17575.439068
HLA A*3301	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.512212	1.046875	-3.465337	32524.587033

HLA A*2301	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.453251	0.987852	-3.465400	28395.627140
HLA B*5401	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.541456	1.075733	-3.465723	34790.112316
HLA B*1502	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.538136	1.071973	-3.466163	34525.184533
HLA B*0803	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.421153	0.954978	-3.466175	26372.591074
HLA A*0201	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.390992	0.924700	-3.466292	24603.248990
HLA A*6802	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.421407	0.954978	-3.466429	26388.004238
HLA A*2601	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.391129	0.924700	-3.466429	24610.970051
HLA B*1801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.192280	0.725355	-3.466925	15569.693697
HLA A*6802	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.033347	0.566374	-3.466973	10798.086604
HLA A*2902	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.387875	0.920569	-3.467306	24427.256637
HLA A*3301	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.485172	1.017829	-3.467343	30561.281987
HLA A*0201	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.394972	0.927533	-3.467440	24829.758149
HLA B*4001	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.422323	0.954583	-3.467740	26443.737921
HLA B*1801	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.481309	1.013420	-3.467889	30290.679427
HLA B*1503	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.222043	0.754093	-3.467950	16674.136205
HLA A*2402	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.561189	1.092768	-3.468422	36407.357250

HLA B*4402	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.393166	0.924700	-3.468466	24726.675842
HLA B*4801	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.393199	0.924700	-3.468499	24728.548673
HLA A*0202	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.543843	1.075247	-3.468595	34981.860822
HLA A*2301	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.544397	1.075733	-3.468664	35026.551871
HLA A*0212	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.436178	0.967178	-3.469000	27300.949860
HLA A*0202	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.755036	0.286028	-3.469009	5689.003630
HLA B*5701	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.409091	0.940065	-3.469026	25650.187539
HLA A*0250	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.170787	0.701666	-3.469121	14817.910932
HLA B*0802	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.486974	1.017829	-3.469145	30688.355969
HLA A*2501	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.396796	0.927533	-3.469263	24934.214415
HLA A*0219	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.442066	0.972498	-3.469568	27673.594106
HLA B*0803	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.464296	0.994492	-3.469804	29127.042793
HLA A*0250	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.537152	1.067238	-3.469914	34447.013424
HLA B*4601	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.356641	0.886699	-3.469942	22732.156724
HLA A*2902	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.424943	0.954978	-3.469965	26603.729297
HLA B*1801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.390539	0.920569	-3.469970	24577.573933

HLA B*5101	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.464684	0.994492	-3.470192	29153.054122
HLA A*2402	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.545946	1.075733	-3.470213	35151.648484
HLA A*3101	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.274303	0.804086	-3.470217	18806.281810
HLA B*5301	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.553972	1.083538	-3.470434	35807.296913
HLA A*3201	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.554051	1.083538	-3.470513	35813.883778
HLA A*0212	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.391211	0.920569	-3.470642	24615.630484
HLA A*6801	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.470835	1.000164	-3.470671	29568.889249
HLA B*4801	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.437907	0.967178	-3.470729	27409.870161
HLA B*4402	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.425800	0.954978	-3.470822	26656.313174
HLA A*0202	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.443456	0.972498	-3.470958	27762.365139
HLA B*1801	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.508906	1.037888	-3.471018	32277.958999
HLA A*0216	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.426004	0.954978	-3.471027	26668.862197
HLA B*3801	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.491912	1.020870	-3.471042	31039.323022
HLA B*0802	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.395804	0.924700	-3.471104	24877.355200
HLA A*2902	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.425563	0.954256	-3.471307	26641.752175
HLA B*4801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.411623	0.940065	-3.471559	25800.212893

HLA A*0202	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-3.512334	0.040514	-3.471820	3253.377136
HLA B*1502	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.486158	1.013420	-3.472739	30630.800858
HLA B*0802	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.475299	1.002409	-3.472890	29874.389028
HLA B*1517	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.337770	0.864656	-3.473114	21765.546597
HLA B*0802	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.467621	0.994492	-3.473129	29350.865694
HLA A*0212	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.413317	0.940065	-3.473253	25901.043919
HLA A*2601	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.329445	0.856017	-3.473428	21352.333925
HLA A*2403	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.394014	0.920569	-3.473445	24775.013483
HLA A*1101	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.427757	0.954256	-3.473501	26776.709262
HLA B*0702	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.427797	0.954256	-3.473541	26779.171979
HLA B*0803	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.473744	1.000164	-3.473579	29767.589842
HLA B*4801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.401166	0.927533	-3.473633	25186.378861
HLA B*5401	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.545636	1.071973	-3.473663	35126.555464
HLA B*3901	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.180566	0.706847	-3.473719	15155.334857
HLA B*4002	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.612645	1.138874	-3.473772	40986.914555
HLA A*3001	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.250500	0.776623	-3.473878	17803.291679

HLA B*3901	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.468558	0.994492	-3.474066	29414.289308
HLA A*2601	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.394752	0.920569	-3.474183	24817.134693
HLA A*0212	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.460049	0.985844	-3.474204	28843.537623
HLA A*3002	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.446833	0.972498	-3.474335	27979.031153
HLA B*2705	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.469056	0.994492	-3.474565	29448.043806
HLA A*0202	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.558241	1.083538	-3.474703	36161.009965
HLA A*3001	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.143044	0.667964	-3.475080	13900.942953
HLA B*1801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.415159	0.940065	-3.475095	26011.132689
HLA A*0219	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.429686	0.954583	-3.475103	26895.903030
HLA B*1509	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.462997	0.987852	-3.475145	29040.034546
HLA A*2902	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.261766	0.786460	-3.475307	18271.158611
HLA B*3501	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.447871	0.972498	-3.475373	28046.013853
HLA B*4402	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.442733	0.967178	-3.475555	27716.144731
HLA A*0250	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.461411	0.985844	-3.475567	28934.183158
HLA A*0206	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-3.633516	0.157927	-3.475590	4300.472230
HLA A*0206	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.313709	0.837899	-3.475809	20592.472853

HLA B*1501	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.138914	0.662917	-3.475997	13769.363542
HLA B*5701	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.362782	0.886699	-3.476083	23055.906135
HLA A*3201	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.569088	1.092768	-3.476321	37075.594530
HLA B*5101	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.396925	0.920569	-3.476356	24941.634542
HLA A*2602	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.470861	0.994492	-3.476369	29570.648910
HLA B*3501	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.147579	0.671022	-3.476557	14046.844253
HLA B*5401	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.454163	0.977336	-3.476827	28455.293211
HLA A*2301	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.397508	0.920569	-3.476939	24975.120007
HLA A*8001	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.432097	0.954978	-3.477119	27045.605063
HLA B*1509	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.495234	1.017829	-3.477405	31277.671378
HLA B*0802	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.431989	0.954583	-3.477406	27038.875469
HLA B*3901	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.495505	1.017829	-3.477676	31297.136437
HLA B*0702	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.432773	0.954978	-3.477795	27087.776260
HLA A*2301	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.524852	1.046875	-3.477977	33485.132387
HLA A*0212	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.405719	0.927533	-3.478186	25451.831172
HLA B*1501	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.402918	0.924700	-3.478218	25288.230865

HLA A*0101	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.403106	0.924700	-3.478406	25299.177755
HLA B*1517	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.478642	1.000164	-3.478478	30105.257713
HLA B*0702	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.446048	0.967178	-3.478870	27928.521406
HLA A*6802	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.406466	0.927533	-3.478933	25495.654781
HLA A*6901	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.192628	0.713674	-3.478954	15582.164776
HLA A*2402	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.434340	0.954978	-3.479362	27185.696246
HLA A*1101	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.259092	0.779687	-3.479405	18159.018613
HLA A*0203	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.434106	0.954583	-3.479523	27170.993063
HLA A*2902	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.344200	0.864656	-3.479544	22090.223937
HLA A*3002	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.555339	1.075733	-3.479606	35920.215846
HLA A*2301	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.482195	1.002409	-3.479786	30352.521164
HLA A*2602	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.517710	1.037888	-3.479821	32938.937480
HLA B*4402	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.407427	0.927533	-3.479894	25552.130062
HLA A*3201	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.499811	1.019585	-3.480227	31609.032947
HLA A*8001	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.407801	0.927533	-3.480268	25574.118754
HLA B*3901	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.493688	1.013420	-3.480269	31166.529963

HLA A*2902	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.375488	0.895143	-3.480345	23740.409741
HLA B*0801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.420732	0.940065	-3.480668	26347.065005
HLA B*1509	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.552651	1.071973	-3.480679	35698.595252
HLA B*4001	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.375852	0.895143	-3.480710	23760.325202
HLA A*0202	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.239246	0.758478	-3.480768	17347.874592
HLA A*2501	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.458667	0.977336	-3.481331	28751.931680
HLA B*5101	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.206884	0.725355	-3.481530	16102.172229
HLA A*2602	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.484025	1.002409	-3.481616	30480.705820
HLA A*3001	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.204850	0.723137	-3.481713	16026.910568
HLA A*2403	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.438541	0.956718	-3.481823	27449.936193
HLA A*6801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.249302	0.767355	-3.481947	17754.239323
HLA A*2902	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.438849	0.956718	-3.482131	27469.396733
HLA B*5301	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.549484	1.067238	-3.482246	35439.209095
HLA A*3301	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.468175	0.985844	-3.482331	29388.362869
HLA B*3901	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.437479	0.954978	-3.482501	27382.895690
HLA B*0802	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.481683	0.999064	-3.482619	30316.745842

HLA A*0219	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.403198	0.920569	-3.482629	25304.516083
HLA B*3801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.460121	0.977336	-3.482785	28848.375279
HLA B*0702	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.407507	0.924700	-3.482807	25556.830457
HLA A*2501	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.437446	0.954583	-3.482864	27380.821830
HLA A*2403	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.455436	0.972498	-3.482938	28538.851124
HLA B*0803	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.502574	1.019585	-3.482990	31810.771605
HLA B*0702	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.347750	0.864656	-3.483094	22271.537041
HLA A*0212	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.438339	0.954978	-3.483361	27437.168067
HLA B*3901	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.469322	0.985844	-3.483478	29466.051413
HLA B*1801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.478078	0.994492	-3.483587	30066.195211
HLA A*0101	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.348276	0.864656	-3.483621	22298.542387
HLA A*3002	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-3.644131	0.160477	-3.483655	4406.878946
HLA A*0250	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.235976	0.751912	-3.484064	17217.725944
HLA B*0801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.331428	0.847335	-3.484093	21450.050452
HLA B*1509	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.207373	0.723137	-3.484237	16120.301508
HLA B*1517	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.471030	0.985844	-3.485186	29582.169277

HLA B*4601	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.409929	0.924700	-3.485229	25699.774396
HLA B*3501	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.473389	0.987852	-3.485537	29743.282828
HLA A*8001	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.452744	0.967178	-3.485566	28362.465205
HLA A*0101	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.134121	0.648415	-3.485706	13618.237910
HLA B*1502	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.523656	1.037888	-3.485768	33393.053437
HLA A*0201	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.395142	0.909340	-3.485802	24839.431522
HLA A*2301	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.339365	0.853458	-3.485907	21845.645324
HLA A*2601	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.395313	0.909340	-3.485974	24849.243095
HLA B*4001	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.372725	0.886699	-3.486026	23589.851985
HLA B*3501	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.453284	0.967178	-3.486106	28397.777863
HLA A*0202	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.276721	0.790540	-3.486181	18911.264102
HLA B*1509	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.440837	0.954583	-3.486254	27595.405877
HLA B*7301	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.579073	1.092768	-3.486306	37937.912906
HLA B*4501	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.625246	1.138874	-3.486372	42193.496342
HLA B*1517	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.453569	0.967178	-3.486391	28416.373036
HLA B*7301	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.562615	1.076055	-3.486561	36527.108340

HLA A*1101	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.443440	0.956718	-3.486722	27761.313820
HLA B*1502	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.579609	1.092768	-3.486842	37984.736475
HLA A*0219	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.475008	0.987852	-3.487156	29854.355224
HLA A*3101	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.190335	0.702788	-3.487547	15500.106964
HLA B*1801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.441826	0.954256	-3.487570	27658.327789
HLA B*0803	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.475473	0.987852	-3.487621	29886.351090
HLA B*1502	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.444469	0.956718	-3.487751	27827.173123
HLA A*0203	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.427884	0.940065	-3.487819	26784.532793
HLA B*4001	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.194766	0.706847	-3.487919	15659.064894
HLA B*1801	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.297192	0.809025	-3.488167	19824.015225
HLA A*2602	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.627059	1.138874	-3.488186	42370.083207
HLA A*0212	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.461002	0.972498	-3.488504	28906.959627
HLA B*5701	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.413411	0.924700	-3.488711	25906.649396
HLA A*2301	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.176637	0.687624	-3.489013	15018.867907
HLA A*8001	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.409640	0.920569	-3.489071	25682.679034
HLA A*2602	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.474972	0.985844	-3.489128	29851.932691

HLA B*2705	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.456355	0.967178	-3.489177	28599.282295
HLA A*0101	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.345262	0.856017	-3.489245	22144.306592
HLA B*4002	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.510257	1.020870	-3.489387	32378.521932
HLA A*2403	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.399227	0.909340	-3.489888	25074.218540
HLA A*0216	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.457629	0.967178	-3.490451	28683.263027
HLA B*1517	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-3.294406	-0.196092	-3.490498	1969.724919
HLA A*1101	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.430713	0.940065	-3.490648	26959.563435
HLA B*1503	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.463429	0.972498	-3.490931	29068.955957
HLA B*3801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.476920	0.985844	-3.491076	29986.113243
HLA A*8001	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.338432	0.847335	-3.491097	21798.777211
HLA A*2902	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.458387	0.967178	-3.491209	28733.427810
HLA B*0802	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.463803	0.972498	-3.491305	29093.971027
HLA B*5701	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.300469	0.809025	-3.491445	19974.188963
HLA A*0219	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.446518	0.954978	-3.491540	27958.755800
HLA B*2705	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.419189	0.927533	-3.491656	26253.585931
HLA A*3301	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.563767	1.071973	-3.491794	36624.064518

HLA B*4801	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.300939	0.809025	-3.491915	19995.812289
HLA B*5801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.356591	0.864656	-3.491936	22729.574324
HLA A*0202	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.259348	0.767355	-3.491994	18169.729743
HLA A*0216	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.339414	0.847335	-3.492079	21848.127298
HLA B*5801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.345088	0.852998	-3.492090	22135.443297
HLA A*2902	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.283050	0.790540	-3.492510	19188.899679
HLA A*2501	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.417542	0.924700	-3.492842	26154.212157
HLA A*0206	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.218237	0.725355	-3.492882	16528.642223
HLA B*5701	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.413465	0.920569	-3.492896	25909.873095
HLA B*4402	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.433022	0.940065	-3.492958	27103.314153
HLA A*8001	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.447223	0.954256	-3.492967	28004.168773
HLA A*2602	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.560411	1.067238	-3.493174	36342.221902
HLA A*3002	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.420728	0.927533	-3.493195	26346.779937
HLA A*1101	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.493388	1.000164	-3.493223	31144.955677
HLA B*7301	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.576912	1.083538	-3.493374	37749.561306
HLA B*1502	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.514439	1.020870	-3.493569	32691.820281

HLA B*3901	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.328940	0.835252	-3.493688	21327.512905
HLA B*2705	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.448280	0.954583	-3.493697	28072.426576
HLA B*5801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.347252	0.853458	-3.493794	22246.008535
HLA B*3501	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.347461	0.853458	-3.494003	22256.722125
HLA A*2601	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.075290	0.581216	-3.494073	11892.956012
HLA A*2603	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.421705	0.927533	-3.494172	26406.140502
HLA A*6901	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.329497	0.835252	-3.494245	21354.875379
HLA A*0301	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.347292	0.852998	-3.494294	22248.054553
HLA B*4402	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.415866	0.920569	-3.495298	26053.523114
HLA A*0219	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.462772	0.967178	-3.495594	29024.956538
HLA B*3901	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.416273	0.920569	-3.495704	26077.918302
HLA B*4402	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.405400	0.909340	-3.496060	25433.112003
HLA B*4601	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.405421	0.909340	-3.496081	25434.350346
HLA A*2403	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.450787	0.954583	-3.496204	28234.939084
HLA B*5301	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.352332	0.856017	-3.496314	22507.729446
HLA A*2902	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.305384	0.809025	-3.496360	20201.530651

HLA B*5301	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.484312	0.987852	-3.496460	30500.829923
HLA A*6901	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.826841	0.330347	-3.496494	6711.833455
HLA B*0801	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.405900	0.909340	-3.496560	25462.435632
HLA A*2603	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.635506	1.138874	-3.496632	43202.185313
HLA A*6802	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.097164	0.600517	-3.496646	12507.298588
HLA B*5801	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.352947	0.856017	-3.496930	22539.654318
HLA A*1101	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.469465	0.972498	-3.496967	29475.776910
HLA B*4403	1:215-223	9	QVLVPRSAI	0.852479	0.308989	-4.658479	1.161468	-3.497011	45549.013955
HLA A*2603	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.564340	1.067238	-3.497102	36672.440679
HLA A*3201	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.496332	0.999064	-3.497268	31356.791760
HLA A*2501	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.485486	0.987852	-3.497635	30583.444661
HLA A*2403	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.306763	0.809025	-3.497739	20265.784700
HLA B*1509	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.483684	0.985844	-3.497840	30456.805095
HLA A*0203	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.422621	0.924700	-3.497921	26461.912491
HLA A*2301	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.517597	1.019585	-3.498012	32930.385182
HLA B*1502	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.418585	0.920569	-3.498016	26217.109844

HLA A*0219	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.252143	0.754093	-3.498050	17870.742501
HLA A*2501	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.438278	0.940065	-3.498214	27433.309106
HLA B*2705	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.422936	0.924700	-3.498236	26481.102351
HLA B*5401	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.498589	1.000164	-3.498425	31520.237194
HLA A*0211	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.345873	0.847335	-3.498538	22175.476052
HLA A*3001	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-3.900277	0.401614	-3.498663	7948.344364
HLA A*0216	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.453150	0.954256	-3.498895	28389.022369
HLA A*2501	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.394432	0.895143	-3.499289	24798.882327
HLA B*2705	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.386094	0.886699	-3.499395	24327.292984
HLA A*2601	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.387090	0.886699	-3.500391	24383.158806
HLA B*5401	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.457551	0.956718	-3.500833	28678.142766
HLA A*2601	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.353903	0.852998	-3.500906	22589.337366
HLA A*2301	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.487098	0.985844	-3.501254	30697.156322
HLA B*1509	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.441669	0.940065	-3.501604	27648.304497
HLA B*3801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.457072	0.954978	-3.502094	28646.510527
HLA A*2403	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.388829	0.886699	-3.502130	24480.967994

HLA B*4403	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.595080	1.092768	-3.502313	39362.300862
HLA A*2402	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.501407	0.999064	-3.502343	31725.356389
HLA B*2705	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.423077	0.920569	-3.502508	26489.699336
HLA B*1801	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.457575	0.954978	-3.502597	28679.694263
HLA A*6802	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.442801	0.940065	-3.502736	27720.493369
HLA A*3002	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.578230	1.075247	-3.502982	37864.303285
HLA A*2501	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.457443	0.954256	-3.503187	28671.006957
HLA A*3201	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.460415	0.956718	-3.503697	28867.890191
HLA B*5701	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.413244	0.909340	-3.503905	25896.700508
HLA B*0802	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.444105	0.940065	-3.504040	27803.848905
HLA B*4601	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.368961	0.864656	-3.504306	23386.290545
HLA A*0301	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.284070	0.779687	-3.504383	19234.006073
HLA A*3301	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.524262	1.019585	-3.504678	33439.694380
HLA A*3001	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.247758	0.742712	-3.505046	17691.247493
HLA A*0203	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.212077	0.706847	-3.505230	16295.842907
HLA B*4001	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.352569	0.847335	-3.505234	22520.031003

HLA A*6901	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.257180	0.751912	-3.505268	18079.228467
HLA B*0801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.230755	0.725355	-3.505400	17011.994560
HLA A*6802	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.296024	0.790540	-3.505484	19770.785691
HLA B*1502	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.523658	1.017829	-3.505830	33393.234090
HLA A*3301	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.644756	1.138874	-3.505882	44132.206122
HLA B*1509	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.500406	0.994492	-3.505914	31652.325913
HLA B*1801	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.491774	0.985844	-3.505929	31029.417364
HLA A*0212	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.207726	0.701666	-3.506060	16133.388174
HLA A*0212	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.431495	0.924700	-3.506795	27008.174675
HLA B*3901	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.474073	0.967178	-3.506895	29790.143893
HLA B*3501	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.416419	0.909340	-3.507079	26086.666645
HLA B*0801	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.431824	0.924700	-3.507124	27028.637996
HLA B*4601	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.402371	0.895143	-3.507228	25256.375026
HLA A*0203	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.416886	0.909340	-3.507547	26114.765837
HLA B*5101	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.493461	0.985844	-3.507616	31150.179329
HLA A*0216	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.495495	0.987852	-3.507643	31296.459188

HLA A*0250 1:216-224 9 VLVPRSAID 1.164467 -0.740753 -3.931605
0.423714 -3.507891 8542.887904

HLA A*2602 1:103-111 9 AIPPRGTQA 1.171695 -0.095962 -4.583735
1.075733 -3.508002 38347.301975

HLA B*0702 1:184-192 9 PVNYQNFAV 0.967153 -0.114155 -4.361039
0.852998 -3.508041 22963.542057

HLA B*3901 1:82-90 9 TSSTPREAP 0.792178 0.117162 -4.417629
0.909340 -3.508289 26159.447863

HLA A*2402 1:15-23 9 LCCSGVATA 1.215808 -0.196223 -4.527909
1.019585 -3.508324 33721.640977

HLA B*1517 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.275795
0.767355 -3.508440 18870.997742

HLA A*0216 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.215516
0.706847 -3.508670 16425.419701

HLA B*3801 1:189-197 9 NFAVTNDGV 0.789539 0.210625 -4.508901
1.000164 -3.508737 32277.609761

HLA B*1502 1:56-64 9 LPSYYPDQK 0.981412 0.093835 -4.584012
1.075247 -3.508765 38371.789439

HLA A*0219 1:129-137 9 YKAFDWDQA 0.955276 -0.207214 -4.256849
0.748062 -3.508787 18065.442992

HLA A*1101 1:185-193 9 VNYQNFAVT 1.248328 -0.327759 -4.429665
0.920569 -3.509096 26894.593527

HLA A*8001 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.318255
0.809025 -3.509230 20809.169877

HLA A*2902 1:218-226 9 VPRSAIDSM 0.858689 0.068844 -4.437148
0.927533 -3.509615 27362.016135

HLA B*5401 1:184-192 9 PVNYQNFAV 0.967153 -0.114155 -4.363024
0.852998 -3.510026 23068.756894

HLA A*3002 1:63-71 9 QKSLENYIA 1.220826 -0.266570 -4.464287
0.954256 -3.510031 29126.412503

HLA B*1517 1:214-222 9 TQVLVPRSA 1.194247 -0.237529 -4.466925
0.956718 -3.510207 29303.902966

HLA A*3002	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.290183	0.779687	-3.510496	19506.668736
HLA B*4801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.796772	0.286028	-3.510745	6262.856523
HLA A*6901	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.258930	0.748062	-3.510869	18152.241436
HLA B*0803	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.319108	0.808230	-3.510878	20850.074863
HLA A*2402	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.213721	0.702788	-3.510934	16357.670995
HLA A*2602	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.529177	1.017829	-3.511348	33820.297395
HLA A*2501	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.466343	0.954978	-3.511365	29264.613673
HLA B*4501	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.532387	1.020870	-3.511517	34071.152055
HLA B*1517	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.451856	0.940065	-3.511791	28304.524982
HLA A*8001	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.364803	0.852998	-3.511805	23163.423765
HLA B*1509	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.558717	1.046875	-3.511843	36200.744072
HLA B*3801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.531435	1.019585	-3.511851	33996.583707
HLA B*5101	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.468617	0.956718	-3.511899	29418.267778
HLA B*7301	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.219910	0.707999	-3.511911	16592.430698
HLA A*6802	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.436681	0.924700	-3.511981	27332.574917
HLA A*0301	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.368235	0.856017	-3.512218	23347.229375

HLA A*6801 1:155-163 9 LPVVFPIVQ 1.161225 -0.206642 -4.466930 0.954583 -3.512347 29304.220030

HLA B*7301 1:8-16 9 LVTAVVLLC 0.979168 0.067707 -4.559434 1.046875 -3.512559 36260.525192

HLA A*0211 1:160-168 9 PIVQGELSK 0.947962 0.037882 -4.498409 0.985844 -3.512564 31507.109812

HLA A*0101 1:134-142 9 WDQAYRKPI 0.842101 0.011357 -4.366104 0.853458 -3.512647 23232.950503

HLA B*7301 1:103-111 9 AIPPRGTQA 1.171695 -0.095962 -4.588441 1.075733 -3.512708 38765.093151

HLA B*1502 1:180-188 9 AGLDPVNYQ 1.025360 -0.030868 -4.507332 0.994492 -3.512840 32161.175255

HLA B*0803 1:210-218 9 AAGPTQVLV 0.899889 0.077447 -4.490197 0.977336 -3.512861 30916.983667

HLA A*0216 1:218-226 9 VPRSAIDSM 0.858689 0.068844 -4.440708 0.927533 -3.513175 27587.196254

HLA A*0201 1:134-142 9 WDQAYRKPI 0.842101 0.011357 -4.366840 0.853458 -3.513382 23272.324075

HLA B*0803 1:68-76 9 NYIAQTRDK 0.633507 0.291193 -4.438194 0.924700 -3.513494 27427.966824

HLA B*1502 1:123-131 9 THPTTTYKA 1.324444 -0.257206 -4.580760 1.067238 -3.513523 38085.561727

HLA A*0216 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.322660 0.809025 -3.513636 21021.322741

HLA A*6801 1:82-90 9 TSSTPREAP 0.792178 0.117162 -4.423002 0.909340 -3.513662 26485.113930

HLA B*2705 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.220554 0.706847 -3.513707 16617.044056

HLA A*3002 1:107-115 9 RGTQAVVLK 0.840868 0.114110 -4.468779 0.954978 -3.513801 29429.251148

HLA A*8001 1:154-162 9 PLPVVFPIV 1.026322 -0.131179 -4.409015 0.895143 -3.513873 25645.747454

HLA B*5801	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.351787	0.837899	-3.513887	22479.497844
HLA A*2602	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.560881	1.046875	-3.514007	36381.564661
HLA A*2301	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.491374	0.977336	-3.514038	31000.893312
HLA A*2601	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.367545	0.853458	-3.514087	23310.124949
HLA A*6801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.322366	0.808230	-3.514136	21007.112168
HLA B*3801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.502102	0.987852	-3.514250	31776.199762
HLA B*0802	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.434909	0.920569	-3.514340	27221.310882
HLA B*4601	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.368268	0.853458	-3.514811	23348.997725
HLA A*2902	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.282216	0.767355	-3.514861	19152.082558
HLA B*3501	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.439627	0.924700	-3.514927	27518.629516
HLA B*3901	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.502821	0.987852	-3.514969	31828.846476
HLA A*0301	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.368534	0.853458	-3.515076	23363.275739
HLA A*0216	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.163593	0.648415	-3.515178	14574.472895
HLA A*0206	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.267092	0.751912	-3.515180	18496.619822
HLA B*4403	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.654374	1.138874	-3.515501	45120.554638
HLA B*0702	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.295199	0.779687	-3.515512	19733.279139

HLA B*1502	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.562458	1.046875	-3.515583	36513.871029
HLA B*4801	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.425011	0.909340	-3.515671	26607.903398
HLA B*3901	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.873779	0.357949	-3.515830	7477.891903
HLA A*0211	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.292483	0.776623	-3.515861	19610.255615
HLA A*2501	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.436460	0.920569	-3.515891	27318.679027
HLA B*1503	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-3.734215	0.218305	-3.515910	5422.693709
HLA B*5401	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.470353	0.954256	-3.516098	29536.114722
HLA B*5101	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.483290	0.967178	-3.516112	30429.136657
HLA B*4601	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.325252	0.809025	-3.516227	21147.134230
HLA A*0250	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.230025	0.713674	-3.516350	16983.396360
HLA B*3901	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.456717	0.940065	-3.516652	28623.118941
HLA B*5401	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.554968	1.037888	-3.517079	35889.525712
HLA B*0802	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.474028	0.956718	-3.517310	29787.081984
HLA B*3801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.535152	1.017829	-3.517323	34288.790219
HLA A*2501	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.370467	0.852998	-3.517470	23467.528870
HLA A*3001	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.258214	0.740601	-3.517613	18122.314641

HLA A*0216	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.472235	0.954583	-3.517652	29664.381905
HLA B*5101	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.260528	0.742712	-3.517816	18219.141512
HLA B*1517	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.206447	0.688457	-3.517990	16085.977738
HLA A*0212	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.272167	0.754093	-3.518074	18714.027262
HLA A*2902	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.198234	0.680076	-3.518157	15784.603014
HLA B*5401	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.532476	1.013420	-3.519056	34078.156979
HLA A*0250	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.594324	1.075247	-3.519076	39293.792040
HLA A*2402	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.505243	0.985844	-3.519399	32006.870927
HLA B*5301	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.595146	1.075733	-3.519413	39368.263793
HLA B*4501	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.533031	1.013420	-3.519611	34121.693502
HLA A*2602	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.215939	0.696230	-3.519709	16441.422237
HLA B*1503	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.227710	0.707999	-3.519711	16893.136941
HLA B*4501	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.612697	1.092768	-3.519929	40991.793008
HLA B*5701	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.415723	0.895143	-3.520580	26044.926785
HLA A*0203	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.376780	0.856017	-3.520763	23811.153077
HLA B*5301	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.592947	1.071973	-3.520975	39169.420301

HLA B*1509	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.374313	0.852998	-3.521316	23676.280021
HLA B*4801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.368961	0.847335	-3.521626	23386.290545
HLA A*3201	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.301355	0.779687	-3.521668	20014.968456
HLA B*7301	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.593720	1.071973	-3.521748	39239.198211
HLA B*3501	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.879794	0.357949	-3.521844	7582.176058
HLA B*1801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.499304	0.977336	-3.521968	31572.118225
HLA B*3501	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.408853	0.886699	-3.522154	25636.176136
HLA A*0202	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.210677	0.688457	-3.522220	16243.384936
HLA B*5101	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.510299	0.987852	-3.522448	32381.675041
HLA A*6901	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.263411	0.740601	-3.522810	18340.481247
HLA B*4501	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.540711	1.017829	-3.522882	34730.500669
HLA B*5801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.358252	0.835252	-3.523000	22816.676677
HLA B*5301	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.540918	1.017829	-3.523089	34747.038764
HLA A*0201	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.332201	0.809025	-3.523177	21488.262396
HLA B*4403	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.480177	0.956718	-3.523458	30211.797354
HLA A*1101	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.478342	0.954583	-3.523759	30084.418067

HLA B*2705	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.496310	0.972498	-3.523812	31355.265067
HLA B*0802	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.491158	0.967178	-3.523980	30985.467703
HLA A*0212	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.433544	0.909340	-3.524204	27135.884663
HLA A*0219	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.464550	0.940065	-3.524485	29144.065765
HLA B*0803	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.377979	0.853458	-3.524521	23876.939795
HLA A*0203	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.315398	0.790540	-3.524858	20672.727590
HLA A*0203	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.362900	0.837899	-3.525001	23062.143473
HLA A*6901	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.362921	0.837899	-3.525022	23063.266373
HLA A*2403	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.389822	0.864656	-3.525167	24537.053976
HLA B*4801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.420415	0.895143	-3.525272	26327.829845
HLA B*3801	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.572276	1.046875	-3.525402	37348.776126
HLA B*1503	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.205588	0.680076	-3.525511	16054.158701
HLA A*2601	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.390255	0.864656	-3.525599	24561.490801
HLA B*0702	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.434965	0.909340	-3.525626	27224.845454
HLA B*1517	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.479897	0.954256	-3.525641	30192.353958
HLA A*0202	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.277562	0.751912	-3.525649	18947.925801

HLA B*2705	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.420850	0.895143	-3.525707	26354.192704
HLA B*0802	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.480224	0.954256	-3.525968	30215.066380
HLA A*0216	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.466639	0.940065	-3.526574	29284.568582
HLA A*6802	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.285494	0.758478	-3.527016	19297.166176
HLA B*0801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.362481	0.835252	-3.527229	23039.946235
HLA A*2902	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.436756	0.909340	-3.527416	27337.307045
HLA B*0803	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.484173	0.956718	-3.527455	30491.096116
HLA B*5801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.281802	0.754093	-3.527710	19133.855764
HLA B*3901	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.500262	0.972498	-3.527764	31641.882267
HLA A*6901	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.161826	0.634040	-3.527786	14515.300935
HLA B*1501	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.318407	0.790540	-3.527868	20816.488559
HLA A*3002	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.514011	0.985844	-3.528167	32659.647762
HLA A*8001	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.414913	0.886699	-3.528214	25996.361563
HLA A*0206	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.483449	0.954583	-3.528866	30440.332758
HLA A*0301	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.366840	0.837899	-3.528941	23272.324075
HLA A*6901	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.287430	0.758478	-3.528952	19383.380109

HLA A*0216	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.109296	0.579719	-3.529577	12861.637307
HLA A*2603	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.547407	1.017829	-3.529578	35270.131293
HLA B*0803	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.450244	0.920569	-3.529675	28199.676360
HLA A*0301	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.364941	0.835252	-3.529689	23170.818327
HLA A*3201	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.502250	0.972498	-3.529752	31787.031668
HLA B*5101	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.484020	0.954256	-3.529765	30480.376027
HLA A*2403	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.383265	0.853458	-3.529807	24169.351936
HLA B*5401	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.425133	0.895143	-3.529990	26615.389633
HLA A*3301	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.605947	1.075733	-3.530214	40359.599192
HLA B*3901	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.455056	0.924700	-3.530356	28513.850573
HLA A*2403	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.306996	0.776623	-3.530373	20276.641536
HLA B*3901	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.307059	0.776623	-3.530437	20279.603501
HLA B*1801	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.497997	0.967178	-3.530819	31477.295183
HLA B*4501	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.598417	1.067238	-3.531179	39665.848172
HLA B*0803	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.485576	0.954256	-3.531320	30589.732523
HLA A*2501	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.498693	0.967178	-3.531515	31527.741011

HLA B*4001 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.387689 0.856017 -3.531672 24416.819116

HLA B*1509 1:107-115 9 RGTQAVVLK 0.840868 0.114110 -4.486673 0.954978 -3.531695 30667.112687

HLA B*4001 1:14-22 9 LLCCSGVAT 1.136854 -0.272198 -4.396443 0.864656 -3.531788 24913.988922

HLA A*0219 1:208-216 9 PEAAGPTQV 0.855949 -0.104037 -4.283807 0.751912 -3.531894 19222.355573

HLA A*0206 1:107-115 9 RGTQAVVLK 0.840868 0.114110 -4.486927 0.954978 -3.531949 30685.035736

HLA A*3301 1:189-197 9 NFAVTNDGV 0.789539 0.210625 -4.532307 1.000164 -3.532143 34064.885712

HLA B*7301 1:21-29 9 ATAAPKTYC 0.926919 0.086501 -4.545640 1.013420 -3.532220 35126.935527

HLA A*0216 1:68-76 9 NYIAQTRDK 0.633507 0.291193 -4.456968 0.924700 -3.532268 28639.692463

HLA A*3001 1:97-105 9 SATYQSAIP 0.500068 0.078015 -4.110368 0.578083 -3.532285 12893.404970

HLA A*0212 1:220-228 9 RSAIDSMLA 1.010961 -0.163626 -4.379694 0.847335 -3.532359 23971.421503

HLA B*1517 1:82-90 9 TSSTPREAP 0.792178 0.117162 -4.441859 0.909340 -3.532519 27660.422667

HLA B*4601 1:149-157 9 QADTDPLPV 0.679726 0.062986 -4.275428 0.742712 -3.532716 18855.078419

HLA A*0211 1:141-149 9 PITYDTLWQ 1.144380 -0.171882 -4.505295 0.972498 -3.532797 32010.680533

HLA B*0801 1:149-157 9 QADTDPLPV 0.679726 0.062986 -4.275647 0.742712 -3.532934 18864.567167

HLA A*2601 1:220-228 9 RSAIDSMLA 1.010961 -0.163626 -4.380436 0.847335 -3.533101 24012.436295

HLA A*0201 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.389183 0.856017 -3.533166 24500.974502

HLA A*6801	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.605162	1.071973	-3.533190	40286.739158
HLA A*0203	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.196218	0.662917	-3.533301	15711.505639
HLA A*2501	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.389437	0.856017	-3.533420	24515.293821
HLA A*0219	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.342555	0.809025	-3.533531	22006.728169
HLA A*1101	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.461200	0.927533	-3.533667	28920.098821
HLA B*4501	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.454264	0.920569	-3.533695	28461.913400
HLA A*2301	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.547135	1.013420	-3.533715	35248.004566
HLA A*3201	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.609135	1.075247	-3.533888	40656.978098
HLA B*5801	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.320611	0.786460	-3.534152	20922.389800
HLA B*5101	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.506683	0.972498	-3.534185	32113.190292
HLA A*0206	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.506726	0.972498	-3.534228	32116.317562
HLA B*1517	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.506942	0.972498	-3.534444	32132.306147
HLA B*0802	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.443938	0.909340	-3.534598	27793.171439
HLA B*1502	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.554423	1.019585	-3.534838	35844.509229
HLA A*0219	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.382332	0.847335	-3.534997	24117.498494
HLA A*2602	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.610350	1.075247	-3.535102	40770.851288

HLA A*0301	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.325665
0.790540	-3.535125	21167.278861

HLA B*3901	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.287086
0.751912	-3.535174	19368.076311

HLA A*2601	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.322477
0.786460	-3.536017	21012.454216

HLA B*4002	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.456705
0.920569	-3.536136	28622.344712

HLA A*3301	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.392449
0.856017	-3.536432	24685.910068

HLA B*5701	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.401358
0.864656	-3.536703	25197.554292

HLA A*0211	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.074608
0.537766	-3.536842	11874.312164

HLA A*2301	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.531438
0.994492	-3.536946	33996.767625

HLA A*0301	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.341331
0.804086	-3.537246	21944.788387

HLA B*3901	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.346465
0.809025	-3.537441	22205.728319

HLA A*2602	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.291560
0.754093	-3.537467	19568.606807

HLA A*6801	1:33-41	9	KGTDTGQAC	1.197565	-0.058691	-4.676640
1.138874	-3.537767	47494.191484

HLA A*2603	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.557841
1.019585	-3.538257	36127.768654

HLA B*7301	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.613524
1.075247	-3.538276	41069.927271

HLA B*5301	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.576285
1.037888	-3.538396	37695.073676

HLA B*1517	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.526276
0.987852	-3.538424	33595.089949

HLA A*2902	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.318118	0.779687	-3.538431	20802.641534
HLA B*1801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.510952	0.972498	-3.538454	32430.412075
HLA B*5101	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.391514	0.852998	-3.538516	24632.815130
HLA B*0702	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.394559	0.856017	-3.538542	24806.127983
HLA A*3101	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.394684	0.856017	-3.538666	24813.241518
HLA A*2902	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.342797	0.804086	-3.538712	22018.994143
HLA B*1503	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.394949	0.856017	-3.538932	24828.414923
HLA A*0212	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.392461	0.853458	-3.539003	24686.577817
HLA A*6801	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.541484	1.002409	-3.539075	34792.370917
HLA A*2301	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.293280	0.754093	-3.539187	19646.252889
HLA A*3301	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.615345	1.076055	-3.539290	41242.481157
HLA A*1101	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.392386	0.852998	-3.539388	24682.304534
HLA B*4501	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.539755	1.000164	-3.539591	34654.114314
HLA A*3001	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.219699	0.680076	-3.539622	16584.353976
HLA A*3001	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.288658	0.748062	-3.540597	19438.300561
HLA A*3101	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.394059	0.853458	-3.540601	24777.560185

HLA A*0203	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.349778	0.809025	-3.540753	22375.760036
HLA A*2402	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.543509	1.002409	-3.541101	34954.997927
HLA A*0201	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.242869	0.701666	-3.541203	17493.196712
HLA B*4601	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.394232	0.852998	-3.541235	24787.481416
HLA A*6801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.535740	0.994492	-3.541248	34335.196232
HLA B*0803	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.481379	0.940065	-3.541315	30295.595902
HLA A*6801	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.617189	1.075733	-3.541456	41418.000630
HLA B*3801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.495768	0.954256	-3.541512	31316.105355
HLA B*1502	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.395327	0.853458	-3.541870	24850.049698
HLA A*0203	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.282799	0.740601	-3.542198	19177.795243
HLA A*8001	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.451586	0.909340	-3.542246	28286.921159
HLA B*0803	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.514784	0.972498	-3.542286	32717.828913
HLA B*5101	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.497293	0.954978	-3.542315	31426.250013
HLA B*0702	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.437529	0.895143	-3.542386	27386.006773
HLA A*3002	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.467250	0.924700	-3.542550	29325.788394
HLA A*0201	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.380575	0.837899	-3.542676	24020.101890

HLA B*4001	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.351704	0.809025	-3.542680	22475.241841
HLA A*3301	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.530578	0.987852	-3.542726	33929.519963
HLA A*3101	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.329387	0.786460	-3.542927	21349.446276
HLA A*0219	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.467837	0.924700	-3.543137	29365.477543
HLA A*3001	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.297415	0.754093	-3.543322	19834.206187
HLA B*5701	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.396843	0.853458	-3.543385	24936.912388
HLA A*2402	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.531266	0.987852	-3.543414	33983.344208
HLA B*4001	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.396504	0.852998	-3.543507	24917.493498
HLA B*3901	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.266667	0.723137	-3.543531	18478.516983
HLA A*2602	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.430241	0.886699	-3.543542	26930.263869
HLA B*1503	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.206664	0.662917	-3.543746	16093.985880
HLA B*3801	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.468624	0.924700	-3.543924	29418.745230
HLA B*4002	1:110-118	9	QAVVLKVYQ	1.073710	0.019058	-4.636927	1.092768	-3.544160	43343.816981
HLA B*1501	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.379424	0.835252	-3.544171	23956.512627
HLA A*0211	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.471826	0.927533	-3.544294	29636.471346
HLA B*5801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.352823	0.808230	-3.544593	22533.192582

HLA B*3801	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.558318	1.013420	-3.544898	36167.466234
HLA A*0206	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.512155	0.967178	-3.544977	32520.364401
HLA B*1501	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.401037	0.856017	-3.545019	25178.885922
HLA B*4801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.431899	0.886699	-3.545201	27033.317503
HLA B*3901	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.401274	0.856017	-3.545257	25192.647395
HLA B*1503	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-3.774871	0.229395	-3.545475	5954.846394
HLA B*4402	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.440724	0.895143	-3.545581	27588.240980
HLA B*5401	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.540192	0.994492	-3.545700	34689.002199
HLA A*6901	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.332229	0.786460	-3.545770	21489.657431
HLA A*3001	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.297791	0.751912	-3.545879	19851.381757
HLA A*0101	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.350360	0.804086	-3.546275	22405.800678
HLA A*6801	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.325989	0.779687	-3.546302	21183.087505
HLA B*4601	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.393723	0.847335	-3.546387	24758.399327
HLA A*8001	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.411449	0.864656	-3.546794	25789.886315
HLA B*4403	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.298926	0.751912	-3.547013	19903.320778
HLA B*2705	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.295568	0.748062	-3.547506	19750.046771

HLA A*2402	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.385579	0.837899	-3.547680	24298.487908
HLA B*4501	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.623674	1.075733	-3.547941	42041.064979
HLA B*3801	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.542685	0.994492	-3.548193	34888.685871
HLA B*5801	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.291048	0.742712	-3.548335	19545.542059
HLA B*4801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.401365	0.852998	-3.548368	25197.963243
HLA A*2603	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.624289	1.075733	-3.548556	42100.695854
HLA A*0203	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.307123	0.758478	-3.548645	20282.565898
HLA B*4002	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.624705	1.076055	-3.548651	42141.028699
HLA B*4001	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.384090	0.835252	-3.548838	24215.290021
HLA A*0219	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.250526	0.701666	-3.548860	17804.351162
HLA A*6801	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.566753	1.017829	-3.548924	36876.758216
HLA A*6801	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.616167	1.067238	-3.548929	41320.646173
HLA A*2403	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.215860	0.666762	-3.549097	16438.398342
HLA A*0212	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.255949	0.706847	-3.549102	18028.050371
HLA A*0206	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.537004	0.987852	-3.549152	34435.275090
HLA A*0202	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.215958	0.666762	-3.549196	16442.133823

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HLA A*0212	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.405609
	0.856017	-3.549591	25445.360490

HLA A*0211	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.504668
	0.954978	-3.549690	31964.476390

HLA A*0219	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.405891
	0.856017	-3.549873	25461.884642

HLA A*3301	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.237677
	0.687624	-3.550053	17285.295881

HLA B*4501	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.633600
	1.083538	-3.550062	43013.054379

HLA A*2301	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.477787
	0.927533	-3.550254	30046.032782

HLA A*3201	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.459680
	0.909340	-3.550340	28819.049691

HLA A*2601	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.388312
	0.837899	-3.550413	24451.848675

HLA A*0206	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.536280
	0.985844	-3.550436	34377.945231

HLA B*1801	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.538434
	0.987852	-3.550583	34548.913416

HLA B*5801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.341320
	0.790540	-3.550780	21944.194800

HLA A*0201	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.264489
	0.713674	-3.550815	18386.079804

HLA B*1509	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.549970
	0.999064	-3.550907	35478.917819

HLA B*3501	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.446062
	0.895143	-3.550919	27929.427962

HLA A*6801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-3.647970
	0.096880	-3.551090	4446.007381

HLA B*4002	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.598273
	1.046875	-3.551399	39652.760474
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HLA B*7301	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.550499	0.999064	-3.551435	35522.129940
HLA B*5301	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.553917	1.002409	-3.551509	35802.841779
HLA A*0101	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.360816	0.809025	-3.551791	22951.743219
HLA B*1503	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.240353	0.688457	-3.551896	17392.134343
HLA A*2301	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.524417	0.972498	-3.551919	33451.636244
HLA A*2603	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.623913	1.071973	-3.551941	42064.270006
HLA A*0211	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.506921	0.954583	-3.552338	32130.741695
HLA A*3101	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.328983	0.776623	-3.552360	21329.589836
HLA B*1509	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.462093	0.909340	-3.552753	28979.612694
HLA A*2603	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.552999	1.000164	-3.552835	35727.189263
HLA B*0803	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.507611	0.954583	-3.553029	32181.886540
HLA B*4601	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.409116	0.856017	-3.553099	25651.713996
HLA A*2601	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.388352	0.835252	-3.553099	24454.097569
HLA B*0802	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.406607	0.853458	-3.553149	25503.931844
HLA A*2501	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.440125	0.886699	-3.553426	27550.208641
HLA B*4002	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.620673	1.067238	-3.553436	41751.628218

HLA A*2602	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.478323	0.924700	-3.553623	30083.116068
HLA B*3501	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.333392	0.779687	-3.553705	21547.281601
HLA A*0211	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.521227	0.967178	-3.554049	33206.780003
HLA B*1801	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.478835	0.924700	-3.554135	30118.615696
HLA A*2603	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.526760	0.972498	-3.554262	33632.550435
HLA B*1501	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.321765	0.767355	-3.554410	20978.038891
HLA A*0203	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.340955	0.786460	-3.554496	21925.801586
HLA A*3201	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.449767	0.895143	-3.554624	28168.724263
HLA B*0702	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.402002	0.847335	-3.554667	25234.932565
HLA B*5701	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.407918	0.852998	-3.554920	25581.037347
HLA A*0301	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.174377	0.619394	-3.554983	14940.908052
HLA B*0803	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.522284	0.967178	-3.555106	33287.718733
HLA A*2603	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.475858	0.920569	-3.555289	29912.878679
HLA A*2301	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.510029	0.954583	-3.555446	32361.535460
HLA A*0301	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.363804	0.808230	-3.555574	23110.227532
HLA A*0301	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.323057	0.767355	-3.555702	21040.550720

HLA A*3201	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.555980	1.000164	-3.555816	35973.305598
HLA A*0301	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.135587	0.579719	-3.555868	13664.287644
HLA B*5801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.360217	0.804086	-3.556131	22920.102619
HLA A*2902	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.412258	0.856017	-3.556240	25837.926028
HLA B*4402	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.409380	0.852998	-3.556382	25667.261274
HLA B*7301	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.263462	0.706847	-3.556616	18342.664217
HLA A*0216	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.219793	0.662917	-3.556875	16587.943145
HLA A*8001	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.410582	0.853458	-3.557125	25738.454630
HLA B*5401	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.545119	0.987852	-3.557267	35084.773563
HLA B*4002	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.633246	1.075733	-3.557512	42977.931652
HLA B*4801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.422283	0.864656	-3.557627	26441.306052
HLA B*5101	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.498019	0.940065	-3.557954	31478.827818
HLA B*4002	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.641725	1.083538	-3.558187	43825.290371
HLA A*0216	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.298872	0.740601	-3.558271	19900.844413
HLA A*2301	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.515036	0.956718	-3.558318	32736.773377
HLA A*0203	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.844556	0.286028	-3.558529	6991.273440

HLA B*0803	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.299156	0.740601	-3.558555	19913.875702
HLA A*6802	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.434891	-0.124403	-3.559294	2722.016074
HLA A*3002	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.317832	0.758478	-3.559354	20788.916186
HLA A*0219	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.468822	0.909340	-3.559482	29432.117049
HLA B*4403	1:142-150	9	ITYDTLWQA	1.233555	-0.212685	-4.580843	1.020870	-3.559973	38092.773763
HLA A*0206	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.416101	0.856017	-3.560084	26067.621594
HLA A*2602	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.369199	0.809025	-3.560174	23399.072278
HLA A*2501	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.339987	0.779687	-3.560300	21876.986151
HLA A*3001	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.261989	0.701666	-3.560324	18280.551294
HLA A*2602	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.413510	0.852998	-3.560512	25912.536453
HLA A*2402	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.573961	1.013420	-3.560541	37493.929274
HLA B*4501	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-3.554592	-0.005967	-3.560560	3585.851064
HLA B*4402	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.416776	0.856017	-3.560759	26108.126616
HLA A*2501	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.398713	0.837899	-3.560814	25044.529056
HLA A*3201	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.546660	0.985844	-3.560816	35209.506670
HLA A*6802	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.301639	0.740601	-3.561038	20028.074476

HLA B*4403	1:102-110	9	SAIPPRGTQ	1.076283	0.007255	-4.644840	1.083538	-3.561302	44140.801972
HLA B*1517	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.486205	0.924700	-3.561505	30634.115222
HLA B*4402	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.426171	0.864656	-3.561516	26679.107731
HLA B*7301	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.581164	1.019585	-3.561580	38121.016871
HLA B*3901	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.448332	0.886699	-3.561633	28075.767887
HLA A*0211	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.516070	0.954256	-3.561814	32814.791214
HLA A*0219	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.415284	0.853458	-3.561826	26018.591777
HLA B*1801	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.471178	0.909340	-3.561838	29592.253279
HLA A*3301	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.629096	1.067238	-3.561859	42569.281531
HLA A*2603	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.608891	1.046875	-3.562016	40634.109758
HLA A*0301	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.348901	0.786460	-3.562442	22330.653769
HLA B*5401	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.310607	0.748062	-3.562545	20445.944705
HLA A*3002	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.366715	0.804086	-3.562630	23265.652295
HLA A*6901	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-3.834195	0.271476	-3.562719	6826.452295
HLA A*0203	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.270295	0.707433	-3.562861	18633.512037
HLA B*1509	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.535714	0.972498	-3.563216	34333.153047

HLA B*4402	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.410721	0.847335	-3.563386	25746.671230
HLA B*3801	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.518109	0.954583	-3.563526	32969.244734
HLA B*0801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.252119	0.688457	-3.563662	17869.775740
HLA A*0211	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.252145	0.688457	-3.563688	17870.839180
HLA A*2601	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.367911	0.804086	-3.563825	23329.805663
HLA A*0101	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.401995	0.837899	-3.564096	25234.523014
HLA B*4402	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.350781	0.786460	-3.564321	22427.508295
HLA A*6901	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.354902	0.790540	-3.564362	22641.334589
HLA B*5801	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.340998	0.776623	-3.564375	21927.936780
HLA B*5401	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.323109	0.758478	-3.564631	21043.055065
HLA B*5101	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.418106	0.853458	-3.564648	26188.192145
HLA A*3301	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.563858	0.999064	-3.564795	36631.792487
HLA B*4002	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.563877	0.999064	-3.564813	36633.377912
HLA A*3001	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.262631	0.697746	-3.564885	18307.569782
HLA B*3901	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.417960	0.852998	-3.564962	26179.409755
HLA A*2902	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.271827	0.706847	-3.564980	18699.353101

HLA B*4001	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.369126	0.804086	-3.565040	23395.148429
HLA B*2705	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.369431	0.804086	-3.565346	23411.607686
HLA A*3001	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.236410	0.671022	-3.565388	17234.966578
HLA A*0101	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.400738	0.835252	-3.565486	25161.592561
HLA A*6901	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.342147	0.776623	-3.565524	21986.022526
HLA B*4002	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.640827	1.075247	-3.565580	43734.815524
HLA A*3101	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.400999	0.835252	-3.565747	25176.706577
HLA A*3001	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.253371	0.687624	-3.565747	17921.377079
HLA A*0201	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.401109	0.835252	-3.565857	25183.108941
HLA B*4601	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.401375	0.835252	-3.566123	25198.508522
HLA B*0802	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.452915	0.886699	-3.566217	28373.668376
HLA B*1509	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.342903	0.776623	-3.566280	22024.355210
HLA A*0219	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.279956	0.713674	-3.566282	19052.668036
HLA B*5301	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.566555	1.000164	-3.566391	36860.004092
HLA A*0202	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.352987	0.786460	-3.566528	22541.727343
HLA A*2902	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.402463	0.835252	-3.567211	25261.704321

HLA B*4601	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.405303	0.837899	-3.567404	25427.471426
HLA A*2301	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.405317	0.837899	-3.567418	25428.296798
HLA A*6901	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.375996	0.808230	-3.567766	23768.167481
HLA B*5701	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.403024	0.835252	-3.567772	25294.387908
HLA B*1801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.432771	0.864656	-3.568115	27087.629719
HLA B*0702	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.377236	0.809025	-3.568212	23836.156441
HLA B*1501	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.236288	0.667964	-3.568324	17230.118819
HLA B*3801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.508408	0.940065	-3.568343	32240.960742
HLA B*7301	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.606250	1.037888	-3.568362	40387.775006
HLA B*0801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.276366	0.707999	-3.568367	18895.821926
HLA A*3201	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.562928	0.994492	-3.568436	36553.399609
HLA A*0101	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.345069	0.776623	-3.568447	22134.485315
HLA A*8001	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.424541	0.856017	-3.568524	26579.129806
HLA A*2402	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.525244	0.956718	-3.568526	33515.398250
HLA A*0211	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.556648	0.987852	-3.568796	36028.617771
HLA B*4402	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.377936	0.809025	-3.568912	23874.614820

HLA A*2601	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.378463	0.809025	-3.569438	23903.563977
HLA A*3301	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.583002	1.013420	-3.569582	38282.630718
HLA B*5701	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.425720	0.856017	-3.569703	26651.410563
HLA B*0801	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.356234	0.786460	-3.569775	22710.891406
HLA B*1517	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.423411	0.853458	-3.569953	26510.056654
HLA B*4501	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.607920	1.037888	-3.570032	40543.422956
HLA A*2403	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.349860	0.779687	-3.570173	22379.997200
HLA A*6802	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.356725	0.786460	-3.570266	22736.584380
HLA A*0206	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.479704	0.909340	-3.570365	30178.963271
HLA B*3801	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.543192	0.972498	-3.570694	34929.478388
HLA A*0202	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.525331	0.954583	-3.570748	33522.107561
HLA B*3801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.457582	0.886699	-3.570883	28680.159729
HLA A*3001	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.296524	0.725355	-3.571170	19793.580825
HLA B*1503	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.294384	0.723137	-3.571247	19696.269954
HLA A*2603	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.584764	1.013420	-3.571344	38438.274852
HLA A*2501	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.267741	0.696230	-3.571510	18524.258298

HLA A*0301	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.330054	0.758478	-3.571576	21382.272959
HLA A*0201	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.362192	0.790540	-3.571653	23024.620177
HLA A*2602	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.273474	0.701666	-3.571808	18770.401896
HLA A*2601	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.339198	0.767355	-3.571843	21837.255976
HLA B*4501	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.647150	1.075247	-3.571902	44376.164536
HLA B*5401	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.557851	0.985844	-3.572006	36128.550451
HLA B*1502	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.557883	0.985844	-3.572039	36131.286875
HLA B*3501	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.274994	0.702905	-3.572088	18836.217141
HLA A*3201	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.527093	0.954978	-3.572115	33658.397030
HLA B*3901	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.330902	0.758478	-3.572424	21424.072699
HLA A*0219	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.279361	0.706847	-3.572514	19026.608450
HLA B*3901	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.437219	0.864656	-3.572563	27366.457260
HLA B*0801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.363130	0.790540	-3.572590	23074.373552
HLA A*0101	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.331179	0.758478	-3.572701	21437.753485
HLA B*0802	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.425706	0.852998	-3.572708	26650.545490
HLA B*3801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.572523	0.999064	-3.573459	37369.997690

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HLA B*3501	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.280440
	0.706847	-3.573593	19073.912873

HLA A*2601	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.353304
	0.779687	-3.573617	22558.196369

HLA A*6901	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.154890
	0.581216	-3.573674	14285.332866

HLA B*1502	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.528487
	0.954583	-3.573904	33766.548717

HLA B*1501	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.271679
	0.697746	-3.573933	18692.981017

HLA B*1517	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.360604
	0.786460	-3.574145	22940.570964

HLA B*4501	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.650244
	1.076055	-3.574190	44693.465914

HLA B*0802	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.469439
	0.895143	-3.574297	29474.022895

HLA B*2705	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.427501
	0.852998	-3.574503	26760.924283

HLA A*2403	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.427548
	0.852998	-3.574550	26763.819912

HLA B*2705	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.439251
	0.864656	-3.574595	27494.820184

HLA B*5101	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.461855
	0.886699	-3.575156	28963.782594

HLA B*3501	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.323327
	0.748062	-3.575266	21053.644904

HLA B*1502	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.552602
	0.977336	-3.575266	35694.539848

HLA A*6801	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.431385
	0.856017	-3.575368	27001.308320

HLA A*2603	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.650834
	1.075247	-3.575586	44754.195597
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HLA A*0301	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.352247	0.776623	-3.575624	22503.346358
HLA B*7301	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.352748	0.776623	-3.576125	22529.292053
HLA B*5101	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.355858	0.779687	-3.576171	22691.241766
HLA A*0211	1:91-99	9	YELNITSAT	0.787532	-0.429583	-3.934433	0.357949	-3.576484	8598.713673
HLA B*1801	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.356204	0.779687	-3.576516	22709.294238
HLA B*0801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.317233	0.740601	-3.576632	20760.257197
HLA B*4001	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.319397	0.742712	-3.576684	20863.953461
HLA A*1101	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.441443	0.864656	-3.576787	27633.949096
HLA B*4501	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.424153	0.847335	-3.576818	26555.415018
HLA A*0219	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.353445	0.776623	-3.576823	22565.519798
HLA A*0201	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.330944	0.754093	-3.576851	21426.159034
HLA A*2501	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.486222	0.909340	-3.576882	30635.275334
HLA B*4002	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.614889	1.037888	-3.577001	41199.219117
HLA B*4001	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.414920	0.837899	-3.577020	25996.783479
HLA A*3001	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.225309	0.648272	-3.577037	16799.994089
HLA A*2403	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.331271	0.754093	-3.577178	21442.277021

HLA B*4403	1:123-131	9	THPTTTYKA	1.324444	-0.257206	-4.644424	1.067238	-3.577187	44098.555160
HLA A*2601	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.367937	0.790540	-3.577397	23331.194032
HLA A*0101	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.368061	0.790540	-3.577522	23337.884608
HLA A*2902	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.291217	0.713674	-3.577543	19553.156766
HLA B*4402	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.413233	0.835252	-3.577981	25896.000026
HLA B*4402	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.386399	0.808230	-3.578169	24344.408036
HLA B*5801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.345572	0.767355	-3.578218	22160.125608
HLA A*2403	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.413491	0.835252	-3.578239	25911.415006
HLA B*0801	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.387508	0.809025	-3.578484	24406.650128
HLA B*1502	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.280191	0.701666	-3.578525	19062.978107
HLA B*3801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.535260	0.956718	-3.578542	34297.324214
HLA B*1501	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.416651	0.837899	-3.578752	26100.641859
HLA A*0201	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.355442	0.776623	-3.578820	22669.524159
HLA A*2301	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.546002	0.967178	-3.578824	35156.212777
HLA A*2602	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.533449	0.954583	-3.578866	34154.567162
HLA A*2902	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.432348	0.853458	-3.578890	27061.265164

HLA A*3002	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.535707	0.956718	-3.578988	34332.595836
HLA B*3901	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.426324	0.847335	-3.578989	26688.490897
HLA B*4801	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.435196	0.856017	-3.579178	27239.283054
HLA B*4601	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.383498	0.804086	-3.579412	24182.300001
HLA B*1503	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.414729	0.835252	-3.579477	25985.394158
HLA B*5301	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.593149	1.013420	-3.579729	39187.648132
HLA B*5401	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.534814	0.954978	-3.579836	34262.088829
HLA A*2603	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.582273	1.002409	-3.579865	38218.482039
HLA B*5701	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.388150	0.808230	-3.579920	24442.722935
HLA A*3001	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.287361	0.707433	-3.579928	19380.339352
HLA B*1517	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.384101	0.804086	-3.580016	24215.945040
HLA B*4402	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.360005	0.779687	-3.580318	22908.945767
HLA A*0216	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.433972	0.853458	-3.580514	27162.615807
HLA A*3201	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.520599	0.940065	-3.580535	33158.849414
HLA B*5101	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.505300	0.924700	-3.580600	32011.026883
HLA A*0216	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.489960	0.909340	-3.580620	30900.095278

HLA B*7301	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.568515	0.987852	-3.580663	37026.686551
HLA A*2402	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.428389	0.847335	-3.581054	26815.704709
HLA B*5301	1:89-97	9	APYELNITS	1.361001	-1.037258	-3.904900	0.323743	-3.581158	8033.419779
HLA B*1509	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.434730	0.853458	-3.581273	27210.121098
HLA A*0211	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.419348	0.837899	-3.581449	26263.245679
HLA B*5701	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.340025	0.758478	-3.581547	21878.879866
HLA A*3201	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.446405	0.864656	-3.581749	27951.496562
HLA B*3901	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.182314	0.600517	-3.581796	15216.457361
HLA B*5301	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.567702	0.985844	-3.581858	36957.444023
HLA B*4801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.417159	0.835252	-3.581907	26131.159227
HLA B*3501	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.386129	0.804086	-3.582043	24329.267184
HLA B*4002	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.599885	1.017829	-3.582056	39800.192567
HLA A*2402	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.576623	0.994492	-3.582131	37724.450486
HLA B*2705	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.391375	0.809025	-3.582351	24624.953997
HLA B*5801	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.357656	0.775271	-3.582385	22785.345543
HLA A*0206	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.507095	0.924700	-3.582395	32143.607228

HLA A*3002	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.549862	0.967178	-3.582684	35470.089814
HLA A*2301	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.537314	0.954256	-3.583058	34459.874287
HLA B*4501	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.629949	1.046875	-3.583074	42652.960787
HLA A*2603	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.538063	0.954978	-3.583085	34519.394919
HLA B*5701	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.421064	0.837899	-3.583164	26367.170065
HLA A*6901	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.286093	0.702905	-3.583187	19323.805406
HLA B*5301	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.582353	0.999064	-3.583290	38225.512449
HLA A*3301	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.538338	0.954978	-3.583360	34541.251129
HLA B*1509	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.291468	0.707999	-3.583469	19564.478546
HLA A*2602	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.583700	1.000164	-3.583535	38344.190282
HLA A*3002	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.297297	0.713674	-3.583623	19828.841870
HLA B*0702	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.370204	0.786460	-3.583745	23453.314023
HLA A*0211	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.351204	0.767355	-3.583849	22449.358392
HLA B*4601	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.363572	0.779687	-3.583884	23097.853493
HLA A*2402	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.504637	0.920569	-3.584068	31962.228454
HLA A*8001	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.422041	0.837899	-3.584142	26426.576569

HLA B*7301	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.584393	1.000164	-3.584228	38405.433295
HLA A*2501	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.338350	0.754093	-3.584257	21794.650088
HLA A*6901	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.280806	0.696230	-3.584576	19090.016957
HLA B*3901	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.479798	0.895143	-3.584655	30185.494572
HLA B*5301	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.579510	0.994492	-3.585019	37976.106741
HLA A*2402	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.552294	0.967178	-3.585116	35669.252250
HLA A*0202	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.540098	0.954978	-3.585120	34681.496465
HLA B*4403	1:122-130	9	GTHPTTTYK	0.923012	0.114876	-4.623166	1.037888	-3.585278	41991.967170
HLA B*2705	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.376003	0.790540	-3.585463	23768.553233
HLA A*2402	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.540154	0.954583	-3.585571	34685.999710
HLA A*0211	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.525656	0.940065	-3.585591	33547.143328
HLA A*2902	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.328348	0.742712	-3.585636	21298.457086
HLA B*1509	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.481029	0.895143	-3.585887	30271.185265
HLA A*0202	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.573752	0.987852	-3.585900	37475.881037
HLA B*0802	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.450632	0.864656	-3.585976	28224.859523
HLA A*2602	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.585053	0.999064	-3.585989	38463.860821

HLA A*6901	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.353380	0.767355	-3.586025	22562.101902
HLA A*6801	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.220403	0.634040	-3.586364	16611.291684
HLA A*3002	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.574447	0.987852	-3.586596	37535.940259
HLA A*0203	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.361896	0.775271	-3.586626	23008.930884
HLA A*0202	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.572758	0.985844	-3.586914	37390.219914
HLA A*0216	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.424997	0.837899	-3.587097	26607.039737
HLA A*1101	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.482373	0.895143	-3.587230	30365.003217
HLA A*3002	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.496658	0.909340	-3.587319	31380.380139
HLA B*5301	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.541601	0.954256	-3.587346	34801.783334
HLA B*5101	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.496722	0.909340	-3.587382	31384.964112
HLA A*0101	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.373996	0.786460	-3.587537	23658.994717
HLA B*4403	1:56-64	9	LPSYYPDQK	0.981412	0.093835	-4.662912	1.075247	-3.587665	46016.380769
HLA B*4601	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.364542	0.776623	-3.587919	23149.518358
HLA A*3301	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.528127	0.940065	-3.588063	33738.611268
HLA B*4403	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.664228	1.076055	-3.588174	46156.000524
HLA A*0201	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.396671	0.808230	-3.588441	24927.066199

HLA A*2402	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.560989	0.972498	-3.588491	36390.619518
HLA A*2602	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.498026	0.909340	-3.588686	31479.338713
HLA A*2403	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.393055	0.804086	-3.588970	24720.389518
HLA A*0212	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.337062	0.748062	-3.589001	21730.132931
HLA A*3001	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.295944	0.706847	-3.589097	19767.149462
HLA A*3001	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.285557	0.696230	-3.589327	19299.985061
HLA B*3501	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-3.373602	-0.215742	-3.589344	2363.752601
HLA A*0211	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.442836	0.853458	-3.589378	27722.742932
HLA A*0202	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.330409	0.740601	-3.589808	21399.747130
HLA A*3001	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.297878	0.707999	-3.589879	19855.355724
HLA B*2705	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.499273	0.909340	-3.589934	31569.897882
HLA A*3002	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.544562	0.954583	-3.589979	35039.818666
HLA A*0250	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.510586	0.920569	-3.590017	32403.054211
HLA B*0803	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.485461	0.895143	-3.590318	30581.624732
HLA B*5401	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.562836	0.972498	-3.590338	36545.688179
HLA A*0250	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.128120	0.537766	-3.590354	13431.370599

HLA A*6802	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.428295	0.837899	-3.590396	26809.902537
HLA A*6801	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.610077	1.019585	-3.590493	40745.273683
HLA A*0219	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.381120	0.790540	-3.590580	24050.268310
HLA B*0801	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.349148	0.758478	-3.590670	22343.342040
HLA B*1517	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.426004	0.835252	-3.590752	26668.862197
HLA A*0202	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.444222	0.853458	-3.590765	27811.370710
HLA A*6801	1:104-112	9	IPPRGTQAV	1.002370	0.073685	-4.666939	1.076055	-3.590885	46445.054337
HLA B*5401	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.371113	0.779687	-3.591426	23502.467954
HLA B*4601	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.377913	0.786460	-3.591453	23873.323265
HLA A*0212	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.426813	0.835252	-3.591561	26718.539209
HLA A*0201	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.339677	0.748062	-3.591616	21861.369255
HLA A*2501	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.456412	0.864656	-3.591756	28602.995791
HLA A*2602	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.548598	0.956718	-3.591880	35367.003486
HLA B*4601	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.400301	0.808230	-3.592071	25136.286710
HLA A*2403	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.448174	0.856017	-3.592157	28065.593316
HLA B*1501	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.334971	0.742712	-3.592259	21625.758131

HLA A*0301	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.367662	0.775271	-3.592391	23316.431062
HLA A*3101	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.430391	0.837899	-3.592492	26939.589627
HLA B*4501	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.591695	0.999064	-3.592631	39056.639095
HLA B*4403	1:103-111	9	AIPPRGTQA	1.171695	-0.095962	-4.668408	1.075733	-3.592675	46602.359247
HLA A*2902	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.430600	0.837899	-3.592701	26952.563628
HLA B*4001	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.401192	0.808230	-3.592962	25187.877716
HLA B*1509	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.560160	0.967178	-3.592982	36321.190999
HLA B*0803	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.503072	0.909340	-3.593733	31847.276197
HLA B*3901	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.397841	0.804086	-3.593755	24994.313371
HLA A*6802	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.307442	0.713674	-3.593768	20297.494184
HLA B*0702	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.402221	0.808230	-3.593991	25247.631951
HLA B*1801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.402449	0.808230	-3.594219	25260.884356
HLA B*4403	1:2-10	9	RIKIFMLVT	1.197683	-0.125710	-4.666268	1.071973	-3.594295	46373.248799
HLA B*3501	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.292124	0.697746	-3.594378	19594.030666
HLA B*1801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.489558	0.895143	-3.594415	30871.523095
HLA B*3801	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.561755	0.967178	-3.594577	36454.855510

HLA B*4403	1:8-16	9	LVTAVVLLC	0.979168	0.067707	-4.641480	1.046875	-3.594606	43800.639950
HLA B*1801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.447751	0.852998	-3.594753	28038.276903
HLA A*2501	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.442249	0.847335	-3.594914	27685.274034
HLA B*5401	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.562228	0.967178	-3.595050	36494.517633
HLA B*1517	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.490376	0.895143	-3.595233	30929.697847
HLA B*4403	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.572937	0.977336	-3.595600	37405.596123
HLA A*3301	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.449142	0.852998	-3.596144	28128.217761
HLA A*0212	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.434070	0.837899	-3.596171	27168.788272
HLA A*6801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.443602	0.847335	-3.596267	27771.678563
HLA A*3001	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.068819	0.472542	-3.596277	11717.078266
HLA A*0202	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.563529	0.967178	-3.596351	36604.058639
HLA B*4402	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.373024	0.776623	-3.596401	23606.065102
HLA B*4001	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.376163	0.779687	-3.596475	23777.298638
HLA A*2902	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.344639	0.748062	-3.596578	22112.582803
HLA B*1801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.483447	0.886699	-3.596748	30440.168079
HLA B*1502	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.521497	0.924700	-3.596797	33227.445606

HLA A*1101	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.450298	0.853458	-3.596840	28203.185392
HLA A*2603	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.461630	0.864656	-3.596974	28948.744177
HLA A*0201	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.383514	0.786460	-3.597055	24183.215783
HLA B*0802	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.351307	0.754093	-3.597214	22454.702764
HLA A*0212	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.387774	0.790540	-3.597234	24421.574901
HLA B*5701	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.384073	0.786460	-3.597614	24214.373024
HLA A*0206	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.364970	0.767355	-3.597615	23172.322594
HLA B*4402	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.435785	0.837899	-3.597886	27276.295915
HLA A*0203	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.352296	0.754093	-3.598204	22505.903056
HLA B*0803	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.462971	0.864656	-3.598316	29038.306460
HLA A*2603	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.555205	0.956718	-3.598487	35909.141064
HLA A*0216	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.454511	0.856017	-3.598494	28478.085451
HLA B*5101	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.463333	0.864656	-3.598677	29062.509019
HLA A*2402	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.378385	0.779687	-3.598698	23899.296942
HLA B*4601	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.346803	0.748062	-3.598742	22223.033855
HLA B*0802	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.446570	0.847335	-3.599234	27962.083581

HLA A*2501	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.452706	0.853458	-3.599249	28360.010307
HLA A*2601	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.407538	0.808230	-3.599308	25558.627895
HLA B*0801	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.437263	0.837899	-3.599364	27369.270345
HLA B*5801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.351314	0.751912	-3.599402	22455.067200
HLA B*4501	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.619355	1.019585	-3.599771	41625.106296
HLA A*2403	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.358729	0.758478	-3.600251	22841.747887
HLA A*2602	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.540638	0.940065	-3.600574	34724.676625
HLA B*4801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.409156	0.808230	-3.600926	25654.073244
HLA B*0801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.409222	0.808230	-3.600992	25657.959538
HLA B*1509	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.349202	0.748062	-3.601140	22346.122338
HLA A*0211	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.391869	0.790540	-3.601329	24652.945732
HLA B*4801	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.349423	0.748062	-3.601361	22357.488892
HLA A*6801	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.578876	0.977336	-3.601540	37920.676671
HLA A*2601	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.378176	0.776623	-3.601553	23887.792675
HLA A*6901	1:94-102	9	NITSATYQS	1.243610	-0.899139	-3.946106	0.344471	-3.601635	8832.949128
HLA A*2501	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.437033	0.835252	-3.601781	27354.763848

HLA A*2601	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.315478	0.713674	-3.601803	20676.530403
HLA A*0203	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.437228	0.835252	-3.601976	27367.049464
HLA A*3001	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.304978	0.702905	-3.602072	20182.632664
HLA A*3301	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.556659	0.954583	-3.602076	36029.592339
HLA A*0219	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.342743	0.740601	-3.602143	22016.254547
HLA A*0219	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.440054	0.837899	-3.602155	27545.737696
HLA A*0202	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.026186	0.423714	-3.602472	10621.493215
HLA A*8001	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.437761	0.835252	-3.602509	27400.678073
HLA B*5801	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.350610	0.748062	-3.602548	22418.652930
HLA B*0702	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.440588	0.837899	-3.602689	27579.585877
HLA A*3301	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.575206	0.972498	-3.602708	37601.587682
HLA A*2601	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.305880	0.702905	-3.602975	20224.603594
HLA A*2402	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.378254	0.775271	-3.602983	23892.057656
HLA A*0219	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.438302	0.835252	-3.603050	27434.793258
HLA B*1501	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.411351	0.808230	-3.603121	25784.027122
HLA B*0801	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.378547	0.775271	-3.603276	23908.219793

HLA A*2403	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.370688	0.767355	-3.603334	23479.465838
HLA B*4801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.355480	0.751912	-3.603568	22671.486477
HLA B*4801	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.441690	0.837899	-3.603790	27649.650698
HLA B*0803	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.383488	0.779687	-3.603801	24181.776712
HLA A*0202	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.185034	0.581216	-3.603818	15312.082382
HLA A*2902	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.380594	0.776623	-3.603971	24021.141482
HLA A*2501	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.408529	0.804086	-3.604443	25617.044214
HLA A*0250	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.561314	0.956718	-3.604595	36417.797614
HLA A*0203	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.330129	0.725355	-3.604774	21385.974902
HLA B*1503	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.408872	0.804086	-3.604786	25637.285671
HLA B*4601	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.363374	0.758478	-3.604896	23087.359504
HLA B*7301	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.582421	0.977336	-3.605085	38231.509998
HLA B*0803	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.491865	0.886699	-3.605166	31035.964818
HLA B*0702	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.345864	0.740601	-3.605263	22174.996189
HLA A*0201	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.372702	0.767355	-3.605347	23588.575835
HLA A*2601	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.312336	0.706847	-3.605489	20527.516169

HLA A*6802 1:207-215 9 LPEAAGPTQ 1.054236 -0.218984 -4.440851 0.835252 -3.605599 27596.301621

HLA A*2402 1:134-142 9 WDQAYRKPI 0.842101 0.011357 -4.459151 0.853458 -3.605693 28783.991762

HLA A*3001 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.272510 0.666762 -3.605748 18728.814260

HLA B*0802 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.414913 0.809025 -3.605888 25996.361563

HLA A*6802 1:208-216 9 PEAAGPTQV 0.855949 -0.104037 -4.357891 0.751912 -3.605978 22797.675497

HLA A*0219 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.373517 0.767355 -3.606162 23632.898642

HLA B*5701 1:111-119 9 AVVLKVYQN 1.224563 -0.434023 -4.396953 0.790540 -3.606413 24943.253772

HLA A*3101 1:78-86 9 LSAATSSTP 0.733359 0.025119 -4.364894 0.758478 -3.606416 23168.311431

HLA B*4501 1:180-188 9 AGLDPVNYQ 1.025360 -0.030868 -4.600926 0.994492 -3.606434 39895.691337

HLA A*0201 1:202-210 9 NPGELLPEA 1.188654 -0.463299 -4.332244 0.725355 -3.606889 21490.354982

HLA A*3001 1:76-84 9 KFLSAATSS 0.874409 -0.909510 -3.572171 -0.035101 -3.607272 3733.972320

HLA A*0301 1:31-39 9 ELKGTDTGQ 0.941370 -0.200769 -4.347908 0.740601 -3.607307 22279.611103

HLA A*6802 1:128-136 9 TYKAFDWDQ 0.746622 0.061608 -4.415704 0.808230 -3.607474 26043.799608

HLA B*4403 1:189-197 9 NFAVTNDGV 0.789539 0.210625 -4.607758 1.000164 -3.607594 40528.291636

HLA B*2705 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.463639 0.856017 -3.607621 29082.955452

HLA A*0219 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.278678 0.671022 -3.607656 18996.678849

HLA B*5701	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.375086	0.767355	-3.607732	23718.457856
HLA A*3201	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.575039	0.967178	-3.607861	37587.147605
HLA A*2601	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.366628	0.758478	-3.608150	23260.995770
HLA B*4403	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.602733	0.994492	-3.608241	40062.011304
HLA A*3001	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.256877	0.648415	-3.608462	18066.615815
HLA A*0211	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.333879	0.725355	-3.608524	21571.424777
HLA B*1509	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.455935	0.847335	-3.608599	28571.601009
HLA B*7301	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.603268	0.994492	-3.608777	40111.456469
HLA A*0216	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.399319	0.790540	-3.608779	25079.509399
HLA A*0216	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.376160	0.767355	-3.608806	23777.170006
HLA B*0802	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.444236	0.835252	-3.608984	27812.273463
HLA B*3501	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.446981	0.837899	-3.609082	27988.568676
HLA A*8001	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.351817	0.742712	-3.609105	22481.078850
HLA A*0250	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.597148	0.987852	-3.609296	39550.139832
HLA A*3201	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.534024	0.924700	-3.609324	34199.866420
HLA A*0216	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.334746	0.725355	-3.609391	21614.529724

HLA A*3301	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.604145	0.994492	-3.609653	40192.478641
HLA A*3301	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.587076	0.977336	-3.609740	38643.440106
HLA B*4601	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.377410	0.767355	-3.610055	23845.700722
HLA A*6801	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.368935	0.758478	-3.610458	23384.898896
HLA B*5301	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.583044	0.972498	-3.610546	38286.358785
HLA A*0211	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.324422	0.713674	-3.610748	21106.788277
HLA A*6802	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.419774	0.809025	-3.610749	26288.974979
HLA B*4001	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.397249	0.786460	-3.610790	24960.262039
HLA A*0206	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.551086	0.940065	-3.611022	35570.205140
HLA A*0202	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.538709	0.927533	-3.611176	34570.788316
HLA A*0250	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.566205	0.954978	-3.611227	36830.304192
HLA B*1509	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.467327	0.856017	-3.611310	29331.024287
HLA A*0212	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.336874	0.725355	-3.611520	21720.730357
HLA A*6901	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.386930	0.775271	-3.611659	24374.190563
HLA A*8001	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.391493	0.779687	-3.611806	24631.615812
HLA A*6901	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.334990	0.723137	-3.611854	21626.694095

HLA B*4403	1:112-120	9	VVLKVYQNA	1.087232	-0.069403	-4.629757	1.017829	-3.611928	42634.043665
HLA B*1501	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.292089	0.680076	-3.612012	19592.440708
HLA A*1101	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.379459	0.767355	-3.612104	23958.456737
HLA B*4002	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.625617	1.013420	-3.612197	42229.577177
HLA A*0201	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.364215	0.751912	-3.612303	23132.117052
HLA A*2402	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.566628	0.954256	-3.612372	36866.186275
HLA A*2402	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.465466	0.852998	-3.612469	29205.620483
HLA B*0702	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.355257	0.742712	-3.612544	22659.837699
HLA B*4501	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.392397	0.779687	-3.612710	24682.972186
HLA B*2705	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.355508	0.742712	-3.612796	22672.958328
HLA B*4601	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.403367	0.790540	-3.612827	25314.374416
HLA B*1517	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.465859	0.852998	-3.612861	29232.018267
HLA A*0301	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.326546	0.713674	-3.612872	21210.264687
HLA A*3002	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.301369	0.688457	-3.612912	20015.618140
HLA A*3201	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.567281	0.954256	-3.613026	36921.672860
HLA B*1503	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.177572	0.564331	-3.613242	15051.240409

HLA A*2501	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.316185	0.702905	-3.613279	20710.227010
HLA A*0211	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.284342	0.671022	-3.613320	19246.080107
HLA A*0212	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.371835	0.758478	-3.613357	23541.534131
HLA B*4501	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.315097	0.701666	-3.613431	20658.417388
HLA B*4801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.321758	0.707999	-3.613759	20977.698427
HLA A*2601	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.367993	0.754093	-3.613900	23334.223489
HLA A*0250	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.581136	0.967178	-3.613958	38118.542185
HLA B*4601	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.368144	0.754093	-3.614051	23342.303964
HLA A*0301	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.356779	0.742712	-3.614067	22739.413611
HLA A*0212	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.327796	0.713674	-3.614122	21271.397052
HLA B*1501	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.315811	0.701666	-3.614146	20692.420304
HLA A*0101	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.366414	0.751912	-3.614502	23249.547203
HLA B*4402	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.405125	0.790540	-3.614585	25417.019030
HLA B*1501	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.366516	0.751912	-3.614603	23254.956263
HLA A*0301	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.368752	0.754093	-3.614659	23375.033221
HLA A*0101	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.303183	0.688457	-3.614726	20099.386862

HLA A*2402	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.542327	0.927533	-3.614795	34860.008587
HLA B*1501	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.362857	0.748062	-3.614796	23059.897837
HLA B*5801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.355424	0.740601	-3.614823	22668.543063
HLA B*0801	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.391932	0.776623	-3.615310	24656.546977
HLA B*3901	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.363454	0.748062	-3.615392	23091.606496
HLA B*5301	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.570514	0.954978	-3.615536	37197.543586
HLA A*2902	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.318325	0.702788	-3.615538	20812.547411
HLA A*0101	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.363872	0.748062	-3.615811	23113.853506
HLA A*0301	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.367819	0.751912	-3.615907	23324.883927
HLA A*3101	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.370155	0.754093	-3.616062	23450.649698
HLA A*0219	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.341498	0.725355	-3.616143	21953.219046
HLA B*5301	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.583488	0.967178	-3.616310	38325.525422
HLA B*0702	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.196298	0.579719	-3.616579	15714.395820
HLA A*2602	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.537173	0.920569	-3.616604	34448.690656
HLA B*0801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.318344	0.701666	-3.616678	20813.448179
HLA B*1502	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.589233	0.972498	-3.616735	38835.831520

HLA B*0802	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.472860	0.856017	-3.616843	29707.100585
HLA B*4001	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.392137	0.775271	-3.616866	24668.154567
HLA A*0203	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.425130	0.808230	-3.616900	26615.245647
HLA A*1101	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.421017	0.804086	-3.616931	26364.317350
HLA B*4001	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.371238	0.754093	-3.617145	23509.207645
HLA A*8001	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.421587	0.804086	-3.617502	26398.998753
HLA B*5701	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.421663	0.804086	-3.617577	26403.569250
HLA A*0206	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.376334	0.758478	-3.617856	23786.690668
HLA B*4002	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.595290	0.977336	-3.617953	39381.257591
HLA B*5401	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.558102	0.940065	-3.618037	36149.469811
HLA A*0101	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.426390	0.808230	-3.618160	26692.533893
HLA A*0216	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.155952	0.537766	-3.618186	14320.307104
HLA A*2603	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.558382	0.940065	-3.618317	36172.749494
HLA B*7301	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.604196	0.985844	-3.618352	40197.262537
HLA B*1509	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.398353	0.779687	-3.618666	25023.807950
HLA A*2602	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.596598	0.977336	-3.619262	39500.104431

HLA B*4002	1:189-197	9	NFAVTNDGV	0.789539	0.210625	-4.619586	1.000164	-3.619421	41647.180494
HLA A*0301	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.367582	0.748062	-3.619520	23312.142720
HLA B*0803	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.466886	0.847335	-3.619550	29301.208065
HLA A*8001	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.406231	0.786460	-3.619772	25481.865644
HLA A*0201	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.395177	0.775271	-3.619906	24841.447283
HLA A*0212	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.157963	0.537766	-3.620198	14386.776300
HLA B*2705	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.220963	0.600517	-3.620445	16632.693388
HLA A*6801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.541179	0.920569	-3.620610	34767.910546
HLA B*3801	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.541256	0.920569	-3.620687	34774.118088
HLA A*0250	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.575324	0.954583	-3.620741	37611.760079
HLA A*0101	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.388098	0.767355	-3.620743	24439.813995
HLA A*0206	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.411327	0.790540	-3.620787	25782.632273
HLA A*0211	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.545549	0.924700	-3.620849	35119.525029
HLA B*0801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.301240	0.680076	-3.621163	20009.663500
HLA B*3501	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.407780	0.786460	-3.621320	25572.873606
HLA B*4002	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.575678	0.954256	-3.621423	37642.497425

HLA A*0250	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.575763	0.954256	-3.621507	37649.829241
HLA B*3501	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.398248	0.776623	-3.621625	25017.716770
HLA B*4002	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.641229	1.019585	-3.621645	43775.292930
HLA B*4403	1:21-29	9	ATAAPKTYC	0.926919	0.086501	-4.635341	1.013420	-3.621921	43185.828078
HLA A*0202	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.531449	0.909340	-3.622110	33997.687232
HLA B*7301	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.594714	0.972498	-3.622216	39329.095349
HLA A*2501	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.430490	0.808230	-3.622260	26945.711411
HLA A*0202	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.376496	0.754093	-3.622403	23795.571478
HLA B*1502	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.517684	0.895143	-3.622541	32936.977382
HLA B*1517	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.271523	0.648415	-3.623109	18686.307829
HLA A*6801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.413677	0.790540	-3.623137	25922.491425
HLA A*0212	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.431387	0.808230	-3.623157	27001.454395
HLA B*5701	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.377365	0.754093	-3.623273	23843.249799
HLA A*3301	1:172-180	9	QQVSIAPNA	1.175074	-0.172665	-4.625758	1.002409	-3.623349	42243.286842
HLA A*0201	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.286452	0.662917	-3.623535	19339.806593
HLA A*3201	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.544402	0.920569	-3.623833	35026.930852

HLA B*1801 1:117-125 9 YQNAGGTHP 0.729126 0.047497 -4.400496 0.776623 -3.623873 25147.575960

HLA B*4001 1:78-86 9 LSAATSSTP 0.733359 0.025119 -4.382422 0.758478 -3.623944 24122.456977

HLA B*4801 1:93-101 9 LNITSATYQ 0.940219 -0.153759 -4.410437 0.786460 -3.623977 25729.823062

HLA A*0212 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.391378 0.767355 -3.624023 24625.087216

HLA B*5301 1:185-193 9 VNYQNFAVT 1.248328 -0.327759 -4.544611 0.920569 -3.624042 35043.799685

HLA A*0216 1:207-215 9 LPEAAGPTQ 1.054236 -0.218984 -4.459668 0.835252 -3.624416 28818.270162

HLA A*2902 1:153-161 9 DPLPVVFPI 0.780193 -0.026100 -4.378524 0.754093 -3.624431 23906.926420

HLA A*8001 1:117-125 9 YQNAGGTHP 0.729126 0.047497 -4.401229 0.776623 -3.624606 25190.058028

HLA A*0212 1:162-170 9 VQGELSKQT 0.977010 -0.314093 -4.287538 0.662917 -3.624620 19388.204359

HLA A*0202 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.433730 0.809025 -3.624705 27147.484509

HLA A*0201 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.331861 0.706847 -3.625014 21471.412884

HLA B*0801 1:129-137 9 YKAFDWDQA 0.955276 -0.207214 -4.373122 0.748062 -3.625061 23611.429371

HLA A*3001 1:162-170 9 VQGELSKQT 0.977010 -0.314093 -4.288066 0.662917 -3.625149 19411.818536

HLA A*3101 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.392531 0.767355 -3.625177 24690.584692

HLA A*2402 1:59-67 9 YYPDQKSLE 0.890200 -0.554928 -3.960466 0.335272 -3.625194 9129.894972

HLA B*0702 1:19-27 9 GVATAAPKT 1.007855 -0.294181 -4.339012 0.713674 -3.625338 21827.925137

HLA A*0101	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.379471	0.754093	-3.625378	23959.104809
HLA B*1509	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.384033	0.758478	-3.625555	24212.146176
HLA A*3101	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.400849	0.775271	-3.625578	25167.991081
HLA A*2603	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.580457	0.954583	-3.625874	38058.992011
HLA B*5801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.351253	0.725355	-3.625898	22451.908957
HLA B*5101	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.473278	0.847335	-3.625943	29735.721120
HLA A*6901	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.334128	0.707999	-3.626129	21583.798420
HLA B*5401	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.480061	0.853458	-3.626604	30203.789734
HLA A*2601	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.369380	0.742712	-3.626667	23408.821460
HLA A*0250	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.014372	0.387379	-3.626994	10336.472783
HLA A*8001	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.417699	0.790540	-3.627159	26163.693799
HLA B*4801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.381472	0.754093	-3.627379	24069.792623
HLA B*0803	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.480402	0.852998	-3.627404	30227.491906
HLA B*1501	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.335505	0.707999	-3.627506	21652.331845
HLA A*2602	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.594716	0.967178	-3.627538	39329.308116
HLA B*3501	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.341306	0.713674	-3.627631	21943.482518

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HLA A*2602	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.247122
	0.619394	-3.627728	17665.329713

HLA A*2602	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.368588
	0.740601	-3.627987	23366.182953

HLA B*0801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.395363
	0.767355	-3.628008	24852.066320

HLA A*6901	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.299099
	0.671022	-3.628077	19911.290305

HLA B*4801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.432235
	0.804086	-3.628150	27054.238951

HLA B*5801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.341909
	0.713674	-3.628235	21974.012671

HLA A*0101	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.403539
	0.775271	-3.628268	25324.373591

HLA A*3002	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.463608
	0.835252	-3.628356	29080.910162

HLA A*0206	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.503994
	-0.124403	-3.628397	3191.491840

HLA A*0201	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.387005
	0.758478	-3.628527	24378.410502

HLA B*0801	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.336111
	0.707433	-3.628677	21682.574218

HLA B*0802	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.437103
	0.808230	-3.628873	27359.203796

HLA A*2601	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.404192
	0.775271	-3.628921	25362.488816

HLA A*2902	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.404258
	0.775271	-3.628987	25366.330938

HLA A*2403	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.309421
	0.680076	-3.629344	20390.162739

HLA A*3001	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.251316
	0.621958	-3.629358	17836.743968
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HLA A*2601	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.381407	0.751912	-3.629494	24066.146882
HLA A*6802	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.354956	0.725355	-3.629601	22644.151968
HLA B*3801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.464921	0.835252	-3.629669	29168.987669
HLA A*0250	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.353062	0.723137	-3.629926	22545.630025
HLA A*0201	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.318492	0.688457	-3.630035	20820.543090
HLA A*0212	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.416508	0.786460	-3.630048	26092.029984
HLA B*0801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.382020	0.751912	-3.630108	24100.151827
HLA B*1517	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.486238	0.856017	-3.630221	30636.435490
HLA B*4001	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.331908	0.701666	-3.630242	21473.736169
HLA A*3101	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.373256	0.742712	-3.630544	23618.711401
HLA B*5401	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.478175	0.847335	-3.630840	30072.864797
HLA B*2705	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.466218	0.835252	-3.630966	29256.224006
HLA A*2403	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.421510	0.790540	-3.630970	26394.286257
HLA B*1801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.339036	0.707999	-3.631037	21829.106035
HLA B*5301	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.587837	0.956718	-3.631119	38711.233882
HLA A*2501	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.406398	0.775271	-3.631127	25491.655163

HLA A*3001	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.265180	0.634040	-3.631140	18415.346268
HLA B*1502	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.484359	0.852998	-3.631361	30504.130224
HLA A*0250	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.559230	0.927533	-3.631697	36243.462816
HLA B*4002	1:180-188	9	AGLDPVNYQ	1.025360	-0.030868	-4.626225	0.994492	-3.631733	42288.789099
HLA A*2603	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.631258	0.999064	-3.632194	42781.681146
HLA B*7301	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.599453	0.967178	-3.632275	39760.594386
HLA A*0203	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.335392	0.702905	-3.632486	21646.710013
HLA A*0211	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.542078	0.909340	-3.632739	34840.023907
HLA A*0211	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.281091	0.648272	-3.632818	19102.517308
HLA B*4001	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.152588	0.519628	-3.632960	14209.796852
HLA B*1517	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.346735	0.713674	-3.633061	22219.547628
HLA B*3501	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.441347	0.808230	-3.633117	27627.820415
HLA B*5701	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.410026	0.776623	-3.633403	25705.475378
HLA A*2902	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.267492	0.634040	-3.633452	18513.638640
HLA B*1801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.330042	0.696230	-3.633812	21381.694588
HLA B*4601	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.385763	0.751912	-3.633850	24308.743338

HLA B*4801	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.413562	0.779687	-3.633874	25915.620684
HLA B*5401	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.543373	0.909340	-3.634033	34944.031693
HLA B*7301	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.588725	0.954583	-3.634142	38790.476955
HLA B*4001	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.382687	0.748062	-3.634625	24137.207965
HLA A*2602	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.622598	0.987852	-3.634746	41937.027545
HLA A*0211	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.375455	0.740601	-3.634854	23738.611747
HLA A*0201	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.306035	0.671022	-3.635013	20231.826132
HLA A*6901	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.315226	0.680076	-3.635150	20664.565089
HLA B*4001	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.402533	0.767355	-3.635179	25265.804544
HLA A*0203	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.343293	0.707999	-3.635294	22044.142881
HLA A*2301	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.544898	0.909340	-3.635558	35066.936454
HLA B*0702	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.403095	0.767355	-3.635740	25298.493436
HLA B*4402	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.439975	0.804086	-3.635889	27540.671503
HLA A*0202	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.361283	0.725355	-3.635928	22976.465635
HLA A*2902	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.284420	0.648415	-3.636005	19249.516346
HLA B*1801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.359220	0.723137	-3.636084	22867.588899

HLA B*0702	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.440311	0.804086	-3.636225	27561.985600
HLA B*3901	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.324093	0.687624	-3.636469	21090.808376
HLA B*4601	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.411940	0.775271	-3.636670	25819.062575
HLA A*2902	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.388643	0.751912	-3.636731	24470.507523
HLA A*3001	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.083377	0.446632	-3.636745	12116.487537
HLA A*2603	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.474801	0.837899	-3.636902	29840.145836
HLA B*2705	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.416762	0.779687	-3.637074	26107.279177
HLA A*3201	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.441194	0.804086	-3.637108	27618.106999
HLA B*0802	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.441316	0.804086	-3.637230	27625.877459
HLA B*3501	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.404624	0.767355	-3.637270	25387.747704
HLA B*1503	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.038990	0.401614	-3.637376	10939.318556
HLA B*0803	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.446511	0.809025	-3.637486	27958.302043
HLA B*0802	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.475489	0.837899	-3.637590	29887.482884
HLA B*4001	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.428286	0.790540	-3.637746	26809.322389
HLA B*1801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.428387	0.790540	-3.637847	26815.559639
HLA B*5401	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.562573	0.924700	-3.637873	36523.551576

HLA A*0212	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.326400	0.688457	-3.637943	21203.151678
HLA A*0250	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.485418	0.847335	-3.638083	30578.646899
HLA B*4801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.428627	0.790540	-3.638087	26830.360781
HLA A*0216	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.446330	0.808230	-3.638100	27946.658117
HLA A*3201	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.626366	0.987852	-3.638514	42302.517987
HLA B*5801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.327049	0.688457	-3.638592	21234.834375
HLA B*1501	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.414426	0.775271	-3.639155	25967.265909
HLA A*2902	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.326826	0.687624	-3.639201	21223.923759
HLA A*6901	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.326868	0.687624	-3.639244	21225.990603
HLA B*3801	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.548638	0.909340	-3.639299	35370.256272
HLA B*0802	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.382048	0.742712	-3.639336	24101.716428
HLA A*6901	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.346185	0.706847	-3.639339	22191.437387
HLA A*2602	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.593704	0.954256	-3.639448	39237.712281
HLA B*5801	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.346324	0.706847	-3.639477	22198.521657
HLA A*2501	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.430100	0.790540	-3.639560	26921.523903
HLA A*0101	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.310642	0.671022	-3.639620	20447.603927

HLA A*3101	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.380227	0.740601	-3.639626	24000.877567
HLA A*3201	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.594439	0.954583	-3.639856	39304.209598
HLA B*1501	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.394084	0.754093	-3.639992	24779.034712
HLA A*2403	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.388053	0.748062	-3.639992	24437.302007
HLA B*7301	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.549352	0.909340	-3.640013	35428.474278
HLA A*0211	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.346911	0.706847	-3.640065	22228.564854
HLA A*3101	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.391991	0.751912	-3.640079	24659.881932
HLA B*1502	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.595078	0.954978	-3.640100	39362.087917
HLA A*0250	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.328607	0.688457	-3.640150	21311.135310
HLA B*4801	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.382955	0.742712	-3.640242	24152.098633
HLA A*6802	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.061564	0.421102	-3.640462	11522.961774
HLA B*4402	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.394615	0.754093	-3.640522	24809.348953
HLA A*6802	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.407939	0.767355	-3.640585	25582.282893
HLA B*4402	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.388697	0.748062	-3.640635	24473.552515
HLA B*1502	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.444845	0.804086	-3.640759	27851.270258
HLA B*7301	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.535920	0.895143	-3.640778	34349.501931

HLA B*1502	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.476098	0.835252	-3.640846	29929.389420
HLA A*0206	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-3.734286	0.093374	-3.640911	5423.573866
HLA B*1501	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.354632	0.713674	-3.640958	22627.252952
HLA B*1503	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.408332	0.767355	-3.640977	25605.405688
HLA B*5701	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.416475	0.775271	-3.641204	26090.053889
HLA A*8001	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.393128	0.751912	-3.641216	24724.535637
HLA A*2403	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.366819	0.725355	-3.641464	23271.190996
HLA A*6901	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.339266	0.697746	-3.641520	21840.682222
HLA B*1502	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.629409	0.987852	-3.641557	42599.921800
HLA B*5101	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.400191	0.758478	-3.641713	25129.896249
HLA A*3301	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.382412	0.740601	-3.641811	24121.934984
HLA A*1101	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.497927	0.856017	-3.641910	31472.186937
HLA B*1503	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-3.770031	0.127871	-3.642159	5888.851790
HLA A*3101	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.329929	0.687624	-3.642305	21376.143024
HLA A*2301	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.529114	0.886699	-3.642415	33815.357726
HLA B*1509	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.396634	0.754093	-3.642541	24924.908650

HLA A*3001	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.243367	0.600517	-3.642850	17513.271108
HLA A*0212	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.222687	0.579719	-3.642968	16698.870765
HLA B*1502	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.597832	0.954256	-3.643576	39612.451772
HLA A*0301	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.369100	0.725355	-3.643745	23393.756253
HLA B*1503	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-3.598936	-0.044895	-3.643831	3971.334123
HLA B*1503	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.452074	0.808230	-3.643844	28318.769129
HLA B*5801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.367018	0.723137	-3.643882	23281.894495
HLA A*3101	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.324100	0.680076	-3.644024	21091.150675
HLA B*0803	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.479420	0.835252	-3.644168	30159.214689
HLA B*3801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.491755	0.847335	-3.644420	31028.074468
HLA A*6801	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.643560	0.999064	-3.644496	44010.849361
HLA B*0702	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.403041	0.758478	-3.644563	25295.345805
HLA B*1502	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.611795	0.967178	-3.644617	40906.725153
HLA B*4402	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.419898	0.775271	-3.644627	26296.513744
HLA A*0301	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.324744	0.680076	-3.644668	21122.437474
HLA B*1517	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.398870	0.754093	-3.644777	25053.608406

HLA A*0301	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.368228	0.723137	-3.645092	23346.850461
HLA A*1101	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.387804	0.742712	-3.645092	24423.292496
HLA B*4402	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.403572	0.758478	-3.645094	25326.291692
HLA A*0301	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.347931	0.702788	-3.645143	22280.816438
HLA A*0206	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.431636	0.786460	-3.645177	27016.942772
HLA A*0202	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.501597	0.856017	-3.645580	31739.261519
HLA A*3101	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.347254	0.701666	-3.645589	22246.128884
HLA A*2603	1:210-218	9	AAGPTQVLV	0.899889	0.077447	-4.622990	0.977336	-3.645654	41974.932735
HLA B*4001	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.386336	0.740601	-3.645735	24340.852381
HLA B*5101	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.432254	0.786460	-3.645795	27055.409860
HLA A*8001	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.399972	0.754093	-3.645879	25117.256084
HLA A*0250	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.585974	0.940065	-3.645909	38545.516781
HLA B*2705	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.400137	0.754093	-3.646044	25126.769595
HLA A*2601	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.394145	0.748062	-3.646084	24782.520304
HLA B*3801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.541402	0.895143	-3.646259	34785.783740
HLA A*2301	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.499325	0.852998	-3.646327	31573.655477

HLA A*0101	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.369669	0.723137	-3.646532	23424.403256
HLA A*3002	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.502572	0.856017	-3.646555	31810.599513
HLA A*0202	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.571374	0.924700	-3.646674	37271.268409
HLA B*4403	1:15-23	9	LCCSGVATA	1.215808	-0.196223	-4.666293	1.019585	-3.646709	46376.008496
HLA B*1509	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.482413	0.835252	-3.647161	30367.795958
HLA A*0212	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.422469	0.775271	-3.647198	26452.608986
HLA B*3501	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.314023	0.666762	-3.647261	20607.406267
HLA A*0219	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.455615	0.808230	-3.647385	28550.587330
HLA A*2501	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.228603	0.581216	-3.647387	16927.900861
HLA A*0101	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.372925	0.725355	-3.647570	23600.702051
HLA A*2403	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.248113	0.600517	-3.647596	17705.705258
HLA B*5401	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.534316	0.886699	-3.647617	34222.816285
HLA A*0216	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.336144	0.688457	-3.647687	21684.216485
HLA B*3901	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.345673	0.697746	-3.647927	22165.281212
HLA A*2501	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.399855	0.751912	-3.647943	25110.462924
HLA A*3001	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.261646	0.613638	-3.648008	18266.118214

HLA B*5801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.356190	0.707999	-3.648190	22708.557121
HLA B*4801	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.406936	0.758478	-3.648458	25523.255443
HLA B*5301	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.501954	0.853458	-3.648496	31765.371548
HLA B*5801	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.356018	0.707433	-3.648585	22699.590785
HLA A*3101	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.371776	0.723137	-3.648639	23538.350419
HLA B*5801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.350579	0.701666	-3.648913	22417.076314
HLA A*2902	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.407474	0.758478	-3.648996	25554.894895
HLA A*0219	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.372276	0.723137	-3.649140	23565.489443
HLA A*0216	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.435727	0.786460	-3.649267	27272.607121
HLA A*1101	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.484525	0.835252	-3.649273	30515.849176
HLA B*5801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.345600	0.696230	-3.649370	22161.564261
HLA A*2403	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.337868	0.688457	-3.649411	21770.492625
HLA A*6801	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.536111	0.886699	-3.649412	34364.557216
HLA B*1801	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.487312	0.837899	-3.649413	30712.272250
HLA A*3301	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.570054	0.920569	-3.649485	37158.122511
HLA A*2301	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.417199	0.767355	-3.649844	26133.562571

HLA B*1801	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.497199	0.847335	-3.649863	31419.450248
HLA B*1509	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.514559	0.864656	-3.649903	32700.841341
HLA A*3002	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.514561	0.864656	-3.649906	32701.018249
HLA A*6802	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.426752	0.776623	-3.650129	26714.781321
HLA A*2602	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.605129	0.954978	-3.650151	40283.688018
HLA A*0101	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.391138	0.740601	-3.650537	24611.502627
HLA A*0219	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.330665	0.680076	-3.650588	21412.369809
HLA B*5101	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.353537	0.702905	-3.650631	22570.281302
HLA B*5801	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.353744	0.702788	-3.650956	22581.028900
HLA A*2501	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.437505	0.786460	-3.651046	27384.525261
HLA B*4403	1:13-21	9	VLLCCSGVA	1.166577	-0.167513	-4.650289	0.999064	-3.651225	44698.060097
HLA B*3801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.504750	0.852998	-3.651752	31970.529313
HLA B*2705	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.460032	0.808230	-3.651802	28842.445362
HLA B*2705	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.438273	0.786460	-3.651814	27433.012285
HLA A*0101	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.359044	0.706847	-3.652197	22858.312447
HLA A*2603	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.460478	0.808230	-3.652248	28872.107145

HLA A*0212	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.404204	0.751912	-3.652291	25363.174867
HLA A*6901	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.359843	0.707433	-3.652410	22900.395857
HLA B*1801	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.438999	0.786460	-3.652540	27478.909189
HLA A*0212	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.332638	0.680076	-3.652562	21509.895614
HLA A*0203	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.375784	0.723137	-3.652648	23756.597814
HLA B*1509	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.439256	0.786460	-3.652796	27495.117673
HLA B*5701	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.395694	0.742712	-3.652981	24871.030568
HLA B*3501	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.443536	0.790540	-3.652996	27767.472114
HLA B*5301	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.577807	0.924700	-3.653107	37827.449728
HLA B*0702	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.429872	0.776623	-3.653249	26907.400291
HLA B*1501	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.360703	0.707433	-3.653269	22945.784006
HLA B*5801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.351244	0.697746	-3.653498	22451.423113
HLA A*3301	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.610390	0.956718	-3.653671	40774.601079
HLA A*0212	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.394500	0.740601	-3.653899	24802.773249
HLA B*1801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.341578	0.687624	-3.653954	21957.257409
HLA B*0702	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.444598	0.790540	-3.654058	27835.454160

HLA B*1503	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.356934	0.702788	-3.654147	22747.534229
HLA A*1101	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.440639	0.786460	-3.654180	27582.868527
HLA B*4002	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.642155	0.987852	-3.654303	43868.699318
HLA B*1801	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.361159	0.706847	-3.654312	22969.878672
HLA A*0202	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.429641	0.775271	-3.654371	26893.138599
HLA B*1517	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.493428	0.837899	-3.655528	31147.820152
HLA A*0219	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.193328	0.537766	-3.655562	15607.305776
HLA A*2402	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.542417	0.886699	-3.655718	34867.175698
HLA B*7301	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.610756	0.954978	-3.655778	40809.027031
HLA A*1101	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.464047	0.808230	-3.655817	29110.344729
HLA A*0101	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.323844	0.667964	-3.655880	21078.717356
HLA B*2705	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.493905	0.837899	-3.656005	31182.045711
HLA A*3201	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.583641	0.927533	-3.656108	38339.004687
HLA B*5801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.090655	0.434427	-3.656228	12321.269148
HLA B*1501	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.379492	0.723137	-3.656355	23960.271382
HLA A*3101	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.404479	0.748062	-3.656417	25379.233749

HLA A*0206	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.344877	0.688457	-3.656420	22124.668393
HLA A*0101	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.354209	0.697746	-3.656463	22605.229710
HLA A*0206	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.364542	0.707999	-3.656543	23149.518358
HLA B*0702	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.408597	0.751912	-3.656685	25621.063505
HLA A*8001	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.415178	0.758478	-3.656700	26012.258452
HLA A*0202	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.597049	0.940065	-3.656985	39541.154454
HLA A*0211	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.513015	0.856017	-3.656998	32584.819144
HLA A*2902	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.397703	0.740601	-3.657102	24986.336873
HLA B*1509	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.399918	0.742712	-3.657206	25114.131002
HLA A*0203	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.276612	0.619394	-3.657219	18906.558527
HLA B*5701	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.405301	0.748062	-3.657239	25427.333866
HLA A*0301	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.365247	0.707999	-3.657248	23187.119761
HLA A*2601	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.382863	0.725355	-3.657508	24147.003424
HLA B*4501	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.511056	0.853458	-3.657598	32438.132570
HLA A*2403	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.444161	0.786460	-3.657702	27807.459118
HLA B*4403	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.645796	0.987852	-3.657945	44238.099364

HLA A*6802	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.433344	0.775271	-3.658073	27123.409350
HLA A*0203	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.059750	0.401614	-3.658136	11474.937236
HLA B*0803	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.444605	0.786460	-3.658146	27835.905924
HLA A*8001	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.425626	0.767355	-3.658272	26645.643940
HLA A*2403	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.401114	0.742712	-3.658402	25183.381418
HLA A*2902	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.354634	0.696230	-3.658404	22627.375364
HLA A*0101	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.360289	0.701666	-3.658624	22923.946793
HLA A*2301	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.523379	0.864656	-3.658723	33371.743219
HLA B*0702	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.434014	0.775271	-3.658743	27165.260978
HLA A*8001	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.406889	0.748062	-3.658827	25520.494033
HLA A*2501	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.401572	0.742712	-3.658860	25209.962100
HLA B*5701	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.410803	0.751912	-3.658891	25751.546724
HLA A*3301	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.523555	0.864656	-3.658899	33385.286273
HLA A*0301	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.366337	0.707433	-3.658904	23245.396916
HLA B*1501	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.355137	0.696230	-3.658907	22653.586614
HLA A*2301	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.434230	0.775271	-3.658959	27178.784759

HLA B*1517	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.435727	0.776623	-3.659104	27272.607121
HLA B*4002	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.586681	0.927533	-3.659148	38608.334531
HLA B*3901	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.497112	0.837899	-3.659212	31413.161775
HLA B*3901	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.439084	0.779687	-3.659397	27484.261393
HLA A*2403	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.361072	0.701666	-3.659406	22965.281346
HLA B*4601	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.400029	0.740601	-3.659428	25120.517453
HLA B*4801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.426871	0.767355	-3.659517	26722.153062
HLA B*5301	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.599671	0.940065	-3.659607	39780.603757
HLA A*0219	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.418113	0.758478	-3.659635	26188.617174
HLA A*2501	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.348375	0.688457	-3.659918	22303.609533
HLA A*0301	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.348460	0.688457	-3.660003	22307.953718
HLA B*0801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.252885	0.592876	-3.660009	17901.319110
HLA A*0301	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.367176	0.706847	-3.660329	23290.334840
HLA B*3901	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.224966	0.564331	-3.660636	16786.729957
HLA A*0219	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.447119	0.786460	-3.660660	27997.503591
HLA B*4801	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.436345	0.775271	-3.661074	27311.438227

HLA B*4002	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.647159	0.985844	-3.661315	44377.124827
HLA A*2301	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.470389	0.809025	-3.661364	29538.511626
HLA B*3501	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.401988	0.740601	-3.661387	25234.113469
HLA A*2601	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.357721	0.696230	-3.661491	22788.797258
HLA B*4002	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.628859	0.967178	-3.661681	42546.028080
HLA B*1801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.363438	0.701666	-3.661772	23090.732052
HLA B*0803	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.517804	0.856017	-3.661786	32946.066091
HLA B*0803	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.384975	0.723137	-3.661839	24264.728186
HLA B*1517	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.470217	0.808230	-3.661987	29526.848523
HLA B*3901	1:77-85	9	FLSAATSST	0.627583	-0.297236	-3.992419	0.330347	-3.662071	9826.950707
HLA B*4601	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.363762	0.701666	-3.662096	23107.977214
HLA A*0219	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.369593	0.707433	-3.662160	23420.348458
HLA B*3501	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.358487	0.696230	-3.662257	22829.023586
HLA B*5101	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.414370	0.751912	-3.662458	25963.894607
HLA A*0301	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.360630	0.697746	-3.662884	22941.936170
HLA B*5101	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.500871	0.837899	-3.662972	31686.248722

HLA A*6802	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-3.759918	0.096880	-3.663039	5753.318815
HLA B*2705	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.350943	0.687624	-3.663319	22435.881651
HLA B*4501	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.651358	0.987852	-3.663506	44808.219876
HLA B*1501	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-3.892923	0.229395	-3.663527	7814.888512
HLA A*1101	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.422269	0.758478	-3.663791	26440.447799
HLA A*0206	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.499088	0.835252	-3.663835	31556.408382
HLA B*4403	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.618253	0.954256	-3.663998	41519.627363
HLA B*1501	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.243816	0.579719	-3.664097	17531.376727
HLA B*5301	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.573660	0.909340	-3.664321	37467.974997
HLA A*0301	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.360621	0.696230	-3.664390	22941.439722
HLA B*0801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.367441	0.702905	-3.664536	23304.576981
HLA A*0211	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.283964	0.619394	-3.664570	19229.324220
HLA B*3801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.518142	0.853458	-3.664684	32971.741868
HLA B*5801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.352602	0.687624	-3.664978	22521.736700
HLA A*0101	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.372587	0.707433	-3.665153	23582.323696
HLA A*0301	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.368087	0.702905	-3.665182	23339.273458

HLA A*2403	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.372039	0.706847	-3.665192	23552.616805
HLA A*0219	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.328146	0.662917	-3.665229	21288.550273
HLA B*0803	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.469357	0.804086	-3.665271	29468.442631
HLA A*0301	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.366995	0.701666	-3.665329	23280.635004
HLA A*0250	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.590191	0.924700	-3.665491	38921.645989
HLA B*4001	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.266030	0.600517	-3.665513	18451.445849
HLA B*1509	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.474575	0.809025	-3.665551	29824.652399
HLA B*7301	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.606100	0.940065	-3.666035	40373.793850
HLA A*6802	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.334067	0.667964	-3.666102	21580.762719
HLA A*0212	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.024170	0.357949	-3.666220	10572.305835
HLA A*2601	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.389376	0.723137	-3.666239	24511.845813
HLA B*1503	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.504165	0.837899	-3.666266	31927.492009
HLA A*6801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.369199	0.702905	-3.666293	23399.072278
HLA B*5701	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.406983	0.740601	-3.666382	25526.017152
HLA B*3501	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.334375	0.667964	-3.666410	21596.062328
HLA A*6801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.380164	0.713674	-3.666489	23997.372086

HLA A*2403	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.369579	0.702905	-3.666674	23419.588261
HLA A*3101	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-3.908702	0.241980	-3.666722	8104.046569
HLA B*5801	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.333519	0.666762	-3.666757	21553.577214
HLA A*0201	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.374758	0.707999	-3.666758	23700.500665
HLA A*1101	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.504900	0.837899	-3.667001	31981.600479
HLA A*6801	1:214-222	9	TQVLVPRSA	1.194247	-0.237529	-4.623970	0.956718	-3.667251	42069.731873
HLA B*7301	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.514690	0.847335	-3.667355	32710.749686
HLA A*0201	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.247096	0.579719	-3.667377	17664.278502
HLA B*7301	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.592162	0.924700	-3.667462	39098.708862
HLA A*2402	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.476645	0.809025	-3.667621	29967.139327
HLA A*6801	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.607777	0.940065	-3.667712	40530.045703
HLA A*0212	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.338799	0.671022	-3.667777	21817.181896
HLA A*3101	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.316805	0.648415	-3.668390	20739.826711
HLA B*0803	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.445223	0.776623	-3.668601	27875.539063
HLA A*0206	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-3.829318	0.160477	-3.668841	6750.213804
HLA B*7301	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.596424	0.927533	-3.668891	39484.294448

HLA A*2501	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.445533	0.776623	-3.668911	27895.452244
HLA A*3101	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.376950	0.707999	-3.668950	23820.429614
HLA B*4002	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.624747	0.954978	-3.669769	42145.132508
HLA B*5801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.373056	0.702905	-3.670151	23607.853056
HLA A*0219	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.445493	0.775271	-3.670223	27892.886870
HLA A*0201	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.410956	0.740601	-3.670355	25760.603662
HLA A*0301	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.358227	0.687624	-3.670602	22815.318925
HLA A*6802	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.290150	0.619394	-3.670756	19505.191387
HLA A*0212	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.378803	0.707999	-3.670804	23922.322100
HLA B*5801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.338808	0.667964	-3.670844	21817.654015
HLA A*2601	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.372554	0.701666	-3.670888	23580.537675
HLA B*3901	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.396298	0.725355	-3.670943	24905.633844
HLA B*4501	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.657018	0.985844	-3.671173	45396.001338
HLA A*0301	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.339374	0.667964	-3.671410	21846.118059
HLA B*5101	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.480604	0.809025	-3.671580	30241.558533
HLA A*2301	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.518971	0.847335	-3.671636	33034.767863

HLA A*6801	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.626058	0.954256	-3.671803	42272.549004
HLA A*2601	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.379825	0.707999	-3.671826	23978.684836
HLA B*1509	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.509766	0.837899	-3.671867	32341.933300
HLA B*1502	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.581277	0.909340	-3.671938	38130.917219
HLA A*0219	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.320224	0.648272	-3.671951	20903.722144
HLA A*3201	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.430506	0.758478	-3.672028	26946.731843
HLA B*4402	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.373879	0.701666	-3.672213	23652.595956
HLA B*5801	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.343270	0.671022	-3.672248	22042.950350
HLA A*0201	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.396147	0.723137	-3.673011	24897.012187
HLA B*5701	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.396241	0.723137	-3.673105	24902.400373
HLA A*2602	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.254447	0.581216	-3.673231	17965.836455
HLA A*0101	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.376188	0.702905	-3.673283	23778.713638
HLA A*2603	1:25-33	9	PKTYCEELK	0.921220	0.066632	-4.661160	0.987852	-3.673308	45831.043146
HLA A*0206	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.120118	0.446632	-3.673486	13186.149230
HLA A*0201	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.381054	0.707433	-3.673621	24046.625526
HLA A*2403	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.425643	0.751912	-3.673730	26646.653009

HLA A*2402	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.583237	0.909340	-3.673897	38303.346800
HLA A*0206	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.482150	0.808230	-3.673920	30349.401453
HLA B*4002	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.628504	0.954583	-3.673921	42511.286708
HLA A*3301	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.628478	0.954256	-3.674223	42508.756989
HLA B*1502	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.560982	0.886699	-3.674284	36390.028915
HLA B*4001	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.387978	0.713674	-3.674304	24433.071874
HLA A*0219	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.362928	0.688457	-3.674471	23063.640686
HLA A*6801	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-3.766676	0.092119	-3.674557	5843.533789
HLA B*4601	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.397806	0.723137	-3.674669	24992.285207
HLA B*3501	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.253395	0.578083	-3.675312	17922.346631
HLA A*0101	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.342760	0.666762	-3.675998	22017.088301
HLA B*4402	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.382903	0.706847	-3.676056	24149.224280
HLA B*4501	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.630692	0.954583	-3.676109	42725.939450
HLA A*1101	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.452744	0.776623	-3.676121	28362.465205
HLA B*1509	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.484424	0.808230	-3.676194	30508.751245
HLA B*1501	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.401636	0.725355	-3.676281	25213.644712

HLA A*0101	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.372854	0.696230	-3.676624	23596.872046
HLA B*4501	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.631956	0.954978	-3.676978	42850.475311
HLA B*5801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.357068	0.680076	-3.676992	22754.549824
HLA B*4501	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.644279	0.967178	-3.677101	44083.766406
HLA B*4601	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.402526	0.725355	-3.677171	25265.394492
HLA B*4001	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.375054	0.697746	-3.677308	23716.661525
HLA B*0803	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.452589	0.775271	-3.677318	28352.340119
HLA B*1501	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.380229	0.702788	-3.677442	24001.007409
HLA A*2601	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.366295	0.688457	-3.677838	23243.133436
HLA B*3901	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.464320	0.786460	-3.677860	29128.618576
HLA B*1801	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.453136	0.775271	-3.677865	28388.100895
HLA A*3301	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.605552	0.927533	-3.678019	40322.934575
HLA B*1801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.418653	0.740601	-3.678052	26221.223284
HLA B*1509	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.384959	0.706847	-3.678112	24263.809317
HLA A*2601	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.358534	0.680076	-3.678458	22831.493769
HLA A*0202	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.516516	0.837899	-3.678617	32848.538187

HLA B*0803	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.469172	0.790540	-3.678632	29455.851062
HLA B*2705	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.446086	0.767355	-3.678731	27930.938954
HLA B*4801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.380467	0.701666	-3.678801	24014.125114
HLA B*1509	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.380535	0.701666	-3.678869	24017.892909
HLA B*3501	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.386876	0.707999	-3.678877	24371.157934
HLA B*2705	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.437451	0.758478	-3.678973	27381.118086
HLA A*0206	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.350057	0.671022	-3.679035	22390.169669
HLA B*4402	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.421775	0.742712	-3.679063	26410.426478
HLA A*0101	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.392797	0.713674	-3.679123	24705.683092
HLA A*0301	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.313196	0.634040	-3.679156	20568.201316
HLA B*2705	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.454722	0.775271	-3.679451	28491.954523
HLA B*5101	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.427626	0.748062	-3.679564	26768.598386
HLA A*0301	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.350610	0.671022	-3.679587	22418.652930
HLA A*2301	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.535636	0.856017	-3.679619	34327.024222
HLA A*0206	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.272541	0.592876	-3.679665	18730.131477
HLA B*4601	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.387344	0.707433	-3.679910	24397.409269

HLA B*4002	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.652796	0.972498	-3.680298	44956.819126
HLA A*0203	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.261519	0.581216	-3.680303	18260.782839
HLA B*4402	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.405672	0.725355	-3.680317	25449.077489
HLA B*4001	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.403461	0.723137	-3.680325	25319.852927
HLA A*3301	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.647888	0.967178	-3.680710	44451.610619
HLA A*0203	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.302675	0.621958	-3.680717	20075.913721
HLA B*4403	1:155-163	9	LPVVFPIVQ	1.161225	-0.206642	-4.635344	0.954583	-3.680761	43186.061709
HLA B*4402	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.281286	0.600517	-3.680768	19111.096662
HLA B*7301	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.567481	0.886699	-3.680782	36938.654848
HLA A*0203	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.273892	0.592876	-3.681016	18788.485753
HLA B*4402	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.448400	0.767355	-3.681045	28080.172949
HLA A*0202	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.489377	0.808230	-3.681147	30858.665886
HLA B*5801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.300573	0.619394	-3.681179	19978.944088
HLA A*0250	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.260967	0.579719	-3.681248	18237.582219
HLA A*8001	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.421914	0.740601	-3.681313	26418.857595
HLA A*0216	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.348213	0.666762	-3.681451	22295.285543

HLA A*3101	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.370094	0.688457	-3.681637	23447.351430
HLA A*2402	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.449055	0.767355	-3.681701	28122.588015
HLA A*0212	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.330099	0.648272	-3.681826	21384.470910
HLA B*4001	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.407253	0.725355	-3.681898	25541.902779
HLA B*1503	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.349942	0.667964	-3.681978	22384.235167
HLA A*3002	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.468615	0.786460	-3.682155	29418.108629
HLA B*0802	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.434073	0.751912	-3.682160	27168.935252
HLA A*2501	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.362387	0.680076	-3.682311	23034.961032
HLA B*0801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.304343	0.621958	-3.682385	20153.174017
HLA B*0803	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.436666	0.754093	-3.682574	27331.687734
HLA A*0216	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.457920	0.775271	-3.682649	28702.510968
HLA B*1801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.486795	0.804086	-3.682709	30675.740996
HLA A*6901	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.350769	0.667964	-3.682805	22426.901652
HLA B*4402	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.390323	0.707433	-3.682889	24565.344477
HLA A*3301	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.592543	0.909340	-3.683203	39132.990070
HLA A*6901	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.276136	0.592876	-3.683260	18885.806600

HLA A*2403	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.390713	0.707433	-3.683279	24587.415087
HLA A*0219	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.283901	0.600517	-3.683383	19226.515655
HLA A*0203	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.386301	0.702788	-3.683513	24338.877242
HLA B*0802	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.406675	0.723137	-3.683539	25507.933388
HLA A*3101	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.408997	0.725355	-3.683642	25644.637553
HLA B*3901	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.491893	0.808230	-3.683663	31037.979697
HLA A*0216	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.442345	0.758478	-3.683867	27691.415460
HLA B*4001	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.380286	0.696230	-3.684056	24004.123838
HLA B*0803	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.521960	0.837899	-3.684061	33262.876572
HLA B*1509	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.332441	0.648272	-3.684168	21500.123078
HLA A*0212	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.371844	0.687624	-3.684220	23542.043565
HLA A*0201	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.387160	0.702905	-3.684255	24387.116433
HLA A*2601	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.382041	0.697746	-3.684295	24101.325268
HLA B*3501	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.436272	0.751912	-3.684360	27306.858304
HLA B*5801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.347283	0.662917	-3.684365	22247.573120
HLA B*1502	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.492596	0.808230	-3.684366	31088.226021

HLA B*2705	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.386059	0.701666	-3.684393	24325.318945
HLA A*2603	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.651633	0.967178	-3.684455	44836.590531
HLA B*4501	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.656999	0.972498	-3.684501	45394.036681
HLA B*4601	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.391679	0.706847	-3.684832	24642.145152
HLA A*0211	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-3.971062	0.286028	-3.685034	9355.391339
HLA A*3002	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.522947	0.837899	-3.685047	33338.540859
HLA B*0802	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.464978	0.779687	-3.685291	29172.775139
HLA B*0801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.383166	0.697746	-3.685420	24163.860912
HLA B*5701	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.399159	0.713674	-3.685485	25070.285035
HLA A*2602	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.580807	0.895143	-3.685664	38089.682723
HLA B*4801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.426270	0.740601	-3.685669	26685.170322
HLA A*0202	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.265662	0.579719	-3.685943	18435.780719
HLA B*4403	1:107-115	9	RGTQAVVLK	0.840868	0.114110	-4.641008	0.954978	-3.686030	43753.037558
HLA B*3501	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.461357	0.775271	-3.686086	28930.583175
HLA A*0250	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.595656	0.909340	-3.686316	39414.507145
HLA B*0802	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.463021	0.776623	-3.686398	29041.605622

HLA A*2601	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.393929	0.707433	-3.686496	24770.188870
HLA B*3901	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.394521	0.707999	-3.686522	24803.980901
HLA A*3201	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.374997	0.688457	-3.686540	23713.582416
HLA B*5301	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.581754	0.895143	-3.686611	38172.815881
HLA A*0216	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.394047	0.707433	-3.686613	24776.889975
HLA B*3501	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.306054	0.619394	-3.686660	20232.701766
HLA A*0216	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.409918	0.723137	-3.686781	25699.079240
HLA A*0211	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.522047	0.835252	-3.686795	33269.535332
HLA A*0212	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.409979	0.723137	-3.686842	25702.694253
HLA B*4403	1:160-168	9	PIVQGELSK	0.947962	0.037882	-4.672773	0.985844	-3.686929	47073.148433
HLA A*3001	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.253381	0.566374	-3.687007	17921.764893
HLA B*7301	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.306733	0.619394	-3.687339	20264.359486
HLA B*4402	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.427978	0.740601	-3.687377	26790.329474
HLA A*0301	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.354171	0.666762	-3.687409	22603.273126
HLA A*8001	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.389143	0.701666	-3.687478	24498.721297
HLA A*2403	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.355494	0.667964	-3.687530	22672.222391

HLA A*3001	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.280541	0.592876	-3.687665	19078.350463
HLA A*2501	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.410961	0.723137	-3.687824	25760.882387
HLA B*4402	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.395872	0.707999	-3.687873	24881.258434
HLA A*6802	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.394789	0.706847	-3.687942	24819.282913
HLA B*5301	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.574642	0.886699	-3.687943	37552.798461
HLA B*4601	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.385819	0.697746	-3.688073	24311.899725
HLA B*0802	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.474547	0.786460	-3.688088	29822.716285
HLA B*5101	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.464905	0.776623	-3.688282	29167.883083
HLA B*0802	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.478934	0.790540	-3.688394	30125.459885
HLA A*2603	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.544414	0.856017	-3.688397	35027.878324
HLA A*2403	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.386242	0.697746	-3.688496	24335.585699
HLA B*4801	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.289051	0.600517	-3.688533	19455.870058
HLA B*4001	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.396540	0.707999	-3.688540	24919.515593
HLA B*1501	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.322810	0.634040	-3.688771	21028.602274
HLA B*4403	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-3.752710	0.063696	-3.689014	5658.615968
HLA B*1501	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.355847	0.666762	-3.689084	22690.627989

HLA B*3901	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.480012	0.790540	-3.689472	30200.358546
HLA A*0101	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.397533	0.707999	-3.689534	24976.606290
HLA B*4002	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.498742	0.809025	-3.689718	31531.323007
HLA A*6901	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.352649	0.662917	-3.689732	22524.173634
HLA A*0212	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.323821	0.634040	-3.689781	21077.577051
HLA A*0250	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.437898	0.748062	-3.689836	27409.277030
HLA B*4403	1:185-193	9	VNYQNFAVT	1.248328	-0.327759	-4.610411	0.920569	-3.689842	40776.586402
HLA A*2403	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.360877	0.671022	-3.689855	22954.971772
HLA A*2301	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.525148	0.835252	-3.689896	33507.965176
HLA B*4601	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.403628	0.713674	-3.689954	25329.580204
HLA B*4801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.353142	0.662917	-3.690225	22549.777364
HLA A*0212	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.398243	0.707433	-3.690810	25017.446085
HLA B*1501	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.362002	0.671022	-3.690980	23014.532975
HLA B*4001	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.362098	0.671022	-3.691076	23019.638290
HLA B*1502	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.443177	0.751912	-3.691265	27744.498124
HLA A*1101	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.325320	0.634040	-3.691280	21150.452196

HLA B*4001	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.358243	0.666762	-3.691481	22816.182940
HLA A*2403	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.432141	0.740601	-3.691540	27048.385167
HLA A*2601	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.394338	0.702788	-3.691550	24793.516540
HLA A*3101	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.389303	0.697746	-3.691557	24507.735360
HLA A*8001	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.414910	0.723137	-3.691774	25996.220926
HLA B*4601	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.380246	0.688457	-3.691789	24001.916326
HLA A*3101	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.398671	0.706847	-3.691824	25042.090389
HLA B*7301	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.292345	0.600517	-3.691827	19603.997344
HLA B*4402	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.394644	0.702788	-3.691856	24810.959596
HLA A*0216	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.340232	0.648272	-3.691959	21889.298230
HLA B*3501	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.380469	0.688457	-3.692012	24014.255028
HLA A*3301	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.587174	0.895143	-3.692032	38652.221486
HLA A*3101	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.395250	0.702905	-3.692344	24845.613706
HLA B*7301	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.545535	0.852998	-3.692537	35118.385091
HLA A*6901	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.395550	0.702788	-3.692763	24862.824402
HLA A*0250	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.530801	0.837899	-3.692902	33946.962164

HLA A*2602	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.557627	0.864656	-3.692972	36109.987334
HLA B*0801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.406680	0.713674	-3.693006	25508.209379
HLA B*4402	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.355980	0.662917	-3.693063	22697.626034
HLA A*0201	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.395971	0.702788	-3.693183	24886.912480
HLA A*8001	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.468612	0.775271	-3.693341	29417.949480
HLA B*4801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.416602	0.723137	-3.693465	26097.676794
HLA A*2602	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.501747	0.808230	-3.693517	31750.252598
HLA A*6901	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.255035	0.561410	-3.693625	17990.151189
HLA A*0212	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.342102	0.648415	-3.693687	21983.762746
HLA A*6802	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.401887	0.707999	-3.693888	25228.244061
HLA B*2705	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.445825	0.751912	-3.693913	27914.171524
HLA A*2501	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.452399	0.758478	-3.693921	28339.918816
HLA B*4403	1:141-149	9	PITYDTLWQ	1.144380	-0.171882	-4.666646	0.972498	-3.694148	46413.657129
HLA B*1501	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.342614	0.648272	-3.694342	22009.704719
HLA B*0702	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.442474	0.748062	-3.694413	27699.656098
HLA B*4601	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.397324	0.702905	-3.694419	24964.583445

HLA B*1501	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.258930	0.564331	-3.694600	18152.241436
HLA A*3002	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.471392	0.776623	-3.694769	29606.825129
HLA A*6901	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.361659	0.666762	-3.694897	22996.362266
HLA A*6802	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.418103	0.723137	-3.694967	26188.050470
HLA B*0801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.343336	0.648272	-3.695063	22046.289600
HLA B*5801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.343711	0.648415	-3.695297	22065.380739
HLA A*3001	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.282568	0.587095	-3.695473	19167.630462
HLA A*0206	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.398414	0.702905	-3.695509	25027.327974
HLA A*0201	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.393692	0.697746	-3.695946	24756.658166
HLA A*1101	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.344715	0.648415	-3.696300	22116.411187
HLA A*2501	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.398057	0.701666	-3.696392	25006.756382
HLA B*0802	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.463784	0.767355	-3.696430	29092.711893
HLA A*0206	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.419567	0.723137	-3.696430	26276.462559
HLA A*0101	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.399246	0.702788	-3.696459	25075.303753
HLA B*1503	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.487049	0.790540	-3.696509	30693.669088
HLA A*2603	1:63-71	9	QKSLENYIA	1.220826	-0.266570	-4.650806	0.954256	-3.696550	44751.290308

HLA B*1501	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.384346	0.687624	-3.696721	24229.573454
HLA B*1501	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.277992	0.581216	-3.696775	18966.693720
HLA A*1101	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.410451	0.713674	-3.696777	25730.658248
HLA B*2705	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.437390	0.740601	-3.696789	27377.267008
HLA A*0211	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.297365	0.600517	-3.696848	19831.952997
HLA A*6802	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.393123	0.696230	-3.696893	24724.268125
HLA B*1801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.464355	0.767355	-3.697001	29130.982411
HLA A*0202	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-3.926478	0.229395	-3.697083	8442.637287
HLA A*0216	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.368358	0.671022	-3.697335	23353.798207
HLA A*1101	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.395332	0.697746	-3.697586	24850.318572
HLA B*5701	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.399263	0.701666	-3.697597	25076.253353
HLA A*6802	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.405038	0.707433	-3.697604	25411.931919
HLA A*0212	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.365613	0.667964	-3.697649	23206.696621
HLA B*4001	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.405143	0.707433	-3.697710	25418.119080
HLA A*2603	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.607115	0.909340	-3.697775	40468.260663
HLA B*1501	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.400886	0.702905	-3.697981	25170.169672

HLA B*4403	1:211-219	9	AGPTQVLVP	0.915670	0.051508	-4.665314	0.967178	-3.698136	46271.505676
HLA B*5101	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.502245	0.804086	-3.698160	31786.687742
HLA B*3801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.563139	0.864656	-3.698484	36571.201428
HLA B*5801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.278556	0.579719	-3.698837	18991.335564
HLA A*2402	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.457408	0.758478	-3.698930	28668.680447
HLA A*0301	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.361847	0.662917	-3.698930	23006.317041
HLA A*3001	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.269064	0.570132	-3.698931	18580.764893
HLA A*2601	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.386789	0.687624	-3.699165	24366.280147
HLA A*6802	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.397019	0.697746	-3.699273	24947.032385
HLA B*1502	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.457779	0.758478	-3.699301	28693.195836
HLA A*2603	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.552778	0.853458	-3.699320	35709.025549
HLA A*0301	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.347863	0.648415	-3.699448	22277.321146
HLA B*4501	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.508537	0.809025	-3.699513	32250.555271
HLA A*2403	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.413350	0.713674	-3.699676	25903.005698
HLA B*5701	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.425055	0.725355	-3.699700	26610.638509
HLA B*1509	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.475158	0.775271	-3.699887	29864.693573

HLA A*2501	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.448289	0.748062	-3.700228	28073.034058
HLA A*0211	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.486844	0.786460	-3.700385	30679.226194
HLA A*0101	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.380462	0.680076	-3.700386	24013.865288
HLA B*4002	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.477035	0.776623	-3.700413	29994.063153
HLA B*0801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.281936	0.581216	-3.700720	19139.756860
HLA A*2403	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.423881	0.723137	-3.700744	26538.755471
HLA A*3201	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.554244	0.853458	-3.700786	35829.774732
HLA A*2603	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.587506	0.886699	-3.700807	38681.716431
HLA B*0702	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.407742	0.706847	-3.700895	25570.660159
HLA B*7301	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.554674	0.853458	-3.701216	35865.264121
HLA B*4601	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.388932	0.687624	-3.701308	24486.796018
HLA A*3101	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.335392	0.634040	-3.701352	21646.710013
HLA A*6801	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.566095	0.864656	-3.701439	36820.940733
HLA A*0250	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.554902	0.853458	-3.701444	35884.089689
HLA B*4001	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.404457	0.702905	-3.701552	25377.998089
HLA B*4002	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.641654	0.940065	-3.701590	43818.178249

HLA A*2403	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.350250	0.648272	-3.701978	22400.104396
HLA A*3001	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.283269	0.581216	-3.702052	19198.556422
HLA B*1502	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.281845	0.579719	-3.702126	19135.719071
HLA A*0216	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.321532	0.619394	-3.702139	20966.806501
HLA B*5101	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.492810	0.790540	-3.702270	31103.534519
HLA A*2301	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.405176	0.702788	-3.702389	25420.044281
HLA A*3301	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.540295	0.837899	-3.702396	34697.260382
HLA B*4601	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.405430	0.702788	-3.702642	25434.900740
HLA A*2603	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.597806	0.895143	-3.702663	39610.094554
HLA A*3101	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.322099	0.619394	-3.702705	20994.160501
HLA B*0801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.398974	0.696230	-3.702743	25059.572754
HLA A*0206	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.410449	0.707433	-3.703015	25730.519049
HLA A*0211	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.426171	0.723137	-3.703035	26679.107731
HLA B*1503	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.444248	0.740601	-3.703647	27813.025780
HLA A*8001	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.411125	0.707433	-3.703692	25770.639681
HLA B*1517	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.444314	0.740601	-3.703713	27817.239130

HLA B*0801	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.374769	0.671022	-3.703747	23701.141759
HLA A*1101	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.457845	0.754093	-3.703752	28697.542521
HLA A*3101	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.370557	0.666762	-3.703794	23472.353722
HLA B*4801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.429350	0.725355	-3.703995	26875.104025
HLA B*4801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.417770	0.713674	-3.704095	26167.940424
HLA A*0212	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.406901	0.702788	-3.704113	25521.184357
HLA B*0802	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.444758	0.740601	-3.704157	27845.695941
HLA B*4601	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.412182	0.707999	-3.704183	25833.453445
HLA B*3501	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.009777	0.305553	-3.704224	10227.671551
HLA B*5701	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.411118	0.706847	-3.704271	25770.221436
HLA B*5801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.352628	0.648272	-3.704355	22523.076981
HLA B*1801	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.375399	0.671022	-3.704377	23735.529789
HLA B*4402	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.400621	0.696230	-3.704390	25154.787410
HLA A*0201	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.392019	0.687624	-3.704395	24661.482871
HLA A*2902	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.392997	0.688457	-3.704540	24717.046380
HLA B*5301	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.551925	0.847335	-3.704590	35638.969341

HLA B*0802 1:78-86 9 LSAATSSTP 0.733359 0.025119 -4.463159
0.758478 -3.704681 29050.876701

HLA B*3801 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.513800
0.809025 -3.704776 32643.749976

HLA B*5801 1:53-61 9 NISLPSYYP 0.515820 0.118220 -4.338824
0.634040 -3.704785 21818.480248

HLA B*3801 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.560935
0.856017 -3.704918 36386.091808

HLA B*4403 1:81-89 9 ATSSTPREA 0.999596 -0.112897 -4.591631
0.886699 -3.704933 39050.934626

HLA A*0250 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.513993
0.809025 -3.704968 32658.234312

HLA A*0201 1:36-44 9 DTGQACQIQ 0.956574 -0.260344 -4.401220
0.696230 -3.704989 25189.512933

HLA B*1517 1:177-185 9 APNAGLDPV 0.672482 0.029184 -4.406732
0.701666 -3.705066 25511.245485

HLA A*2601 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.372128
0.666762 -3.705366 23557.459151

HLA A*6802 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.011158
0.305553 -3.705606 10260.257727

HLA B*5401 1:117-125 9 YQNAGGTHP 0.729126 0.047497 -4.482263
0.776623 -3.705640 30357.283447

HLA A*2501 1:202-210 9 NPGELLPEA 1.188654 -0.463299 -4.431009
0.725355 -3.705654 26977.946579

HLA B*1509 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.473079
0.767355 -3.705724 29722.050572

HLA B*1503 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.275957
0.570132 -3.705825 18878.043267

HLA B*1801 1:78-86 9 LSAATSSTP 0.733359 0.025119 -4.464332
0.758478 -3.705854 29129.406500

HLA B*4002 1:81-89 9 ATSSTPREA 0.999596 -0.112897 -4.592700
0.886699 -3.706002 39147.176886

HLA B*5701	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.413583	0.707433	-3.706149	25916.882520
HLA A*8001	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.431521	0.725355	-3.706166	27009.781946
HLA A*2602	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.492702	0.786460	-3.706242	31095.795215
HLA B*5101	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.514554	0.808230	-3.706324	32700.487527
HLA A*0203	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.373155	0.666762	-3.706393	23613.217732
HLA B*0802	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.481685	0.775271	-3.706414	30316.909852
HLA B*5701	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.409279	0.702788	-3.706491	25661.291116
HLA A*2402	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.571240	0.864656	-3.706585	37259.777076
HLA B*4403	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.631580	0.924700	-3.706880	42813.400748
HLA B*4501	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.355196	0.648272	-3.706923	22656.650656
HLA A*8001	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.420864	0.713674	-3.707190	26355.048157
HLA B*4601	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.326591	0.619394	-3.707197	21212.444957
HLA A*3101	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.375314	0.667964	-3.707350	23730.907602
HLA B*4403	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.634925	0.927533	-3.707392	43144.495264
HLA A*3002	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.498044	0.790540	-3.707504	31480.701141
HLA B*4501	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.647883	0.940065	-3.707818	44451.129665

HLA B*0702	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.378881	0.671022	-3.707859	23926.593246
HLA B*1801	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.450662	0.742712	-3.707950	28226.844607
HLA A*0219	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.287843	0.579719	-3.708124	19401.844599
HLA A*6801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.512456	0.804086	-3.708370	32542.891440
HLA B*4403	1:116-124	9	VYQNAGGTH	1.000005	-0.059940	-4.648541	0.940065	-3.708476	44518.513879
HLA A*6802	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.269933	0.561410	-3.708523	18617.994496
HLA B*4002	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.633260	0.924700	-3.708560	42979.326710
HLA B*4001	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.396462	0.687624	-3.708838	24915.067201
HLA B*4001	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.397369	0.688457	-3.708912	24967.149633
HLA A*0211	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.416529	0.707433	-3.709096	26093.300409
HLA B*3801	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.489036	0.779687	-3.709349	30834.468793
HLA A*2301	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.489424	0.779687	-3.709737	30862.004906
HLA A*6801	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.518948	0.809025	-3.709923	33032.980767
HLA B*1509	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.514049	0.804086	-3.709963	32662.474846
HLA B*5701	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.406356	0.696230	-3.710125	25489.172958
HLA B*5401	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.519204	0.809025	-3.710179	33052.465331

HLA B*4402 1:105-113 9 PPRGTQAVV 0.903475 -0.180338 -4.433349 0.723137 -3.710212 27123.702821

HLA B*2705 1:49-57 9 AYNINISLP 0.584960 0.117828 -4.413087 0.702788 -3.710299 25887.315624

HLA A*3301 1:161-169 9 IVQGELSKQ 0.821593 -0.054238 -4.478234 0.767355 -3.710879 30076.932344

HLA B*4801 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.418441 0.707433 -3.711008 26208.459540

HLA A*1101 1:208-216 9 PEAAGPTQV 0.855949 -0.104037 -4.463046 0.751912 -3.711134 29043.333904

HLA B*4001 1:98-106 9 ATYQSAIPP 0.417465 0.201929 -4.330752 0.619394 -3.711358 21416.656264

HLA B*5701 1:169-177 9 QTGQQVSIA 0.950594 -0.262137 -4.399906 0.688457 -3.711449 25113.451688

HLA A*0216 1:135-143 9 DQAYRKPIT 1.136670 -0.428671 -4.419555 0.707999 -3.711556 26275.751805

HLA B*4001 1:17-25 9 CSGVATAAP 0.698375 -0.030411 -4.379579 0.667964 -3.711614 23965.067891

HLA A*6801 1:211-219 9 AGPTQVLVP 0.915670 0.051508 -4.678795 0.967178 -3.711617 47730.389304

HLA A*6901 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.276037 0.564331 -3.711706 18881.515942

HLA A*6802 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.360444 0.648272 -3.712172 22932.133312

HLA B*5301 1:14-22 9 LLCCSGVAT 1.136854 -0.272198 -4.577203 0.864656 -3.712548 37774.893199

HLA A*0216 1:41-49 9 CQIQMSDPA 0.720301 -0.119784 -4.313328 0.600517 -3.712811 20574.433474

HLA B*2705 1:162-170 9 VQGELSKQT 0.977010 -0.314093 -4.376050 0.662917 -3.713132 23771.125077

HLA B*1801 1:129-137 9 YKAFDWDQA 0.955276 -0.207214 -4.461223 0.748062 -3.713162 28921.663409

HLA B*1501	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.361798	0.648415	-3.713383	23003.703496
HLA B*3801	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.521645	0.808230	-3.713415	33238.772214
HLA A*3002	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.456355	0.742712	-3.713643	28599.282295
HLA A*3101	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.427332	0.713674	-3.713658	26750.502611
HLA B*0803	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.481206	0.767355	-3.713851	30283.470039
HLA A*0203	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.362698	0.648272	-3.714425	23051.416296
HLA B*0702	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.421994	0.707433	-3.714560	26423.717427
HLA B*3901	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.482023	0.767355	-3.714669	30340.536655
HLA A*0202	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.377605	0.662917	-3.714688	23856.410342
HLA B*5101	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.038680	0.323743	-3.714937	10931.509518
HLA A*0301	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.363442	0.648272	-3.715170	23090.981890
HLA A*0201	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.381949	0.666762	-3.715187	24096.240770
HLA B*4403	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.568649	0.853458	-3.715191	37038.105997
HLA B*4402	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.428991	0.713674	-3.715316	26852.868355
HLA A*3001	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.021031	0.305553	-3.715478	10496.168788
HLA A*2603	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.568503	0.852998	-3.715505	37025.685014

HLA A*2902	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.102934	0.387379	-3.715555	12674.588060
HLA A*6802	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.395659	0.680076	-3.715582	24869.012408
HLA A*2902	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.440994	0.725355	-3.715639	27605.409992
HLA A*2603	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.495415	0.779687	-3.715728	31290.703164
HLA A*3201	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.483224	0.767355	-3.715869	30424.527695
HLA A*2902	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.423545	0.707433	-3.716111	26518.232653
HLA B*5701	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.403912	0.687624	-3.716288	25346.166289
HLA A*0219	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.424421	0.707999	-3.716422	26571.797520
HLA B*1503	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.294506	0.578083	-3.716423	19701.811574
HLA B*4601	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.379363	0.662917	-3.716445	23953.143210
HLA B*4501	1:68-76	9	NYIAQTRDK	0.633507	0.291193	-4.641253	0.924700	-3.716553	43777.661189
HLA A*6901	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.317118	0.600517	-3.716600	20754.754702
HLA B*5401	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-3.351047	-0.365615	-3.716662	2244.124586
HLA A*2501	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.424834	0.707999	-3.716835	26597.109653
HLA B*4402	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.405301	0.688457	-3.716844	25427.333866
HLA A*8001	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.396958	0.680076	-3.716881	24943.523654

HLA B*5701	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.419842	0.702905	-3.716936	26293.099696
HLA A*0211	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.525331	0.808230	-3.717101	33522.107561
HLA B*3801	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.459849	0.742712	-3.717136	28830.277243
HLA A*8001	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.380410	0.662917	-3.717493	24011.007386
HLA A*3002	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.424367	0.706847	-3.717520	26568.491464
HLA A*2902	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.440703	0.723137	-3.717566	27586.897768
HLA B*4501	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.645122	0.927533	-3.717589	44169.466896
HLA B*4001	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.397874	0.680076	-3.717798	24996.206474
HLA B*4601	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.388930	0.671022	-3.717907	24486.663547
HLA B*1503	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.493329	0.775271	-3.718058	31140.743693
HLA A*0101	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.381080	0.662917	-3.718163	24048.056554
HLA A*2601	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.389205	0.671022	-3.718182	24502.167459
HLA B*4601	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.414565	0.696230	-3.718335	25975.555553
HLA B*1517	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.441495	0.723137	-3.718358	27637.238217
HLA B*0803	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.466517	0.748062	-3.718455	29276.331574
HLA A*2301	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.523278	0.804086	-3.719192	33363.981012

HLA B*0801	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.422210	0.702788	-3.719422	26436.872044
HLA A*0202	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.339043	0.619394	-3.719649	21829.460317
HLA A*0201	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.388006	0.667964	-3.720042	24434.658088
HLA B*4402	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.417805	0.697746	-3.720059	26170.063995
HLA B*0802	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.421900	0.701666	-3.720234	26418.000070
HLA B*5701	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.418019	0.697746	-3.720273	26182.950687
HLA A*3002	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.301775	0.581216	-3.720559	20034.359742
HLA B*4501	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.468760	0.748062	-3.720699	29427.977503
HLA B*0803	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.122491	0.401614	-3.720877	13258.395388
HLA B*5101	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.488280	0.767355	-3.720925	30780.802389
HLA A*0212	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.418674	0.697746	-3.720928	26222.500001
HLA B*5701	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.428946	0.707999	-3.720947	26850.108347
HLA B*1509	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.461564	0.740601	-3.720963	28944.359444
HLA A*2402	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.401065	0.680076	-3.720988	25180.520555
HLA B*0801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.408668	0.687624	-3.721043	25625.222056
HLA B*4501	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.630389	0.909340	-3.721049	42696.132458

HLA B*4001	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.369499	0.648415	-3.721085	23415.280946
HLA A*0206	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.369626	0.648272	-3.721354	23422.122346
HLA A*0250	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.577462	0.856017	-3.721444	37797.379267
HLA A*6901	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.369932	0.648415	-3.721517	23438.600581
HLA A*6801	1:218-226	9	VPRSAIDSM	0.858689	0.068844	-4.649053	0.927533	-3.721520	44571.048020
HLA A*1101	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.469733	0.748062	-3.721671	29493.961035
HLA A*2402	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.577781	0.856017	-3.721764	37825.198730
HLA A*3201	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.530136	0.808230	-3.721906	33895.029176
HLA A*0202	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.424823	0.702788	-3.722035	26596.390225
HLA A*0201	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-3.762710	0.040514	-3.722195	5790.414175
HLA A*0216	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.418545	0.696230	-3.722315	26214.698816
HLA B*1502	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.502086	0.779687	-3.722398	31774.996445
HLA B*5401	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.560315	0.837899	-3.722416	36334.161893
HLA B*5701	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.370954	0.648272	-3.722681	23493.823634
HLA B*5701	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.393887	0.671022	-3.722865	24767.776916
HLA A*6801	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.575932	0.852998	-3.722934	37664.497159

HLA A*0250	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.531205	0.808230	-3.722975	33978.564545
HLA B*7301	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.532006	0.809025	-3.722982	34041.305109
HLA B*4801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.410634	0.687624	-3.723010	25741.518140
HLA A*0101	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.410902	0.687624	-3.723278	25757.398535
HLA A*0201	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.371574	0.648272	-3.723301	23527.401737
HLA A*0250	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.558616	0.835252	-3.723364	36192.323844
HLA A*1101	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.425100	0.701666	-3.723434	26613.373901
HLA A*1101	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.498831	0.775271	-3.723561	31537.805750
HLA B*1502	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.430619	0.706847	-3.723772	26953.730136
HLA A*3002	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.420185	0.696230	-3.723954	26313.875342
HLA B*0802	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.472209	0.748062	-3.724148	29662.616666
HLA B*5101	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.499569	0.775271	-3.724298	31591.424713
HLA B*1502	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.472433	0.748062	-3.724371	29677.865374
HLA B*4601	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.392522	0.667964	-3.724558	24690.050404
HLA B*3901	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.499868	0.775271	-3.724597	31613.137247
HLA A*0211	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.500114	0.775271	-3.724843	31631.099822

HLA B*4002	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.426561	0.701666	-3.724896	26703.077441
HLA A*3301	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.504719	0.779687	-3.725032	31968.280951
HLA A*6802	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.412819	0.687624	-3.725195	25871.355130
HLA A*6801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.344611	0.619394	-3.725218	22111.147330
HLA B*0803	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.483870	0.758478	-3.725392	30469.824545
HLA B*0801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.055742	0.330347	-3.725395	11369.519146
HLA B*4601	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.405491	0.680076	-3.725415	25438.478592
HLA A*0206	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.500720	0.775271	-3.725450	31675.279799
HLA B*1517	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.477430	0.751912	-3.725518	30021.335990
HLA B*3901	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.011605	0.286028	-3.725577	10270.809452
HLA B*7301	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.581606	0.856017	-3.725589	38159.807923
HLA A*0211	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.484070	0.758478	-3.725592	30483.839028
HLA B*0803	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.477651	0.751912	-3.725739	30036.606610
HLA B*4801	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.428558	0.702788	-3.725771	26826.151782
HLA B*1501	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.303939	0.578083	-3.725857	20134.430192
HLA B*4801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.423906	0.697746	-3.726160	26540.334807

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HLA A*2603	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.493813
	0.767355	-3.726458	31175.467440

HLA B*1801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.424332
	0.697746	-3.726586	26566.335563

HLA B*2705	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.290928
	0.564331	-3.726597	19540.150103

HLA B*1509	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.429470
	0.702788	-3.726682	26882.520006

HLA B*1503	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.414363
	0.687624	-3.726738	25963.473225

HLA A*2601	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.360905
	0.634040	-3.726865	22956.462026

HLA B*3501	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.414586
	0.687624	-3.726962	25976.820308

HLA A*0301	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.308455
	0.581216	-3.727239	20344.876302

HLA A*6802	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.430053
	0.702788	-3.727265	26918.611212

HLA B*4002	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.592012
	0.864656	-3.727356	39085.173946

HLA A*0203	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.151089
	0.423714	-3.727375	14160.836149

HLA B*1517	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.375655
	0.648272	-3.727383	23749.530234

HLA B*4002	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.636749
	0.909340	-3.727409	43325.999765

HLA A*8001	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.435640
	0.707999	-3.727641	27267.148621

HLA B*2705	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.450796
	0.723137	-3.727660	28235.550082

HLA A*2601	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.395734
	0.667964	-3.727769	24873.318015
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HLA B*5801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.349921	0.621958	-3.727963	22383.145328
HLA A*0203	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.294403	0.566374	-3.728029	19697.122409
HLA A*0206	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.265889	0.537766	-3.728123	18445.457604
HLA A*0203	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.362216	0.634040	-3.728176	23025.865817
HLA A*3301	1:81-89	9	ATSSTPREA	0.999596	-0.112897	-4.614983	0.886699	-3.728284	41208.135410
HLA A*8001	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.435252	0.706847	-3.728405	27242.819959
HLA B*4601	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.395222	0.666762	-3.728459	24844.000814
HLA A*6802	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.321415	0.592876	-3.728539	20961.135863
HLA A*8001	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.395320	0.666762	-3.728558	24849.646393
HLA A*3002	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.469343	0.740601	-3.728742	29467.486121
HLA B*0803	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.471545	0.742712	-3.728832	29617.237987
HLA B*5401	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.431848	0.702905	-3.728942	27030.100255
HLA A*0201	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.377415	0.648415	-3.729000	23845.958729
HLA B*1501	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.351234	0.621958	-3.729277	22450.937279
HLA A*0216	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.310527	0.581216	-3.729311	20442.184301
HLA A*0250	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.377814	0.648272	-3.729542	23867.899495

HLA B*5401	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.516213	0.786460	-3.729753	32825.621988
HLA A*6802	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.309484	0.579719	-3.729765	20393.141287
HLA B*2705	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.443480	0.713674	-3.729806	27763.867093
HLA A*0101	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.316991	0.587095	-3.729895	20748.692418
HLA A*3001	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.294835	0.564800	-3.730035	19716.739073
HLA B*3801	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.568075	0.837899	-3.730176	36989.247472
HLA B*5401	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.437240	0.706847	-3.730393	27367.789738
HLA A*3002	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.432085	0.701666	-3.730419	27044.873505
HLA B*4801	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.088578	0.357949	-3.730629	12262.485299
HLA A*2902	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.378904	0.648272	-3.730632	23927.887683
HLA B*2705	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.438936	0.707999	-3.730937	27474.895720
HLA A*2902	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.432888	0.701666	-3.731223	27094.957763
HLA B*7301	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.438708	0.707433	-3.731275	27460.481797
HLA B*3501	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.434106	0.702788	-3.731318	27170.993063
HLA B*1502	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.587377	0.856017	-3.731359	38670.208634
HLA B*4402	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.411644	0.680076	-3.731568	25801.469110

HLA B*5401	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.522162	0.790540	-3.731622	33278.355741
HLA A*2603	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.518149	0.786460	-3.731689	32972.276993
HLA A*0250	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.522319	0.790540	-3.731779	33290.420086
HLA A*0101	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.365829	0.634040	-3.731790	23218.249696
HLA A*2601	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.394996	0.662917	-3.732079	24831.101448
HLA B*3801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.486191	0.754093	-3.732098	30633.120875
HLA A*2402	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.398880	0.666762	-3.732117	25054.150561
HLA A*8001	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.428366	0.696230	-3.732135	26814.254048
HLA B*4402	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.419837	0.687624	-3.732213	26292.815212
HLA A*3002	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.585732	0.853458	-3.732274	38524.044485
HLA A*2601	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.312022	0.579719	-3.732303	20512.640649
HLA A*0212	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.435252	0.702905	-3.732347	27242.819959
HLA A*2902	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.403588	0.671022	-3.732566	25327.250798
HLA A*0201	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.366680	0.634040	-3.732640	23263.764402
HLA B*3801	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.536809	0.804086	-3.732723	34419.816406
HLA A*6801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.420605	0.687624	-3.732981	26339.369255

HLA B*4002	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.481213	0.748062	-3.733151	30283.961534
HLA A*3001	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.294602	0.561410	-3.733192	19706.182028
HLA B*4501	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.185936	0.452621	-3.733315	15343.924726
HLA B*1517	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.508617	0.775271	-3.733346	32256.487862
HLA B*5401	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.400181	0.666762	-3.733419	25129.352455
HLA A*6802	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.311606	0.578083	-3.733523	20493.008164
HLA B*4801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.429757	0.696230	-3.733526	26900.268500
HLA B*7301	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.598189	0.864656	-3.733533	39645.038612
HLA A*6801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.381985	0.648415	-3.733570	24098.196219
HLA A*2402	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.569020	0.835252	-3.733768	37069.778315
HLA B*0702	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.382205	0.648415	-3.733791	24110.453981
HLA A*2601	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.353758	0.619394	-3.734364	22581.761877
HLA A*6802	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.315647	0.581216	-3.734430	20684.585729
HLA A*8001	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.423072	0.688457	-3.734615	26489.412725
HLA A*0101	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.354052	0.619394	-3.734658	22597.037645
HLA B*0702	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.383343	0.648272	-3.735070	24173.667187

HLA A*0203 1:170-178 9 TGQQVSIAP 0.814303 -0.116557 -4.432980
0.697746 -3.735234 27100.675015

HLA B*3501 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.442820
0.707433 -3.735386 27721.693114

HLA A*0219 1:53-61 9 NISLPSYYP 0.515820 0.118220 -4.369553
0.634040 -3.735514 23418.194631

HLA A*0301 1:120-128 9 AGGTHPTTT 0.991249 -0.369291 -4.357672
0.621958 -3.735714 22786.208422

HLA A*3101 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.406849
0.671022 -3.735827 25518.147069

HLA A*3101 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.443313
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HLA B*1503 1:114-122 9 LKVYQNAGG 0.762278 -0.528116 -3.970075
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HLA B*0801 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.402824
0.666762 -3.736062 25282.759196

HLA A*0219 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.402839
0.666762 -3.736076 25283.579871

HLA B*0801 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.442965
0.706847 -3.736119 27730.992893

HLA B*4501 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.592165
0.856017 -3.736148 39098.920383

HLA A*3101 1:36-44 9 DTGQACQIQ 0.956574 -0.260344 -4.432592
0.696230 -3.736362 27076.494886

HLA B*3501 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.300739
0.564331 -3.736409 19986.619517

HLA B*0801 1:41-49 9 CQIQMSDPA 0.720301 -0.119784 -4.337041
0.600517 -3.736524 21729.074938

HLA B*1503 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.407984
0.671022 -3.736962 25584.912577

HLA B*1502 1:105-113 9 PPRGTQAVV 0.903475 -0.180338 -4.460157
0.723137 -3.737020 28850.716372

HLA A*2902	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.356497	0.619394	-3.737104	22724.656277
HLA B*5401	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.489083	0.751912	-3.737171	30837.805195
HLA B*1801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.385474	0.648272	-3.737201	24292.573283
HLA A*2403	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.445270	0.707999	-3.737271	27878.555298
HLA B*4001	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.400318	0.662917	-3.737400	25137.238619
HLA A*3101	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.158612	0.421102	-3.737510	14408.273664
HLA A*2602	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.541714	0.804086	-3.737629	34810.821649
HLA B*0702	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.425262	0.687624	-3.737638	26623.310058
HLA A*2601	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.386113	0.648415	-3.737698	24328.345871
HLA A*2603	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.357381	0.619394	-3.737987	22770.927961
HLA B*5701	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.406074	0.667964	-3.738110	25472.631096
HLA A*0101	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.386409	0.648272	-3.738136	24344.934844
HLA B*4001	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.441088	0.702788	-3.738301	27611.384327
HLA B*2705	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.445754	0.707433	-3.738321	27909.641515
HLA B*1502	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.505701	0.767355	-3.738347	32040.653699
HLA A*2301	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.528928	0.790540	-3.738388	33800.908764

HLA A*2501	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.452246	0.713674	-3.738572	28329.955040	
HLA A*1101	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.418789	0.680076	-3.738713	26229.452102	
HLA B*4801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.441960	0.702905	-3.739054	27666.857928	
HLA B*0801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.407230	0.667964	-3.739265	25540.521028	
HLA B*1503	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.442199	0.702905	-3.739294	27682.128954	
HLA B*5701	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.406104	0.666762	-3.739342	25474.422612	
HLA A*3101	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.402270	0.662917	-3.739353	25250.500439	
HLA B*1517	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.487415	0.748062	-3.739354	30719.583720	
HLA B*7301	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.525820	0.786460	-3.739360	33559.849776	
HLA A*0203	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.427099	0.687624	-3.739475	26736.179439	
HLA A*0101	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.332396	0.592876	-3.739520	21497.913239	
HLA A*2902	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.447542	0.707999	-3.739543	28024.780279	
HLA A*2501	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.446405	0.706847	-3.739558	27951.496562	
HLA B*2705	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.464952	0.725355	-3.739597	29171.039154	
HLA B*1502	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.526085	0.786460	-3.739626	33580.371771	
HLA B*3801	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.507083	0.767355	-3.739728	32142.737773	

HLA A*1101	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.442681	0.702788	-3.739893	27712.846220
HLA B*5801	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.353572	0.613638	-3.739934	22572.112917
HLA A*0216	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.442770	0.702788	-3.739983	27718.543895
HLA B*4002	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.635217	0.895143	-3.740074	43173.447434
HLA A*2301	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.526534	0.786460	-3.740075	33615.087927
HLA B*5301	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.526598	0.786460	-3.740138	33619.998341
HLA A*3301	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.436471	0.696230	-3.740241	27319.417992
HLA B*3801	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.526826	0.786460	-3.740366	33637.645375
HLA A*2602	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.593880	0.853458	-3.740422	39253.635886
HLA A*0219	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.428098	0.687624	-3.740474	26797.722062
HLA B*0801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.388894	0.648415	-3.740480	24484.676576
HLA B*1503	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.026641	0.286028	-3.740614	10632.646521
HLA A*2601	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.389195	0.648272	-3.740923	24501.637249
HLA A*0250	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.516227	0.775271	-3.740956	32826.687503
HLA B*4402	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.409048	0.667964	-3.741084	25647.689897
HLA A*0202	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.279347	0.537766	-3.741581	19025.990869

HLA B*4402	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.444643	0.702905	-3.741737	27838.315455
HLA B*1502	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.495862	0.754093	-3.741769	31322.882755
HLA B*0702	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.430276	0.688457	-3.741819	26932.449304
HLA B*1801	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.342527	0.600517	-3.742010	22005.299567
HLA B*4403	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.528578	0.786460	-3.742119	33773.673726
HLA A*0203	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.410167	0.667964	-3.742202	25713.820559
HLA A*0203	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.100312	0.357949	-3.742362	12598.296576
HLA A*0250	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.519112	0.776623	-3.742490	33045.492470
HLA A*0219	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.440271	0.697746	-3.742525	27559.450892
HLA B*5401	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.517844	0.775271	-3.742573	32949.096218
HLA B*3801	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.519211	0.776623	-3.742588	33053.001766
HLA B*5701	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.362098	0.619394	-3.742705	23019.638290
HLA B*5701	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.405646	0.662917	-3.742729	25447.563090
HLA A*2902	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.324098	0.581216	-3.742882	21091.036575
HLA A*2602	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.590494	0.847335	-3.743159	38948.817941
HLA A*3002	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.411630	0.667964	-3.743666	25800.631625

HLA B*0702	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.441429	0.697746	-3.743683	27633.052131
HLA A*0101	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.344289	0.600517	-3.743772	22094.765619
HLA A*1101	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.432736	0.688457	-3.744279	27085.431692
HLA B*5801	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.344849	0.600517	-3.744331	22123.232136
HLA B*4801	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.415688	0.671022	-3.744666	26042.813369
HLA A*0212	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.411651	0.666762	-3.744889	25801.887863
HLA B*4002	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-3.990069	0.245175	-3.744895	9773.931536
HLA B*0802	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.470309	0.725355	-3.744954	29533.078923
HLA A*2403	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.441473	0.696230	-3.745243	27635.892620
HLA B*2705	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.412081	0.666762	-3.745319	25827.444631
HLA B*1503	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.412124	0.666762	-3.745361	25829.959779
HLA B*3901	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.416501	0.671022	-3.745479	26091.606522
HLA A*0202	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.453024	0.707433	-3.745590	28380.730181
HLA B*0702	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.365214	0.619394	-3.745820	23185.363671
HLA B*3901	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.459496	0.713674	-3.745822	28806.891443
HLA B*0702	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.442082	0.696230	-3.745852	27674.642104

HLA A*0101	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.368019	0.621958	-3.746061	23335.612122
HLA A*3301	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.555186	0.809025	-3.746162	35907.586982
HLA A*8001	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.433821	0.687624	-3.746197	27153.212844
HLA B*4801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.426303	0.680076	-3.746226	26687.191492
HLA B*4801	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.412998	0.666762	-3.746236	25881.994366
HLA B*0801	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.380295	0.634040	-3.746255	24004.643282
HLA B*5101	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.459957	0.713674	-3.746283	28837.452692
HLA B*0801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.324495	0.578083	-3.746412	21110.328321
HLA B*4501	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.611701	0.864656	-3.747045	40897.874077
HLA B*4002	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.594399	0.847335	-3.747064	39300.595031
HLA A*8001	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.326840	0.579719	-3.747121	21224.612685
HLA B*1502	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.595127	0.847335	-3.747792	39366.560006
HLA A*2902	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.445583	0.697746	-3.747837	27898.621562
HLA B*1509	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.414889	0.666762	-3.748127	25994.955227
HLA A*0202	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.583634	0.835252	-3.748382	38338.382463
HLA A*0219	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.416743	0.667964	-3.748779	26106.149301

HLA B*5701	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.428986	0.680076	-3.748910	26852.577814
HLA B*3801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.501009	0.751912	-3.749097	31696.364063
HLA B*3901	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.397378	0.648272	-3.749106	24967.689917
HLA A*3301	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.553443	0.804086	-3.749357	35763.737890
HLA B*1502	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.587257	0.837899	-3.749358	38659.540827
HLA A*2602	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.529055	0.779687	-3.749368	33810.784602
HLA B*1517	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.445599	0.696230	-3.749369	27899.678081
HLA B*2705	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.447117	0.697746	-3.749371	27997.352128
HLA A*2902	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.329093	0.579719	-3.749374	21335.013890
HLA A*2501	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.452652	0.702788	-3.749865	28356.481763
HLA A*3101	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.398440	0.648272	-3.750168	25028.817364
HLA B*0702	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.458543	0.707999	-3.750543	28743.688989
HLA B*1502	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.413491	0.662917	-3.750574	25911.415006
HLA A*8001	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.453367	0.702788	-3.750579	28403.155381
HLA B*4801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.439265	0.688457	-3.750808	27495.712662
HLA B*5301	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-3.535171	-0.215742	-3.750913	3429.030945

HLA A*1101	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.491515	0.740601	-3.750914	31010.957630
HLA A*0212	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.370371	0.619394	-3.750977	23462.324222
HLA A*2402	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.541522	0.790540	-3.750982	34795.382613
HLA A*8001	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.448832	0.697746	-3.751086	28108.138420
HLA B*0802	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.459203	0.707999	-3.751204	28787.417767
HLA B*7301	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.476568	0.725355	-3.751213	29961.789881
HLA A*2403	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.414203	0.662917	-3.751286	25953.923735
HLA A*0201	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.370688	0.619394	-3.751294	23479.465838
HLA B*4402	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.422344	0.671022	-3.751322	26445.025472
HLA B*5301	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.509886	0.758478	-3.751408	32350.857811
HLA B*5101	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.458864	0.707433	-3.751431	28765.000409
HLA A*1101	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.474907	0.723137	-3.751770	29847.411155
HLA A*0219	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.400247	0.648415	-3.751832	25133.159260
HLA A*0301	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.365508	0.613638	-3.751869	23201.047754
HLA B*3501	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.374102	0.621958	-3.752144	23664.755083
HLA A*3201	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.590142	0.837899	-3.752243	38917.224443

HLA B*1517	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.455124	0.702788	-3.752336	28518.324370
HLA A*2602	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.466063	0.713674	-3.752389	29245.779857
HLA B*3901	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.493113	0.740601	-3.752512	31125.248496
HLA A*1101	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.459649	0.706847	-3.752802	28817.022960
HLA B*1509	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.543406	0.790540	-3.752866	34946.678400
HLA A*0212	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.449528	0.696230	-3.753297	28153.184804
HLA B*3801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.476887	0.723137	-3.753751	29983.842227
HLA B*2705	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.442268	0.688457	-3.753811	27686.472254
HLA A*6801	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.589251	0.835252	-3.753999	38837.512337
HLA A*2602	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.589329	0.835252	-3.754077	38844.446475
HLA B*4402	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-3.748190	-0.005967	-3.754157	5600.023011
HLA B*4801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.422248	0.667964	-3.754283	26439.160471
HLA A*2902	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.089636	0.335272	-3.754364	12292.374075
HLA A*0206	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.388568	0.634040	-3.754528	24466.271642
HLA B*4501	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.649746	0.895143	-3.754603	44642.236517
HLA B*5401	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.558901	0.804086	-3.754815	36216.022972

HLA A*2301	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.506745	0.751912	-3.754832	32117.707558
HLA A*2501	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.421630	0.666762	-3.754868	26401.569560
HLA B*3501	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.334593	0.579719	-3.754874	21606.930466
HLA B*5301	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.534729	0.779687	-3.755042	34255.416731
HLA A*0250	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.541566	0.786460	-3.755107	34798.959341
HLA B*1517	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.423333	0.667964	-3.755369	26505.324333
HLA A*8001	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.423343	0.667964	-3.755378	26505.897903
HLA B*0801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.418538	0.662917	-3.755621	26214.273364
HLA A*6901	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.377598	0.621958	-3.755640	23856.023164
HLA B*5301	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.593687	0.837899	-3.755788	39236.226407
HLA B*4501	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.608863	0.852998	-3.755865	40631.471932
HLA A*0219	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.458693	0.702788	-3.755905	28753.642723
HLA B*5401	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.564154	0.808230	-3.755924	36656.770915
HLA B*4501	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.481419	0.725355	-3.756065	30298.382259
HLA A*1101	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.481478	0.725355	-3.756123	30302.480309
HLA B*5301	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.404415	0.648272	-3.756143	25375.526951

HLA A*3002 1:135-143 9 DQAYRKPIT 1.136670 -0.428671 -4.464278 0.707999 -3.756278 29125.782228

HLA B*1502 1:64-72 9 KSLENYIAQ 0.805806 0.003219 -4.565500 0.809025 -3.756476 36770.578313

HLA A*6802 1:10-18 9 TAVVLLCCS 1.085894 -0.909066 -3.933395 0.176828 -3.756567 8578.177242

HLA A*0202 1:88-96 9 EAPYELNIT 1.024679 -0.321774 -4.459731 0.702905 -3.756826 28822.479868

HLA A*2403 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.327890 0.570132 -3.757758 21276.000586

HLA B*4001 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.406036 0.648272 -3.757764 25470.426325

HLA B*0702 1:17-25 9 CSGVATAAP 0.698375 -0.030411 -4.425934 0.667964 -3.757970 26664.534280

HLA A*2501 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.465509 0.707433 -3.758075 29208.464606

HLA B*2705 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.429157 0.671022 -3.758135 26863.184580

HLA A*0211 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.351129 0.592876 -3.758253 22445.472376

HLA B*7301 1:162-170 9 VQGELSKQT 0.977010 -0.314093 -4.421204 0.662917 -3.758287 26375.730062

HLA A*0203 1:34-42 9 GTDTGQACQ 0.815488 -0.167073 -4.406840 0.648415 -3.758425 25517.594873

HLA B*4601 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.406727 0.648272 -3.758454 25510.969460

HLA B*0702 1:49-57 9 AYNINISLP 0.584960 0.117828 -4.461383 0.702788 -3.758595 28932.304850

HLA B*5401 1:149-157 9 QADTDPLPV 0.679726 0.062986 -4.501317 0.742712 -3.758605 31718.835094

HLA B*4601 1:120-128 9 AGGTHPTTT 0.991249 -0.369291 -4.380666 0.621958 -3.758709 24025.170323

HLA B*4601	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.407178	0.648415	-3.758763	25537.481438
HLA B*5101	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.465845	0.706847	-3.758998	29231.069430
HLA B*4403	1:82-90	9	TSSTPREAP	0.792178	0.117162	-4.668448	0.909340	-3.759108	46606.645375
HLA A*0201	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.381155	0.621958	-3.759197	24052.220028
HLA B*0802	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.461987	0.702788	-3.759199	28972.558611
HLA A*8001	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.462114	0.702905	-3.759208	28981.023717
HLA B*3901	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.378963	0.619394	-3.759569	23931.124082
HLA A*6802	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.426352	0.666762	-3.759590	26690.223534
HLA B*4002	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.615779	0.856017	-3.759762	41283.778511
HLA A*2301	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.536686	0.776623	-3.760064	34410.134983
HLA A*2902	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.463018	0.702905	-3.760113	29041.448510
HLA A*8001	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.408773	0.648272	-3.760501	25631.461148
HLA B*1503	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.474190	0.713674	-3.760516	29798.203052
HLA B*4403	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.569563	0.809025	-3.760538	37116.132797
HLA A*0211	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.463418	0.702788	-3.760630	29068.169669
HLA B*1517	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.467496	0.706847	-3.760649	29342.451299

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HLA B*4801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.380307
	0.619394	-3.760913	24005.292604

HLA B*1517	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.325738
	0.564331	-3.761407	21170.829051

HLA B*5701	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.341343
	0.579719	-3.761624	21945.381989

HLA A*2402	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.565775
	0.804086	-3.761690	36793.859876

HLA A*8001	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.410249
	0.648415	-3.761834	25718.689832

HLA A*0203	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.458082
	0.696230	-3.761852	28713.227109

HLA A*3002	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.234679
	0.472542	-3.762137	17166.386054

HLA B*4402	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.428955
	0.666762	-3.762193	26850.689377

HLA A*3001	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.301893
	0.539612	-3.762281	20039.779658

HLA B*4002	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.615721
	0.852998	-3.762723	41278.195372

HLA A*0301	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.363581
	0.600517	-3.763064	23098.353326

HLA B*0803	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.464738
	0.701666	-3.763072	29156.681788

HLA B*2705	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.382659
	0.619394	-3.763265	24135.641061

HLA A*0216	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.397360
	0.634040	-3.763320	24966.609361

HLA A*8001	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.434566
	0.671022	-3.763544	27199.818787

HLA B*1501	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.639155
	-0.124403	-3.763558	4356.672473
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HLA B*5801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.356493	0.592876	-3.763617	22724.410402
HLA A*0203	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.210263	0.446632	-3.763631	16227.926312
HLA A*3301	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.611057	0.847335	-3.763722	40837.295673
HLA B*0802	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.471194	0.707433	-3.763761	29593.373936
HLA B*4402	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.412340	0.648415	-3.763925	25842.818802
HLA B*3801	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.522611	0.758478	-3.764133	33312.759666
HLA A*6801	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.659853	0.895143	-3.764711	45693.395146
HLA B*5301	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.532300	0.767355	-3.764945	34064.332855
HLA A*3301	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.555494	0.790540	-3.764954	35933.043546
HLA B*0802	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.478967	0.713674	-3.765292	30127.741627
HLA A*0219	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.461583	0.696230	-3.765352	28945.612157
HLA B*1502	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.508462	0.742712	-3.765750	32244.972652
HLA A*0206	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.506366	0.740601	-3.765765	32089.745466
HLA B*5301	1:64-72	9	KSLENYIAQ	0.805806	0.003219	-4.574837	0.809025	-3.765813	37569.664235
HLA B*3801	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.506467	0.740601	-3.765866	32097.211219
HLA B*7301	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.603830	0.837899	-3.765931	40163.352661

HLA A*3001 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.303730
0.537766 -3.765964 20124.738197

HLA B*7301 1:111-119 9 AVVLKVYQN 1.224563 -0.434023 -4.556920
0.790540 -3.766380 36051.234523

HLA B*0702 1:120-128 9 AGGTHPTTT 0.991249 -0.369291 -4.388497
0.621958 -3.766539 24462.301170

HLA B*7301 1:95-103 9 ITSATYQSA 0.951011 -0.171324 -4.546230
0.779687 -3.766543 35174.666166

HLA A*1101 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.433436
0.666762 -3.766674 27129.132605

HLA B*0802 1:170-178 9 TGQQVSIAP 0.814303 -0.116557 -4.464583
0.697746 -3.766837 29146.273175

HLA B*1801 1:53-61 9 NISLPSYYP 0.515820 0.118220 -4.401232
0.634040 -3.767192 25190.194304

HLA A*2402 1:208-216 9 PEAAGPTQV 0.855949 -0.104037 -4.519373
0.751912 -3.767461 33065.342171

HLA B*1509 1:36-44 9 DTGQACQIQ 0.956574 -0.260344 -4.463754
0.696230 -3.767523 29090.665917

HLA B*7301 1:75-83 9 DKFLSAATS 1.204544 -0.986239 -3.985944
0.218305 -3.767638 9681.521114

HLA A*2301 1:129-137 9 YKAFDWDQA 0.955276 -0.207214 -4.515821
0.748062 -3.767759 32795.979023

HLA B*3901 1:34-42 9 GTDTGQACQ 0.815488 -0.167073 -4.416489
0.648415 -3.768074 26090.900768

HLA B*5801 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.334464
0.566374 -3.768090 21600.502412

HLA B*4601 1:91-99 9 YELNITSAT 0.787532 -0.429583 -4.126217
0.357949 -3.768268 13372.642962

HLA B*1509 1:170-178 9 TGQQVSIAP 0.814303 -0.116557 -4.466329
0.697746 -3.768583 29263.663779

HLA A*3201 1:183-191 9 DPVNYQNFA 1.302206 -0.446189 -4.624606
0.856017 -3.768589 42131.454698

HLA A*2301	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.527138	0.758478	-3.768660	33661.856884
HLA A*6801	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.522803	0.754093	-3.768710	33327.540848
HLA B*1801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.482545	0.713674	-3.768871	30376.997390
HLA A*1101	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.476347	0.707433	-3.768913	29946.557298
HLA A*0219	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.472195	0.702905	-3.769290	29661.653853
HLA A*3301	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.403567	0.634040	-3.769527	25326.017669
HLA B*5801	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.356852	0.587095	-3.769757	22743.227480
HLA A*2301	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.436695	0.666762	-3.769932	27333.462128
HLA B*3501	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.432865	0.662917	-3.769948	27093.491996
HLA B*5101	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.510950	0.740601	-3.770349	32430.236630
HLA A*2501	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.468159	0.697746	-3.770413	29387.249976
HLA B*0702	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.450559	0.680076	-3.770483	28220.126426
HLA A*0101	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.384282	0.613638	-3.770644	24226.034571
HLA B*4501	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.459318	0.688457	-3.770861	28795.049878
HLA A*2902	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.438835	0.667964	-3.770871	27468.505109
HLA A*3001	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.290503	0.519628	-3.770875	19521.025950

HLA B*3501	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.451078	0.680076	-3.771002	28253.886177
HLA B*7301	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.606311	0.835252	-3.771059	40393.456234
HLA B*5101	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.459572	0.688457	-3.771115	28811.878821
HLA A*3101	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.393187	0.621958	-3.771229	24727.879788
HLA B*1503	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.468984	0.697746	-3.771238	29443.105590
HLA A*3002	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.459186	0.687624	-3.771562	28786.327630
HLA B*4801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.419886	0.648272	-3.771614	26295.802447
HLA A*3301	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.625088	0.853458	-3.771630	42178.205550
HLA A*2603	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.607126	0.835252	-3.771874	40469.355321
HLA A*6901	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.385579	0.613638	-3.771941	24298.487908
HLA A*6801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-3.932728	0.160477	-3.772251	8565.007776
HLA B*0702	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.372812	0.600517	-3.772295	23594.574342
HLA A*0212	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.365174	0.592876	-3.772298	23183.231455
HLA B*4402	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.420631	0.648272	-3.772359	26340.936725
HLA B*0802	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.460843	0.688457	-3.772386	28896.327508
HLA A*0101	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.063909	0.291433	-3.772476	11585.343294

HLA B*0802	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.469209	0.696230	-3.772979	29458.400819
HLA B*5801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.354256	0.581216	-3.773040	22607.675678
HLA B*3501	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.407084	0.634040	-3.773044	25531.955838
HLA B*1517	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.498446	0.725355	-3.773091	31509.837130
HLA A*2602	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.352844	0.579719	-3.773125	22534.289727
HLA A*2601	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.373721	0.600517	-3.773204	23644.024329
HLA A*0250	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.527413	0.754093	-3.773320	33683.170137
HLA B*3801	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.563915	0.790540	-3.773375	36636.548970
HLA B*4601	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.373914	0.600517	-3.773397	23654.515403
HLA A*0216	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.476359	0.702905	-3.773453	29947.367347
HLA B*4403	1:154-162	9	PLPVVFPIV	1.026322	-0.131179	-4.668638	0.895143	-3.773495	46627.072930
HLA B*5401	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.441516	0.667964	-3.773551	27638.583879
HLA B*5301	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.564208	0.790540	-3.773668	36661.332307
HLA A*3002	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.549103	0.775271	-3.773833	35408.163706
HLA B*4403	1:183-191	9	DPVNYQNFA	1.302206	-0.446189	-4.629914	0.856017	-3.773897	42649.499711
HLA B*0801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.393565	0.619394	-3.774171	24749.426960

HLA A*0301	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.367162	0.592876	-3.774286	23289.578863
HLA A*2603	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.354178	0.579719	-3.774460	22603.639972
HLA B*7301	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.526377	0.751912	-3.774465	33602.905923
HLA B*3801	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.549937	0.775271	-3.774667	35476.230802
HLA A*3101	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.354681	0.579719	-3.774962	22629.823728
HLA B*4601	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.409032	0.634040	-3.774992	25646.718657
HLA A*2301	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.517834	0.742712	-3.775122	32948.383222
HLA A*6801	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.523221	0.748062	-3.775160	33359.649403
HLA B*5301	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.579261	0.804086	-3.775176	37954.335652
HLA B*5401	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.482770	0.707433	-3.775337	30392.777762
HLA A*0201	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.368454	0.592876	-3.775578	23358.978782
HLA B*5301	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.583824	0.808230	-3.775594	38355.186062
HLA B*4402	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.395496	0.619394	-3.776103	24859.730977
HLA B*1801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.464651	0.688457	-3.776194	29150.846199
HLA A*2402	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.562803	0.786460	-3.776344	36542.920370
HLA A*3201	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.611736	0.835252	-3.776484	40901.193006

HLA B*0802	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.444469	0.667964	-3.776505	27827.173123
HLA B*1517	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.484528	0.707999	-3.776529	30516.014264
HLA B*4001	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.410637	0.634040	-3.776597	25741.657399
HLA A*6802	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.439768	0.662917	-3.776850	27527.563329
HLA B*3901	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.439859	0.662917	-3.776942	27533.371864
HLA B*5701	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.425636	0.648415	-3.777221	26646.220546
HLA A*0216	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.464912	0.687624	-3.777288	29168.356472
HLA B*4501	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.585631	0.808230	-3.777401	38515.083863
HLA B*3901	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.466068	0.688457	-3.777611	29246.096291
HLA B*0803	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.480416	0.702788	-3.777629	30228.473087
HLA A*0216	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.475565	0.697746	-3.777819	29892.657347
HLA B*1509	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.465551	0.687624	-3.777927	29211.309007
HLA B*0702	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.441133	0.662917	-3.778216	27614.222589
HLA A*0301	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.356352	0.578083	-3.778269	22717.035407
HLA A*2601	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.400407	0.621958	-3.778449	25142.406758
HLA B*4403	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.625946	0.847335	-3.778610	42261.573319

HLA B*1517	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.356807	0.578083	-3.778725	22740.889871
HLA B*3901	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.481704	0.702905	-3.778798	30318.221970
HLA A*2501	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.466566	0.687624	-3.778942	29279.657779
HLA B*1517	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.459273	0.680076	-3.779197	28792.090248
HLA A*2902	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.442197	0.662917	-3.779280	27681.979197
HLA B*4001	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.393248	0.613638	-3.779610	24731.358185
HLA B*5101	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.487648	0.707999	-3.779649	30736.040891
HLA A*0212	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-3.820310	0.040514	-3.779795	6611.646162
HLA A*0202	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.372695	0.592876	-3.779819	23588.193003
HLA B*1501	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.393591	0.613638	-3.779953	24750.899812
HLA B*4501	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.584066	0.804086	-3.779980	38376.564240
HLA A*6802	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.428892	0.648415	-3.780477	26846.767664
HLA B*7301	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.534586	0.754093	-3.780493	34244.114198
HLA B*1517	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.443449	0.662917	-3.780532	27761.914569
HLA B*4501	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.400191	0.619394	-3.780797	25129.896249
HLA A*0216	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.403048	0.621958	-3.781090	25295.756343

HLA A*0211	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.415138	0.634040	-3.781098	26009.866264
HLA A*3002	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.504282	0.723137	-3.781146	31936.129386
HLA A*0211	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.362376	0.581216	-3.781159	23034.337957
HLA B*5701	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.215653	0.434427	-3.781226	16430.574373
HLA A*0301	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.368421	0.587095	-3.781326	23357.209676
HLA B*3901	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.484182	0.702788	-3.781395	30491.755937
HLA B*5801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.359516	0.578083	-3.781434	22883.181815
HLA B*0802	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.488313	0.706847	-3.781466	30783.133768
HLA A*0201	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.395273	0.613638	-3.781635	24846.957862
HLA A*2601	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.395306	0.613638	-3.781668	24848.839804
HLA A*0250	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.452735	0.671022	-3.781712	28361.851461
HLA B*5701	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.415871	0.634040	-3.781831	26053.805009
HLA B*5401	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.549200	0.767355	-3.781845	35416.018301
HLA A*6801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.470422	0.688457	-3.781964	29540.748911
HLA A*6802	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.347024	0.564800	-3.782224	22234.337799
HLA B*1801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.343695	0.561410	-3.782285	22064.545156

HLA B*5801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.352454	0.570132	-3.782321	22514.062082
HLA B*4002	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.445423	0.662917	-3.782506	27888.360315
HLA B*3901	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.490077	0.707433	-3.782644	30908.454713
HLA B*2705	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.462981	0.680076	-3.782904	29038.934843
HLA B*5801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.347623	0.564331	-3.783293	22265.031718
HLA B*4801	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.417448	0.634040	-3.783408	26148.553114
HLA B*5101	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.450185	0.666762	-3.783423	28195.862690
HLA A*2402	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.526140	0.742712	-3.783427	33584.550351
HLA B*0702	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.486356	0.702905	-3.783450	30644.723597
HLA B*0802	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.486849	0.702905	-3.783944	30679.558138
HLA A*0250	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.509477	0.725355	-3.784122	32320.419606
HLA B*1509	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.509606	0.725355	-3.784251	32330.037781
HLA B*1502	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.471967	0.687624	-3.784343	29646.092709
HLA B*1503	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.509714	0.725355	-3.784359	32338.084271
HLA A*0211	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.451243	0.666762	-3.784480	28264.587731
HLA B*1503	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.480743	0.696230	-3.784512	30251.212679

HLA B*4801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.432945	0.648415	-3.784530	27098.475929
HLA A*2403	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.404020	0.619394	-3.784627	25352.474591
HLA B*0803	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.498542	0.713674	-3.784868	31516.826959
HLA A*0216	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.304623	0.519628	-3.784995	20166.152340
HLA B*1502	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.385629	0.600517	-3.785111	24301.248560
HLA A*0211	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.433563	0.648415	-3.785148	27137.059105
HLA B*1501	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.355503	0.570132	-3.785371	22672.713013
HLA A*8001	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.385922	0.600517	-3.785405	24317.687500
HLA B*5301	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.488393	0.702905	-3.785487	30788.796422
HLA B*3901	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.057185	0.271476	-3.785709	11407.347751
HLA B*4002	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.565479	0.779687	-3.785792	36768.788034
HLA A*3301	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.572319	0.786460	-3.785859	37352.413252
HLA B*0803	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.466239	0.680076	-3.786163	29257.648497
HLA A*3101	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.364359	0.578083	-3.786276	23139.751985
HLA B*5101	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.457333	0.671022	-3.786310	28663.717856
HLA A*1101	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.494405	0.707999	-3.786406	31217.997692

HLA B*4402	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.420521	0.634040	-3.786481	26334.240004
HLA A*2501	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.434963	0.648415	-3.786548	27224.698171
HLA A*2403	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.028549	0.241980	-3.786570	10679.456668
HLA B*1517	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.489720	0.702905	-3.786815	30883.049041
HLA B*0802	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.474474	0.687624	-3.786850	29817.715239
HLA B*1501	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.239524	0.452621	-3.786903	17358.952436
HLA A*2403	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.408999	0.621958	-3.787041	25644.776288
HLA B*3501	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.208224	0.421102	-3.787122	16151.902115
HLA A*6802	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.351491	0.564331	-3.787160	22464.180005
HLA B*4801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.351780	0.564331	-3.787449	22479.133012
HLA A*0206	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.454302	0.666762	-3.787539	28464.377119
HLA B*4501	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.625675	0.837899	-3.787776	42235.288997
HLA A*2603	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.541902	0.754093	-3.787809	34825.890724
HLA B*0803	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.494786	0.706847	-3.787939	31245.369201
HLA B*5101	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.485738	0.697746	-3.787992	30601.153262
HLA B*0801	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.240677	0.452621	-3.788056	17405.123545

HLA B*4601	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.401972	0.613638	-3.788333	25233.157891
HLA A*0206	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.486285	0.697746	-3.788539	30639.750464
HLA A*1101	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.491651	0.702905	-3.788746	31020.689575
HLA B*4001	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.410801	0.621958	-3.788843	25751.407411
HLA A*2402	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.537135	0.748062	-3.789073	34445.708967
HLA A*1101	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.476716	0.687624	-3.789091	29972.003289
HLA A*6802	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.236218	0.446632	-3.789586	17227.322654
HLA B*5801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.351007	0.561410	-3.789596	22439.159033
HLA B*3901	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.469679	0.680076	-3.789603	29490.291405
HLA A*0301	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.355999	0.566374	-3.789625	22698.608388
HLA B*4002	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.627637	0.837899	-3.789738	42426.508238
HLA B*0702	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.456592	0.666762	-3.789830	28614.913179
HLA B*4001	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.371153	0.581216	-3.789937	23504.629531
HLA A*0301	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.360155	0.570132	-3.790023	22916.878971
HLA B*1501	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.327866	0.537766	-3.790101	21274.849609
HLA B*7301	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.598374	0.808230	-3.790144	39661.985779

HLA B*0801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.211729	0.421102	-3.790627	16282.800641
HLA B*4001	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.370359	0.579719	-3.790640	23461.689587
HLA B*1501	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.357134	0.566374	-3.790760	22757.996874
HLA A*0250	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.457704	0.666762	-3.790942	28688.229001
HLA B*4403	1:14-22	9	LLCCSGVAT	1.136854	-0.272198	-4.655728	0.864656	-3.791072	45261.373914
HLA A*1101	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.462149	0.671022	-3.791127	28983.375575
HLA A*3101	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.384045	0.592876	-3.791169	24212.801110
HLA A*3002	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.494165	0.702905	-3.791260	31200.776081
HLA A*2603	1:220-228	9	RSAIDSMLA	1.010961	-0.163626	-4.638614	0.847335	-3.791279	43512.504791
HLA B*0803	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.479058	0.687624	-3.791434	30134.098820
HLA A*3101	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.405324	0.613638	-3.791686	25428.709494
HLA A*3301	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.627071	0.835252	-3.791819	42371.229310
HLA A*2501	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.459999	0.667964	-3.792035	28840.260962
HLA A*0101	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.371830	0.579719	-3.792111	23541.279418
HLA A*3002	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.540241	0.748062	-3.792179	34692.943359
HLA B*2705	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.495192	0.702905	-3.792287	31274.625769

HLA A*2603	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.373618	0.581216	-3.792402	23638.396890
HLA A*3101	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.393032	0.600517	-3.792514	24719.052209
HLA A*2603	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.535260	0.742712	-3.792548	34297.324214
HLA B*1801	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.495413	0.702788	-3.792625	31290.533886
HLA B*5801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.357526	0.564800	-3.792726	22778.566911
HLA A*6901	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.370871	0.578083	-3.792789	23489.375590
HLA A*8001	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.412537	0.619394	-3.793144	25854.565241
HLA A*2403	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.427579	0.634040	-3.793539	26765.702239
HLA B*5101	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.456623	0.662917	-3.793706	28616.925695
HLA B*0802	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.442160	0.648415	-3.793745	27679.583197
HLA B*1517	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.481563	0.687624	-3.793938	30308.382473
HLA A*0101	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.375178	0.581216	-3.793962	23723.462639
HLA A*8001	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.375195	0.581216	-3.793978	23724.361045
HLA B*0702	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.428027	0.634040	-3.793988	26793.373234
HLA B*3501	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.442585	0.648415	-3.794170	27706.700041
HLA A*2402	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.570904	0.776623	-3.794282	37230.963532

HLA B*5101 1:49-57 9 AYNINISLP 0.584960 0.117828 -4.497184
0.702788 -3.794397 31418.430410

HLA A*2301 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.501343
0.706847 -3.794496 31720.722700

HLA A*2403 1:115-123 9 KVYQNAGGT 0.678003 -0.098284 -4.374252
0.579719 -3.794534 23672.950018

HLA A*6901 1:203-211 9 PGELLPEAA 1.144110 -0.557015 -4.381968
0.587095 -3.794873 24097.283657

HLA B*5701 1:120-128 9 AGGTHPTTT 0.991249 -0.369291 -4.416905
0.621958 -3.794947 26115.896085

HLA B*0803 1:170-178 9 TGQQVSIAP 0.814303 -0.116557 -4.492751
0.697746 -3.795005 31099.328137

HLA A*0216 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.359502
0.564331 -3.795172 22882.439054

HLA A*3201 1:117-125 9 YQNAGGTHP 0.729126 0.047497 -4.571994
0.776623 -3.795372 37324.537666

HLA A*0219 1:165-173 9 ELSKQTGQQ 0.723302 -0.142086 -4.376609
0.581216 -3.795393 23801.751387

HLA A*2601 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.388291
0.592876 -3.795415 24450.658168

HLA A*6801 1:27-35 9 TYCEELKGT 0.991738 -0.153839 -4.633563
0.837899 -3.795664 43009.331406

HLA B*4002 1:128-136 9 TYKAFDWDQ 0.746622 0.061608 -4.603898
0.808230 -3.795668 40169.654255

HLA A*0202 1:11-19 9 AVVLLCCSG 0.891360 -0.444728 -4.242350
0.446632 -3.795718 17472.294597

HLA A*0216 1:146-154 9 TLWQADTDP 0.196026 0.057761 -4.049690
0.253787 -3.795902 11212.173873

HLA B*1509 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.503641
0.707433 -3.796207 31888.997738

HLA B*5101 1:36-44 9 DTGQACQIQ 0.956574 -0.260344 -4.492549
0.696230 -3.796319 31084.862525

HLA A*3201	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.537119	0.740601	-3.796518	34444.404560
HLA B*0803	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.522209	0.725355	-3.796854	33281.956580
HLA A*0101	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.375246	0.578083	-3.797164	23727.184828
HLA B*1502	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.505239	0.707999	-3.797239	32006.524621
HLA B*1502	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.155233	0.357949	-3.797284	14296.620505
HLA B*4001	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.384402	0.587095	-3.797307	24232.719561
HLA B*1801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.460244	0.662917	-3.797326	28856.491880
HLA A*2301	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.520715	0.723137	-3.797578	33167.640478
HLA A*0219	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.390685	0.592876	-3.797809	24585.818956
HLA B*0802	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.464625	0.666762	-3.797863	29149.111519
HLA A*2602	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.546120	0.748062	-3.798058	35165.723624
HLA A*0212	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.420323	0.621958	-3.798365	26322.275636
HLA A*6901	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.363330	0.564800	-3.798529	23084.986525
HLA B*3901	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.122308	0.323743	-3.798565	13252.801905
HLA B*1509	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.417993	0.619394	-3.798599	26181.392618
HLA A*2602	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.521894	0.723137	-3.798757	33257.838396

HLA A*0202	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.070408	0.271476	-3.798932	11760.007067
HLA A*3201	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.574269	0.775271	-3.798998	37520.510470
HLA B*3901	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.433088	0.634040	-3.799048	27107.419990
HLA B*7301	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.557806	0.758478	-3.799328	36124.837064
HLA A*2501	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.433657	0.634040	-3.799617	27142.932080
HLA A*1101	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.467799	0.667964	-3.799835	29362.935830
HLA A*0203	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.413848	0.613638	-3.800210	25932.730807
HLA A*0101	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.370439	0.570132	-3.800307	23466.005439
HLA A*2301	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.540922	0.740601	-3.800322	34747.414721
HLA B*1517	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.498084	0.697746	-3.800338	31483.596495
HLA B*4403	1:184-192	9	PVNYQNFAV	0.967153	-0.114155	-4.653364	0.852998	-3.800366	45015.714832
HLA B*4601	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.370911	0.570132	-3.800779	23491.535963
HLA A*0301	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.365595	0.564800	-3.800794	23205.692278
HLA B*1501	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.393800	0.592876	-3.800924	24762.819748
HLA B*4601	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.380749	0.579719	-3.801030	24029.719826
HLA B*4601	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.393934	0.592876	-3.801058	24770.456880

HLA A*2601	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.379165	0.578083	-3.801082	23942.260640
HLA B*3801	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.549310	0.748062	-3.801248	35425.024492
HLA B*0803	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.508746	0.707433	-3.801313	32266.087011
HLA B*0803	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.468131	0.666762	-3.801369	29385.342257
HLA B*0802	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.420791	0.619394	-3.801397	26350.628613
HLA B*4001	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.379480	0.578083	-3.801397	23959.623279
HLA B*5301	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.549550	0.748062	-3.801488	35444.577723
HLA A*0202	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.449934	0.648415	-3.801519	28179.546008
HLA A*0219	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.420941	0.619394	-3.801548	26359.753647
HLA A*2301	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.527053	0.725355	-3.801699	33655.301673
HLA B*4501	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.592376	0.790540	-3.801836	39117.961892
HLA A*6801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.482082	0.680076	-3.802006	30344.640406
HLA B*1509	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.490519	0.688457	-3.802062	30939.906432
HLA B*2705	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.450745	0.648415	-3.802330	28232.189756
HLA B*5101	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.450644	0.648272	-3.802371	28225.623000
HLA B*1801	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.469355	0.666762	-3.802593	29468.283211

HLA B*0802	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.482723	0.680076	-3.802647	30389.489509
HLA A*0212	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.416311	0.613638	-3.802672	26080.175658
HLA A*0203	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.389858	0.587095	-3.802762	24539.045198
HLA B*1517	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.510269	0.707433	-3.802835	32379.397765
HLA B*1503	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.369286	0.566374	-3.802912	23403.756443
HLA A*2403	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.416585	0.613638	-3.802947	26096.688514
HLA A*0202	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-3.895103	0.092119	-3.802984	7854.220848
HLA A*2601	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.341531	0.537766	-3.803765	21954.881811
HLA A*2403	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.452192	0.648415	-3.803777	28326.430235
HLA A*3201	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.474839	0.671022	-3.803816	29842.728858
HLA B*0803	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.452385	0.648415	-3.803970	28338.998936
HLA A*2602	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.580847	0.776623	-3.804225	38093.185921
HLA B*3801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.505894	0.701666	-3.804228	32054.870436
HLA B*4002	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.639481	0.835252	-3.804229	43599.453346
HLA A*3301	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.471359	0.666762	-3.804597	29604.582839
HLA A*0101	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.368928	0.564331	-3.804598	23384.519370

HLA A*3101	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.366010	0.561410	-3.804600	23227.923539
HLA A*2501	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.452944	0.648272	-3.804671	28375.510417
HLA B*4402	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.426876	0.621958	-3.804918	26722.442191
HLA A*2501	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.467849	0.662917	-3.804932	29366.271874
HLA A*0101	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.369786	0.564800	-3.804986	23430.740284
HLA A*0301	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.366407	0.561410	-3.804997	23249.169873
HLA B*5301	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.556934	0.751912	-3.805022	36052.404741
HLA A*0201	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.392287	0.587095	-3.805192	24676.696973
HLA A*0216	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.473163	0.667964	-3.805199	29727.839684
HLA A*0216	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.398083	0.592876	-3.805207	25008.244548
HLA B*1801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.473180	0.667964	-3.805215	29728.965476
HLA B*4002	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.398349	0.592876	-3.805473	25023.537199
HLA B*1517	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.472259	0.666762	-3.805497	29665.986758
HLA A*8001	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.427557	0.621958	-3.805600	26764.399076
HLA A*3301	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.580925	0.775271	-3.805654	38099.987165
HLA A*3201	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-3.966250	0.160477	-3.805774	9252.310813

HLA B*4403	1:27-35	9	TYCEELKGT	0.991738	-0.153839	-4.643755	0.837899	-3.805856	44030.615585
HLA B*4001	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.398804	0.592876	-3.805929	25049.813650
HLA B*4403	1:128-136	9	TYKAFDWDQ	0.746622	0.061608	-4.614182	0.808230	-3.805952	41132.185863
HLA B*5301	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.582631	0.776623	-3.806008	38249.922142
HLA B*3901	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.472823	0.666762	-3.806060	29704.529302
HLA B*0801	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.419884	0.613638	-3.806246	26295.660190
HLA B*5701	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.419999	0.613638	-3.806361	26302.631688
HLA A*0201	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.372807	0.566374	-3.806434	23594.319055
HLA B*0803	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.495272	0.688457	-3.806815	31280.378835
HLA B*0702	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.399744	0.592876	-3.806868	25104.079029
HLA A*0250	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.514456	0.707433	-3.807022	32693.058319
HLA B*7301	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.093240	0.286028	-3.807212	12394.810118
HLA B*3901	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.503549	0.696230	-3.807319	31882.270326
HLA B*1501	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.394484	0.587095	-3.807389	24801.834005
HLA B*2705	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-3.899454	0.091985	-3.807469	7933.308721
HLA B*0802	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.470480	0.662917	-3.807563	29544.744486

HLA B*0803	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.503838	0.696230	-3.807608	31903.492371
HLA A*0250	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.514521	0.706847	-3.807674	32698.010937
HLA B*4801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.429667	0.621958	-3.807709	26894.739024
HLA A*0211	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.505784	0.697746	-3.808038	32046.721047
HLA A*0203	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.260869	0.452621	-3.808248	18233.438832
HLA A*2403	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.208858	0.400567	-3.808291	16175.511954
HLA B*4002	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.612537	0.804086	-3.808451	40976.716029
HLA B*3801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.533855	0.725355	-3.808500	34186.547755
HLA B*1503	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.430896	0.621958	-3.808938	26970.941999
HLA B*4402	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.401939	0.592876	-3.809063	25231.246843
HLA B*4402	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.054267	0.245175	-3.809092	11330.957765
HLA A*2602	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.489241	0.680076	-3.809165	30848.984771
HLA B*7301	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.522862	0.713674	-3.809188	33332.048610
HLA A*3101	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.375655	0.566374	-3.809281	23749.530234
HLA B*4601	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.373778	0.564331	-3.809447	23647.094405
HLA A*3201	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.561443	0.751912	-3.809531	36428.635120

HLA A*6802	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.347405	0.537766	-3.809639	22253.832559
HLA B*4001	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.374297	0.564331	-3.809966	23675.383436
HLA A*2602	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.552766	0.742712	-3.810054	35708.059653
HLA A*6901	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.133919	0.323743	-3.810176	13611.903492
HLA A*2603	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.513112	0.702905	-3.810206	32592.047436
HLA A*6801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.458521	0.648272	-3.810249	28742.289522
HLA A*0206	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.513062	0.702788	-3.810275	32588.344940
HLA B*5701	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.410862	0.600517	-3.810345	25755.029785
HLA B*4501	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.587017	0.776623	-3.810394	38638.214041
HLA A*2902	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.411015	0.600517	-3.810497	25764.087948
HLA B*3501	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.391782	0.581216	-3.810566	24648.011547
HLA B*0801	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.397811	0.587095	-3.810715	24992.555619
HLA A*0301	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.348511	0.537766	-3.810745	22310.608915
HLA A*0101	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.372161	0.561410	-3.810751	23559.243424
HLA A*6802	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.432755	0.621958	-3.810797	27086.603951
HLA B*0802	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.459111	0.648272	-3.810839	28781.344674

HLA A*2402	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.517804	0.706847	-3.810957	32946.066091
HLA B*4501	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.482131	0.671022	-3.811109	30348.087986
HLA B*5401	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.459393	0.648272	-3.811121	28800.035207
HLA B*0803	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.519185	0.707999	-3.811186	33051.034880
HLA A*3201	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.512935	0.701666	-3.811270	32578.826167
HLA B*4402	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.376163	0.564800	-3.811362	23777.298638
HLA B*1801	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.518948	0.707433	-3.811514	33032.980767
HLA B*2705	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.097601	0.286028	-3.811573	12519.890259
HLA B*2705	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.391364	0.579719	-3.811645	24624.287915
HLA A*3002	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.566219	0.754093	-3.812127	36831.499699
HLA B*2705	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.508488	0.696230	-3.812258	32246.891568
HLA A*0206	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.460711	0.648415	-3.812296	28887.574582
HLA A*8001	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.446426	0.634040	-3.812386	27952.857525
HLA B*1801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.432184	0.619394	-3.812790	27051.019213
HLA B*4501	1:207-215	9	LPEAAGPTQ	1.054236	-0.218984	-4.648113	0.835252	-3.812861	44474.702530
HLA A*6802	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.426535	0.613638	-3.812897	26701.488421

HLA B*1509	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.461327	0.648415	-3.812912	28928.548600
HLA B*1509	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.526722	0.713674	-3.813048	33629.639387
HLA A*0201	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.391328	0.578083	-3.813246	24622.289776
HLA B*0702	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.143594	0.330347	-3.813247	13918.551495
HLA B*1517	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.484384	0.671022	-3.813362	30505.945542
HLA B*5801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.353239	0.539612	-3.813626	22554.779583
HLA B*1801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.516626	0.702905	-3.813721	32856.891476
HLA A*3201	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.527495	0.713674	-3.813821	33689.548518
HLA A*2902	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.435884	0.621958	-3.813926	27282.494212
HLA A*3002	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.462365	0.648272	-3.814093	28997.804475
HLA A*2602	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.572770	0.758478	-3.814292	37391.231312
HLA A*0219	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.436377	0.621958	-3.814419	27313.506831
HLA A*2301	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.494720	0.680076	-3.814644	31240.636608
HLA A*0250	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.573284	0.758478	-3.814806	37435.557414
HLA A*2402	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.511089	0.696230	-3.814858	32440.589477
HLA A*0201	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.202355	0.387379	-3.814976	15935.095129

HLA A*6901	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.385119	0.570132	-3.814986	24272.736946
HLA B*5101	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.502692	0.687624	-3.815067	31819.377406
HLA A*3002	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.522533	0.707433	-3.815100	33306.812992
HLA B*1502	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.481901	0.666762	-3.815139	30332.002631
HLA A*0202	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.173320	0.357949	-3.815370	14904.579394
HLA B*5801	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.353213	0.537766	-3.815447	22553.437415
HLA A*3101	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.402578	0.587095	-3.815483	25268.401697
HLA B*5101	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.416177	0.600517	-3.815659	26072.134719
HLA A*6801	1:134-142	9	WDQAYRKPI	0.842101	0.011357	-4.669242	0.853458	-3.815784	46691.945572
HLA B*1502	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.397005	0.581216	-3.815788	24946.222634
HLA A*0203	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.380284	0.564331	-3.815953	24003.993979
HLA A*0203	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.353727	0.537766	-3.815961	22580.173790
HLA B*5401	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.513779	0.697746	-3.816033	32642.160623
HLA A*0211	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.503671	0.687624	-3.816047	31891.240524
HLA A*2601	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.403226	0.587095	-3.816131	25306.158871
HLA A*0250	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.464689	0.648415	-3.816274	29153.369554

HLA B*1502	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.606976	0.790540	-3.816436	40455.345924
HLA B*4801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.396199	0.579719	-3.816480	24899.975545
HLA B*7301	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.620680	0.804086	-3.816595	41752.305838
HLA B*1509	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.519584	0.702905	-3.816679	33081.445276
HLA B*3901	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.484662	0.667964	-3.816697	30525.425745
HLA A*0211	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.524770	0.707999	-3.816771	33478.792708
HLA B*5301	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.592402	0.775271	-3.817131	39120.289824
HLA A*0202	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.525221	0.707999	-3.817222	33513.585153
HLA B*5101	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.485334	0.667964	-3.817369	30572.692104
HLA A*3201	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.603875	0.786460	-3.817415	40167.481180
HLA B*1801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.410296	0.592876	-3.817420	25721.472688
HLA B*0803	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.480473	0.662917	-3.817555	30232.398126
HLA B*2705	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.485545	0.667964	-3.817581	30587.581267
HLA A*2403	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.398936	0.581216	-3.817720	25057.403736
HLA A*3101	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.399049	0.581216	-3.817832	25063.911354
HLA B*4801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.410918	0.592876	-3.818043	25758.373966

HLA B*4601 1:165-173 9 ELSKQTGQQ 0.723302 -0.142086 -4.399305
0.581216 -3.818089 25078.695348

HLA A*3101 1:152-160 9 TDPLPVVFP 0.730366 -0.165566 -4.383037
0.564800 -3.818237 24156.672172

HLA B*4403 1:207-215 9 LPEAAGPTQ 1.054236 -0.218984 -4.653839
0.835252 -3.818587 45064.934786

HLA B*1502 1:169-177 9 QTGQQVSIA 0.950594 -0.262137 -4.507069
0.688457 -3.818612 32141.694458

HLA A*0203 1:97-105 9 SATYQSAIP 0.500068 0.078015 -4.396744
0.578083 -3.818661 24931.246982

HLA A*2603 1:111-119 9 AVVLKVYQN 1.224563 -0.434023 -4.609260
0.790540 -3.818720 40668.637106

HLA B*4601 1:97-105 9 SATYQSAIP 0.500068 0.078015 -4.396810
0.578083 -3.818727 24935.023776

HLA A*2601 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.388866
0.570132 -3.818734 24483.087115

HLA B*0801 1:138-146 9 YRKPITYDT 0.544186 -0.159948 -4.203031
0.384238 -3.818794 15959.942125

HLA B*0802 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.489915
0.671022 -3.818893 30896.919286

HLA B*0803 1:98-106 9 ATYQSAIPP 0.417465 0.201929 -4.438461
0.619394 -3.819068 27444.887619

HLA B*1503 1:115-123 9 KVYQNAGGT 0.678003 -0.098284 -4.398913
0.579719 -3.819194 25056.048195

HLA A*2601 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.385732
0.566374 -3.819358 24307.033799

HLA A*2501 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.490387
0.671022 -3.819365 30930.534489

HLA B*5701 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.385936
0.566374 -3.819563 24318.476849

HLA B*2705 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.467962
0.648272 -3.819689 29373.898541

HLA A*2601	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.384649	0.564800	-3.819848	24246.488586
HLA B*7301	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.543119	0.723137	-3.819983	34923.620976
HLA A*2601	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.384656	0.564331	-3.820325	24246.882102
HLA A*0202	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.488597	0.667964	-3.820633	30803.290899
HLA A*2301	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.518511	0.697746	-3.820765	32999.758399
HLA B*0801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.400837	0.579719	-3.821118	25167.310310
HLA B*0801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.382619	0.561410	-3.821209	24133.421453
HLA B*5101	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.501512	0.680076	-3.821436	31733.080709
HLA A*2403	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.414508	0.592876	-3.821633	25972.183175
HLA B*3501	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.408907	0.587095	-3.821812	25639.366178
HLA B*5401	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.535606	0.713674	-3.821931	34324.610137
HLA B*4001	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.392482	0.570132	-3.822350	24687.779811
HLA B*5401	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.563088	0.740601	-3.822487	36566.849072
HLA B*0803	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.493698	0.671022	-3.822676	31167.204400
HLA B*5701	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.415552	0.592876	-3.822676	26034.643104
HLA B*4001	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.362406	0.539612	-3.822794	23035.957986

HLA B*1503	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.257568	0.434427	-3.823141	18095.373765
HLA B*4402	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.436981	0.613638	-3.823343	27351.508345
HLA A*2403	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.401436	0.578083	-3.823353	25202.053121
HLA B*4601	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.410707	0.587095	-3.823612	25745.835524
HLA B*3801	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.526811	0.702788	-3.824024	33636.553537
HLA A*0202	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.411323	0.587095	-3.824227	25782.353312
HLA A*0201	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.405486	0.581216	-3.824270	25438.203354
HLA B*7301	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.591749	0.767355	-3.824394	39061.499116
HLA A*2601	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.385821	0.561410	-3.824411	24312.031250
HLA B*7301	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.512090	0.687624	-3.824465	32515.438690
HLA B*5701	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.388991	0.564331	-3.824660	24490.108013
HLA A*0211	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.446718	0.621958	-3.824760	27971.615327
HLA A*2301	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.526750	0.701666	-3.825085	33631.822650
HLA A*0201	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.386691	0.561410	-3.825280	24360.744383
HLA B*3501	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.117021	0.291433	-3.825588	13092.463300
HLA B*3801	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.514127	0.688457	-3.825670	32668.306478

HLA A*0101	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.392069	0.566374	-3.825695	24664.284763
HLA A*2301	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.521981	0.696230	-3.825751	33264.496148
HLA B*1502	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.523713	0.697746	-3.825967	33397.389383
HLA A*1101	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.489006	0.662917	-3.826089	30832.300326
HLA A*8001	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.419052	0.592876	-3.826177	26245.349542
HLA B*3801	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.539915	0.713674	-3.826240	34666.864954
HLA B*3801	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.533543	0.706847	-3.826696	34161.958859
HLA A*0250	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.489760	0.662917	-3.826843	30885.889427
HLA A*3002	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.578815	0.751912	-3.826903	37915.343233
HLA B*1503	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.460960	0.634040	-3.826920	28904.144862
HLA A*6901	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.366664	0.539612	-3.827051	23262.883438
HLA B*1509	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.489981	0.662917	-3.827064	30901.599810
HLA A*1101	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.407119	0.579719	-3.827401	25534.027798
HLA A*2402	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.550640	0.723137	-3.827503	35533.662059
HLA A*2301	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.541219	0.713674	-3.827544	34771.108233
HLA B*3801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.507839	0.680076	-3.827763	32198.778714

HLA A*3201	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.274409	0.446632	-3.827777	18810.860663
HLA A*1101	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.524056	0.696230	-3.827825	33423.778525
HLA A*0203	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.212138	0.384238	-3.827900	16298.135195
HLA A*0201	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.392261	0.564331	-3.827931	24675.228536
HLA A*0201	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.398135	0.570132	-3.828002	25011.221146
HLA B*1509	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.428822	0.600517	-3.828304	26842.410876
HLA A*2501	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.428826	0.600517	-3.828309	26842.701307
HLA B*4801	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.442251	0.613638	-3.828613	27685.423809
HLA A*3002	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.462708	0.634040	-3.828668	29020.717259
HLA A*0202	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.704273	-0.124403	-3.828676	5061.430035
HLA A*8001	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.442543	0.613638	-3.828904	27704.002149
HLA A*0301	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.368600	0.539612	-3.828987	23366.815004
HLA B*3501	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.442756	0.613638	-3.829118	27717.644185
HLA B*0802	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.463237	0.634040	-3.829197	29056.063511
HLA B*1509	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.509345	0.680076	-3.829269	32310.629496
HLA A*0201	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.394148	0.564800	-3.829347	24782.654375

HLA B*2705	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.463432	0.634040	-3.829392	29069.113218
HLA B*1509	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.463728	0.634040	-3.829688	29088.934818
HLA B*0803	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.532638	0.702905	-3.829733	34090.880128
HLA B*4501	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.537814	0.707999	-3.829815	34499.605507
HLA B*4601	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.396265	0.566374	-3.829891	24903.747602
HLA B*0801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.394594	0.564331	-3.830264	24808.141040
HLA B*4501	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.423394	0.592876	-3.830518	26509.052758
HLA A*1101	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.452528	0.621958	-3.830570	28348.352441
HLA A*3002	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.497340	0.666762	-3.830577	31429.650448
HLA B*5701	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.408668	0.578083	-3.830585	25625.222056
HLA B*1801	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.510685	0.680076	-3.830608	32410.417518
HLA A*0211	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.533940	0.702905	-3.831034	34193.206439
HLA B*1501	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.254852	0.423714	-3.831138	17982.561462
HLA B*0702	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.395670	0.564331	-3.831340	24869.685110
HLA B*3501	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.397989	0.566374	-3.831615	25002.833461
HLA A*3101	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.401765	0.570132	-3.831632	25221.147995

HLA A*0206 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.396004
0.564331 -3.831673 24888.797448

HLA B*1502 1:55-63 9 SLPSYYPDQ 0.698032 -0.017956 -4.511751
0.680076 -3.831675 32490.118246

HLA B*4002 1:111-119 9 AVVLKVYQN 1.224563 -0.434023 -4.622367
0.790540 -3.831827 41914.799720

HLA A*2301 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.539341
0.707433 -3.831908 34621.134432

HLA B*5101 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.402096
0.570132 -3.831964 25240.393884

HLA A*0301 1:26-34 9 KTYCEELKG 0.984658 -0.550231 -4.266575
0.434427 -3.832148 18474.618692

HLA B*5101 1:98-106 9 ATYQSAIPP 0.417465 0.201929 -4.451597
0.619394 -3.832204 28287.686315

HLA A*0202 1:105-113 9 PPRGTQAVV 0.903475 -0.180338 -4.555341
0.723137 -3.832205 35920.410171

HLA B*7301 1:90-98 9 PYELNITSA 1.095994 -0.320723 -4.607951
0.775271 -3.832680 40546.274417

HLA B*5701 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.402923
0.570132 -3.832791 25288.504479

HLA B*1503 1:11-19 9 AVVLLCCSG 0.891360 -0.444728 -4.279545
0.446632 -3.832913 19034.638828

HLA B*5801 1:164-172 9 GELSKQTGQ 0.717063 -0.197435 -4.352900
0.519628 -3.833272 22537.215709

HLA A*0211 1:36-44 9 DTGQACQIQ 0.956574 -0.260344 -4.529706
0.696230 -3.833476 33861.489373

HLA B*5401 1:135-143 9 DQAYRKPIT 1.136670 -0.428671 -4.541832
0.707999 -3.833833 34820.239057

HLA A*6802 1:203-211 9 PGELLPEAA 1.144110 -0.557015 -4.420995
0.587095 -3.833900 26363.033728

HLA A*2603 1:65-73 9 SLENYIAQT 1.098356 -0.294270 -4.638034
0.804086 -3.833948 43454.400358

HLA A*3101 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.306592
0.472542 -3.834050 20257.782878

HLA A*8001 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.398396
0.564331 -3.834065 25026.244837

HLA B*0702 1:40-48 9 ACQIQMSDP 0.533748 0.079890 -4.447763
0.613638 -3.834125 28039.035333

HLA B*4801 1:203-211 9 PGELLPEAA 1.144110 -0.557015 -4.421315
0.587095 -3.834220 26382.437334

HLA B*7301 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.482521
0.648272 -3.834249 30375.354073

HLA A*2301 1:135-143 9 DQAYRKPIT 1.136670 -0.428671 -4.542562
0.707999 -3.834563 34878.872568

HLA A*2902 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.427901
0.592876 -3.835025 26785.547121

HLA B*3501 1:94-102 9 NITSATYQS 1.243610 -0.899139 -4.179499
0.344471 -3.835028 15118.157670

HLA B*4402 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.401518
0.566374 -3.835144 25206.825483

HLA A*2602 1:90-98 9 PYELNITSA 1.095994 -0.320723 -4.610578
0.775271 -3.835307 40792.251784

HLA A*1101 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.428591
0.592876 -3.835715 26828.183630

HLA B*5401 1:169-177 9 QTGQQVSIA 0.950594 -0.262137 -4.524194
0.688457 -3.835737 33434.448545

HLA B*0702 1:165-173 9 ELSKQTGQQ 0.723302 -0.142086 -4.417004
0.581216 -3.835787 26121.830692

HLA B*4001 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.374036
0.537766 -3.836270 23661.170691

HLA B*1509 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.429165
0.592876 -3.836289 26863.620564

HLA B*1509 1:17-25 9 CSGVATAAP 0.698375 -0.030411 -4.504266
0.667964 -3.836302 31934.920013

HLA B*3801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.534135	0.697746	-3.836389	34208.563347
HLA B*0803	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.470506	0.634040	-3.836466	29546.502710
HLA B*4002	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.623018	0.786460	-3.836559	41977.657780
HLA B*2705	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.458517	0.621958	-3.836559	28741.978538
HLA B*5701	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.417833	0.581216	-3.836617	26171.762976
HLA B*0801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.407039	0.570132	-3.836907	25529.331597
HLA A*2402	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.539964	0.702905	-3.837058	34670.803599
HLA B*4001	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.398548	0.561410	-3.837138	25035.046683
HLA B*1502	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.612422	0.775271	-3.837151	40965.855174
HLA A*2501	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.456585	0.619394	-3.837192	28614.448772
HLA A*3002	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.415350	0.578083	-3.837267	26022.533291
HLA B*1509	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.508382	0.671022	-3.837360	32239.042179
HLA A*2301	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.540272	0.702905	-3.837366	34695.383350
HLA B*0702	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.404058	0.566374	-3.837684	25354.669152
HLA A*2403	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.375622	0.537766	-3.837856	23747.731550
HLA B*1501	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.399385	0.561410	-3.837975	25083.308653

HLA A*0206	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.460027	0.621958	-3.838069	28842.133294
HLA B*1501	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.402902	0.564800	-3.838102	25287.273237
HLA A*3301	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.614760	0.776623	-3.838137	41186.962364
HLA B*4403	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.592409	0.754093	-3.838316	39120.924738
HLA B*1517	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.472637	0.634040	-3.838597	29691.836856
HLA A*2403	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.403543	0.564800	-3.838743	25324.647597
HLA B*1517	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.460702	0.621958	-3.838744	28886.949474
HLA B*5701	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.426016	0.587095	-3.838921	26669.583585
HLA A*6802	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.409156	0.570132	-3.839024	25654.073244
HLA A*0203	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.183559	0.344471	-3.839088	15260.149223
HLA B*1503	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.452810	0.613638	-3.839171	28366.761789
HLA A*2603	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.615796	0.776623	-3.839173	41285.341925
HLA A*3001	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.263082	0.423714	-3.839368	18326.595711
HLA A*2902	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.453073	0.613638	-3.839435	28383.954633
HLA B*4402	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.426815	0.587095	-3.839720	26718.683754
HLA A*3101	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.274223	0.434427	-3.839796	18802.822972

HLA B*1517	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.453550	0.613638	-3.839911	28415.143228
HLA B*4403	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.616724	0.776623	-3.840101	41373.659158
HLA A*2902	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.401727	0.561410	-3.840317	25218.964991
HLA B*4801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.421818	0.581216	-3.840601	26412.998398
HLA A*1101	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.489631	0.648272	-3.841358	30876.700886
HLA A*3001	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-3.645550	-0.196092	-3.841643	4421.302296
HLA B*1517	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.412462	0.570132	-3.842330	25850.089778
HLA B*1801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.490761	0.648415	-3.842346	30957.151527
HLA B*3501	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.435360	0.592876	-3.842484	27249.600312
HLA B*1509	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.406854	0.564331	-3.842523	25518.423171
HLA A*0250	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.545347	0.702788	-3.842559	35103.189454
HLA B*5301	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.549484	0.706847	-3.842637	35439.209095
HLA A*3002	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.540481	0.697746	-3.842735	34712.092510
HLA A*3002	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.568247	0.725355	-3.842892	37003.858221
HLA B*1503	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.491311	0.648272	-3.843038	30996.365435
HLA A*2402	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.556746	0.713674	-3.843072	36036.804956

HLA B*1503	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.491701	0.648415	-3.843286	31024.213964
HLA A*1101	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.444077	0.600517	-3.843559	27802.043975
HLA A*2902	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.407921	0.564331	-3.843590	25581.175738
HLA A*0301	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.363410	0.519628	-3.843782	23089.233081
HLA B*1501	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.363588	0.519628	-3.843960	23098.728207
HLA B*1801	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.363715	0.519628	-3.844087	23105.477117
HLA B*0802	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.423892	0.579719	-3.844173	26539.473339
HLA A*6901	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.202134	0.357949	-3.844184	15926.993722
HLA A*3301	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.552294	0.707999	-3.844295	35669.252250
HLA A*3002	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.457946	0.613638	-3.844307	28704.219070
HLA A*0101	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.382083	0.537766	-3.844317	24103.672321
HLA B*4801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.422494	0.578083	-3.844412	26454.183195
HLA A*2403	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.384064	0.539612	-3.844452	24213.849042
HLA B*5401	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.463878	0.619394	-3.844484	29099.008108
HLA B*4002	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.551382	0.706847	-3.844535	35594.459694
HLA B*3501	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.116082	0.271476	-3.844606	13064.162422

HLA A*2301	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.512797	0.667964	-3.844833	32568.429203
HLA A*0202	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.493106	0.648272	-3.844833	31124.743348
HLA B*1502	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.558511	0.713674	-3.844837	36183.514076
HLA B*4601	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.409814	0.564800	-3.845014	25692.962685
HLA B*5301	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.558701	0.713674	-3.845027	36199.373203
HLA B*2705	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-3.938536	0.093374	-3.845161	8680.319057
HLA A*2402	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.585828	0.740601	-3.845227	38532.590276
HLA B*5801	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.318309	0.472542	-3.845767	20811.759270
HLA A*0206	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.513777	0.667964	-3.845812	32641.984033
HLA B*4403	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.446438	0.600517	-3.845921	27953.613645
HLA A*2602	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.494661	0.648415	-3.846246	31236.411684
HLA B*0802	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.427623	0.581216	-3.846407	26768.453571
HLA B*3801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.554599	0.707999	-3.846600	35859.055791
HLA B*4501	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.621874	0.775271	-3.846603	41867.208331
HLA B*7301	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.517693	0.671022	-3.846671	32937.690131
HLA A*0212	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.411224	0.564331	-3.846893	25776.495831

HLA A*0212	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.434160	0.587095	-3.847064	27174.374091
HLA B*5401	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.549937	0.702788	-3.847150	35476.230802
HLA B*4501	1:93-101	9	LNITSATYQ	0.940219	-0.153759	-4.633697	0.786460	-3.847237	43022.595967
HLA B*4801	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.299978	0.452621	-3.847357	19951.617573
HLA A*3001	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.231653	0.384238	-3.847415	17047.187520
HLA B*1801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.066038	0.218305	-3.847732	11642.266614
HLA A*0203	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.417920	0.570132	-3.847787	26177.002195
HLA A*0212	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.426068	0.578083	-3.847985	26672.757922
HLA B*1501	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.282514	0.434427	-3.848087	19165.245631
HLA A*2602	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.600085	0.751912	-3.848173	39818.498519
HLA B*2705	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.461869	0.613638	-3.848231	28964.722754
HLA B*3801	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.555696	0.707433	-3.848263	35949.765300
HLA A*3201	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.528449	0.680076	-3.848373	33763.626071
HLA A*2602	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.573750	0.725355	-3.848395	37475.678297
HLA A*0206	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.544752	0.696230	-3.848522	35055.176515
HLA A*0216	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.462358	0.613638	-3.848720	28997.333854

HLA A*2902	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.426909	0.578083	-3.848826	26724.466184
HLA A*0206	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.536590	0.687624	-3.848966	34402.503474
HLA A*2902	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.419116	0.570132	-3.848983	26249.183401
HLA B*4402	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.429009	0.579719	-3.849291	26854.030548
HLA B*7301	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.547362	0.697746	-3.849616	35266.506137
HLA A*2902	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.436906	0.587095	-3.849811	27346.773759
HLA A*2601	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.389468	0.539612	-3.849855	24517.018007
HLA A*0212	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.414664	0.564800	-3.849863	25981.458269
HLA A*6801	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.556974	0.706847	-3.850127	36055.720565
HLA A*2402	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.558433	0.707999	-3.850434	36177.054942
HLA A*0206	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-3.805574	-0.044895	-3.850468	6391.070868
HLA B*4403	1:111-119	9	AVVLKVYQN	1.224563	-0.434023	-4.641142	0.790540	-3.850602	43766.531486
HLA B*0802	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.473159	0.621958	-3.851201	29727.518037
HLA B*4402	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.432444	0.581216	-3.851228	27067.268166
HLA B*4403	1:65-73	9	SLENYIAQT	1.098356	-0.294270	-4.655418	0.804086	-3.851332	45229.064061
HLA B*0801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.298138	0.446632	-3.851507	19867.282400

HLA A*2402	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.540657	0.688457	-3.852200	34726.179510
HLA A*8001	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.418622	0.566374	-3.852249	26219.379248
HLA A*2301	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.540908	0.688457	-3.852451	34746.286861
HLA A*6801	1:117-125	9	YQNAGGTHP	0.729126	0.047497	-4.629298	0.776623	-3.852676	42589.091517
HLA B*4403	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.515774	0.662917	-3.852856	32792.430763
HLA B*1501	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.211146	0.357949	-3.853197	16260.969429
HLA B*0803	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.432919	0.579719	-3.853200	27096.863380
HLA B*5101	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.487241	0.634040	-3.853202	30707.288155
HLA A*0212	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.420049	0.566374	-3.853675	26305.620038
HLA B*4002	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.628953	0.775271	-3.853682	42555.235848
HLA B*5301	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.561123	0.707433	-3.853690	36401.842794
HLA A*0201	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.393572	0.539612	-3.853960	24749.828638
HLA B*3801	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.550238	0.696230	-3.854008	35500.805387
HLA A*2402	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.579367	0.725355	-3.854012	37963.576570
HLA A*0250	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.550304	0.696230	-3.854074	35506.183346
HLA A*3301	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.612753	0.758478	-3.854275	40997.115619

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HLA A*1101	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.275400
	0.421102	-3.854298	18853.854412

HLA A*2501	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.434197
	0.579719	-3.854478	27176.726358

HLA B*0801	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.421047
	0.566374	-3.854673	26366.171579

HLA B*7301	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.595485
	0.740601	-3.854884	39398.944566

HLA A*3002	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.455472
	0.600517	-3.854954	28541.167098

HLA A*3001	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.276157
	0.421102	-3.855055	18886.726153

HLA B*3501	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.416602
	0.561410	-3.855192	26097.676794

HLA A*1101	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.433314
	0.578083	-3.855231	27121.501867

HLA A*2403	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.442423
	0.587095	-3.855327	27696.359549

HLA B*3801	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.543006
	0.687624	-3.855382	34914.553373

HLA A*0201	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.141573
	0.286028	-3.855546	13853.945775

HLA B*5301	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.596572
	0.740601	-3.855972	39497.753898

HLA B*0803	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.420657
	0.564331	-3.856326	26342.504289

HLA A*2403	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.420847
	0.564331	-3.856517	26354.050131

HLA A*6801	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.564535
	0.707999	-3.856536	36688.911066

HLA A*3002	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.527596
	0.671022	-3.856574	33697.386469
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HLA B*4002	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.610723	0.754093	-3.856630	40805.936336
HLA B*3801	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.505133	0.648415	-3.856718	31998.733741
HLA B*4801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.418141	0.561410	-3.856731	26190.317360
HLA A*0202	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.554686	0.697746	-3.856940	35866.234270
HLA B*5701	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.421834	0.564800	-3.857034	26413.998657
HLA A*0202	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.544715	0.687624	-3.857090	35052.142333
HLA A*0219	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.215150	0.357949	-3.857200	16411.563436
HLA A*6801	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.524009	0.666762	-3.857246	33420.162342
HLA B*4402	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.435405	0.578083	-3.857322	27252.401385
HLA B*3501	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.427487	0.570132	-3.857355	26760.055655
HLA B*4001	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.423782	0.566374	-3.857408	26532.726143
HLA A*0219	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.471296	0.613638	-3.857657	29600.258902
HLA A*0219	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.419165	0.561410	-3.857755	26252.165679
HLA A*0212	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.419245	0.561410	-3.857835	26256.994848
HLA B*5401	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.545527	0.687624	-3.857903	35117.815136
HLA A*3201	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.520992	0.662917	-3.858075	33188.820362

HLA B*4402	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.422419	0.564331	-3.858089	26449.603937
HLA A*2501	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.451172	0.592876	-3.858296	28260.000854
HLA B*0803	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.526454	0.667964	-3.858490	33608.905463
HLA B*3501	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.396662	0.537766	-3.858896	24926.526794
HLA A*8001	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.446107	0.587095	-3.859011	27932.298916
HLA B*4002	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.584487	0.725355	-3.859132	38413.744959
HLA B*1502	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.130615	0.271476	-3.859139	13508.759982
HLA A*8001	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.437557	0.578083	-3.859474	27387.784694
HLA A*0101	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.399258	0.539612	-3.859646	25075.982035
HLA B*5101	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.508091	0.648415	-3.859676	32217.422635
HLA A*2501	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.481894	0.621958	-3.859936	30331.510357
HLA B*0702	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.447281	0.587095	-3.860186	28007.956515
HLA B*4403	1:95-103	9	ITSATYQSA	0.951011	-0.171324	-4.639996	0.779687	-3.860308	43651.139096
HLA B*4801	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.426719	0.566374	-3.860345	26712.758061
HLA B*4601	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.421851	0.561410	-3.860440	26414.998953
HLA B*0801	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.398349	0.537766	-3.860583	25023.537199

HLA B*1501	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.018625	0.157927	-3.860698	10438.183643
HLA A*6802	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.245026	0.384238	-3.860788	17580.288877
HLA B*5701	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.422363	0.561410	-3.860953	26446.170014
HLA B*0803	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.461540	0.600517	-3.861023	28942.793628
HLA B*5401	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.448160	0.587095	-3.861065	28064.682340
HLA A*0201	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.399239	0.537766	-3.861473	25074.896793
HLA B*3901	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.483492	0.621958	-3.861534	30443.297121
HLA A*0202	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.019621	0.157927	-3.861695	10462.154157
HLA B*0802	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.426122	0.564331	-3.861791	26676.076952
HLA B*3801	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.528581	0.666762	-3.861818	33773.856439
HLA B*1517	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.462386	0.600517	-3.861869	28999.216384
HLA A*0301	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.285916	0.423714	-3.862203	19315.966523
HLA A*3201	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.560172	0.697746	-3.862426	36322.173480
HLA B*1503	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.443682	0.581216	-3.862466	27776.787250
HLA B*5301	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.529351	0.666762	-3.862589	33833.839446
HLA A*2902	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.207289	0.344471	-3.862817	16117.162288

HLA A*2603	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.621406	0.758478	-3.862929	41822.159690
HLA A*0212	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.444300	0.581216	-3.863084	27816.336215
HLA B*1502	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.482538	0.619394	-3.863144	30376.504386
HLA A*0219	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.450289	0.587095	-3.863194	28202.575094
HLA A*3201	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.566076	0.702788	-3.863288	36819.347190
HLA B*4402	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.433502	0.570132	-3.863369	27133.242353
HLA B*4801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.433795	0.570132	-3.863663	27151.597037
HLA B*1503	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-3.955734	0.091985	-3.863749	9030.960001
HLA A*2602	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.571816	0.707999	-3.863817	37309.194778
HLA A*3101	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.383768	0.519628	-3.864140	24197.349392
HLA A*0203	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.429193	0.564800	-3.864392	26865.364571
HLA B*7301	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.498514	0.634040	-3.864474	31514.780995
HLA A*2501	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.431037	0.566374	-3.864663	26979.698008
HLA A*3002	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.484589	0.619394	-3.865195	30520.306860
HLA A*2301	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.528303	0.662917	-3.865386	33752.303206
HLA B*0802	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.465939	0.600517	-3.865421	29237.395588

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HLA B*1517	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.289375
	0.423714	-3.865661	19470.400547

HLA A*3201	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.613895
	0.748062	-3.865833	41105.047311

HLA B*7301	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.567603
	0.701666	-3.865938	36949.047679

HLA A*2902	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.432315
	0.566374	-3.865941	27059.215663

HLA B*5101	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.487911
	0.621958	-3.865953	30754.669734

HLA B*4403	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.572854
	0.706847	-3.866007	37398.514189

HLA B*5401	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.562270
	0.696230	-3.866040	36498.071569

HLA A*1101	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.430856
	0.564800	-3.866056	26968.461646

HLA B*4002	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.624606
	0.758478	-3.866129	42131.454698

HLA B*1509	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.432820
	0.566374	-3.866447	27090.707256

HLA B*7301	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.569577
	0.702788	-3.866789	37117.337581

HLA A*0212	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.436995
	0.570132	-3.866863	27352.396171

HLA A*6801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.446661
	0.579719	-3.866942	27967.983803

HLA B*1801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.406725
	0.539612	-3.867112	25510.831449

HLA B*7301	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.555837
	0.688457	-3.867380	35961.436249

HLA B*0803	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.481156
	0.613638	-3.867518	30280.029800
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HLA A*3301	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.570467	0.702788	-3.867680	37193.519112
HLA B*4501	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.610394	0.742712	-3.867682	40775.042254
HLA A*0250	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.570608	0.702905	-3.867703	37205.593841
HLA B*1801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.432052	0.564331	-3.867721	27042.825246
HLA A*0216	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.437926	0.570132	-3.867793	27411.056462
HLA B*0702	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.191575	0.323743	-3.867833	15544.445096
HLA A*2402	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.516161	0.648272	-3.867889	32821.715395
HLA B*5401	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.438048	0.570132	-3.867915	27418.768667
HLA A*0206	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.097370	0.229395	-3.867975	12513.254359
HLA B*4601	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.406006	0.537766	-3.868240	25468.635090
HLA A*0211	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.536355	0.667964	-3.868391	34383.897135
HLA B*4402	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.429888	0.561410	-3.868478	26908.419273
HLA B*1502	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.593957	0.725355	-3.868603	39260.644320
HLA B*0801	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.292474	0.423714	-3.868760	19609.831262
HLA B*0802	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.435400	0.566374	-3.869026	27252.106522
HLA A*3201	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.565470	0.696230	-3.869240	36767.992382

HLA A*6901	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.388939	0.519628	-3.869311	24487.193434
HLA A*2402	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.571092	0.701666	-3.869426	37247.080250
HLA A*3001	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.270072	0.400567	-3.869504	18623.938000
HLA B*4403	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.617607	0.748062	-3.869546	41457.903729
HLA B*4501	1:153-161	9	DPLPVVFPI	0.780193	-0.026100	-4.624169	0.754093	-3.870077	42089.081691
HLA A*0203	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.431493	0.561410	-3.870083	27008.028564
HLA B*4501	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.610690	0.740601	-3.870090	40802.845874
HLA A*2603	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.622210	0.751912	-3.870298	41899.609927
HLA B*0802	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.484039	0.613638	-3.870401	30481.695219
HLA B*1503	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.390076	0.519628	-3.870448	24551.394381
HLA A*0202	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.566882	0.696230	-3.870652	36887.732303
HLA A*0301	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.343422	0.472542	-3.870880	22050.702957
HLA B*7301	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.613660	0.742712	-3.870948	41082.815950
HLA A*1101	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.484878	0.613638	-3.871239	30540.622330
HLA A*6801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.449325	0.578083	-3.871243	28140.089568
HLA A*2902	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.410897	0.539612	-3.871285	25757.119847

HLA A*0201	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.390988	0.519628	-3.871360	24602.982790
HLA A*2601	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.391260	0.519628	-3.871632	24618.427167
HLA B*0702	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.409755	0.537766	-3.871989	25689.488018
HLA A*2301	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.543014	0.671022	-3.871991	34915.120030
HLA A*0250	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.580135	0.707999	-3.872136	38030.794857
HLA A*2902	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.256414	0.384238	-3.872176	18047.371609
HLA B*1509	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.494170	0.621958	-3.872212	31201.113668
HLA B*3501	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.344776	0.472542	-3.872234	22119.522236
HLA B*0801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.437082	0.564800	-3.872282	27357.871736
HLA A*2402	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.273283	0.400567	-3.872716	18762.178489
HLA A*0202	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.434195	0.561410	-3.872785	27176.579336
HLA A*2402	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.535869	0.662917	-3.872951	34345.413980
HLA A*8001	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.434629	0.561410	-3.873219	27203.792073
HLA A*0219	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.439676	0.566374	-3.873302	27521.756021
HLA B*3801	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.576254	0.702905	-3.873349	37692.422729
HLA A*1101	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.434909	0.561410	-3.873499	27221.310882

HLA A*2402	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.571435	0.697746	-3.873689	37276.511247
HLA A*3101	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.326384	0.452621	-3.873763	21202.348747
HLA A*2902	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.294976	0.421102	-3.873874	19723.140034
HLA B*1502	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.581446	0.707433	-3.874013	38145.772562
HLA B*1501	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.346716	0.472542	-3.874174	22218.586007
HLA A*2501	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.487951	0.613638	-3.874313	30757.498314
HLA A*0101	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.393979	0.519628	-3.874351	24773.003114
HLA A*0212	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.394190	0.519628	-3.874562	24785.067778
HLA B*1503	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.347151	0.472542	-3.874609	22240.834154
HLA B*0801	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.232597	0.357949	-3.874648	17084.301667
HLA A*0219	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.438997	0.564331	-3.874667	27478.760532
HLA B*7301	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.454485	0.579719	-3.874766	28476.390806
HLA A*8001	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.445176	0.570132	-3.875044	27872.523155
HLA A*0206	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-3.967444	0.092119	-3.875325	9277.773205
HLA A*3001	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.307424	0.432006	-3.875417	20296.615745
HLA B*4501	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.578340	0.702788	-3.875553	37873.932068

HLA B*4801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.440618	0.564800	-3.875818	27581.525577
HLA A*2402	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.583676	0.707433	-3.876243	38342.115960
HLA A*2301	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.524955	0.648272	-3.876683	33493.103974
HLA B*1801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.498843	0.621958	-3.876885	31538.658842
HLA A*6801	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.349470	0.472542	-3.876928	22359.908054
HLA B*0802	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.469815	0.592876	-3.876940	29499.546131
HLA A*2603	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.600177	0.723137	-3.877040	39826.900538
HLA A*0219	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.447441	0.570132	-3.877309	28018.261767
HLA A*3101	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.278927	0.401614	-3.877313	19007.575585
HLA B*5701	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.415133	0.537766	-3.877367	26009.584844
HLA B*0803	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.525848	0.648272	-3.877576	33562.028508
HLA B*1502	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.441920	0.564331	-3.877589	27664.313576
HLA B*7301	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.573926	0.696230	-3.877695	37490.886827
HLA B*5101	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.457553	0.579719	-3.877835	28678.297912
HLA B*4002	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.645745	0.767355	-3.878390	44232.834567
HLA A*3002	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.471326	0.592876	-3.878450	29602.340719

HLA A*0216	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.443348	0.564800	-3.878548	27755.457198
HLA B*5301	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.549611	0.671022	-3.878589	35449.563606
HLA A*3201	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.601932	0.723137	-3.878795	39988.174147
HLA A*2603	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.559049	0.680076	-3.878972	36228.368330
HLA B*2705	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.466075	0.587095	-3.878980	29246.570950
HLA B*2705	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.460222	0.581216	-3.879006	28855.086920
HLA A*2603	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.654334	0.775271	-3.879064	45116.405176
HLA B*4501	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.637578	0.758478	-3.879100	43408.818085
HLA A*3301	1:129-137	9	YKAFDWDQA	0.955276	-0.207214	-4.627236	0.748062	-3.879174	42387.278004
HLA A*2403	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.446107	0.566374	-3.879733	27932.298916
HLA B*2705	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.446588	0.566374	-3.880215	27963.293782
HLA A*3301	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.622950	0.742712	-3.880238	41971.072557
HLA A*3201	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.548471	0.667964	-3.880507	35356.673090
HLA A*3201	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.528881	0.648272	-3.880609	33797.251779
HLA A*0206	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.447091	0.566374	-3.880717	27995.686089
HLA B*3901	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.494396	0.613638	-3.880757	31217.322155

HLA A*0211	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.304665	0.423714	-3.880951	20168.116175
HLA A*0202	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.503098	0.621958	-3.881140	31849.171446
HLA A*6801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.211762	0.330347	-3.881415	16284.033922
HLA B*5401	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.459513	0.578083	-3.881430	28807.982358
HLA B*5301	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.584226	0.702788	-3.881438	38390.684519
HLA B*5301	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.569901	0.688457	-3.881444	37145.058422
HLA A*0219	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.459572	0.578083	-3.881489	28811.878821
HLA A*2902	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.419508	0.537766	-3.881742	26272.908981
HLA B*4501	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.569527	0.687624	-3.881903	37113.121006
HLA B*1509	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.463469	0.581216	-3.882253	29071.629497
HLA A*1101	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.316732	0.434427	-3.882305	20736.348797
HLA B*5101	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.460518	0.578083	-3.882436	28874.762581
HLA B*2705	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.460591	0.578083	-3.882509	28879.605474
HLA A*3001	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.174297	0.291433	-3.882864	14938.160130
HLA B*4801	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.403003	0.519628	-3.883375	25293.156379
HLA B*3901	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.461684	0.578083	-3.883601	28952.346420

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HLA A*6801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.551728
	0.667964	-3.883763	35622.777579

HLA B*4501	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.546761
	0.662917	-3.883844	35217.698243

HLA B*0801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.423516
	0.539612	-3.883904	26516.511181

HLA A*3002	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.546961
	0.662917	-3.884043	35233.896494

HLA A*3301	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.609513
	0.725355	-3.884159	40692.405433

HLA A*3301	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.607295
	0.723137	-3.884159	40485.121692

HLA B*0802	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.462295
	0.578083	-3.884212	28993.098610

HLA B*1502	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.580547
	0.696230	-3.884316	38066.816823

HLA A*3301	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.636246
	0.751912	-3.884334	43275.869574

HLA B*3801	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.503890
	0.619394	-3.884496	31907.289672

HLA B*4501	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.652006
	0.767355	-3.884652	44875.174320

HLA A*0206	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.455028
	0.570132	-3.884895	28511.999552

HLA B*5401	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.565101
	0.680076	-3.885025	36736.776651

HLA B*1517	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.423046
	0.537766	-3.885281	26487.836419

HLA A*1101	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.472534
	0.587095	-3.885438	29684.769997

HLA B*4002	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.588258
	0.702788	-3.885470	38748.738842
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HLA A*8001	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.405108	0.519628	-3.885480	25416.056525
HLA A*0216	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.446988	0.561410	-3.885577	27989.022925
HLA A*2403	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.446995	0.561410	-3.885585	27989.477182
HLA B*4501	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.599439	0.713674	-3.885765	39759.303805
HLA B*1501	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.425445	0.539612	-3.885833	26634.546703
HLA A*3002	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.287472	0.401614	-3.885858	19385.267716
HLA B*3801	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.556934	0.671022	-3.885912	36052.404741
HLA B*1503	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.423878	0.537766	-3.886112	26538.611899
HLA B*5301	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.594190	0.707999	-3.886191	39281.677129
HLA A*0216	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.464543	0.578083	-3.886460	29143.592771
HLA B*5701	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.426082	0.539612	-3.886470	26673.623716
HLA B*4002	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.629186	0.742712	-3.886473	42578.033644
HLA A*0216	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.473593	0.587095	-3.886498	29757.285107
HLA B*5401	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.520595	0.634040	-3.886555	33158.490644
HLA B*4601	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.406212	0.519628	-3.886585	25480.762836
HLA B*4001	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.451442	0.564800	-3.886642	28277.587924

HLA A*2501 1:18-26 9 SGVATAAPK 0.424227 0.140104 -4.451008
0.564331 -3.886677 28249.301037

HLA B*5401 1:195-203 9 DGVIFFFNP 0.675455 -0.114045 -4.448245
0.561410 -3.886834 28070.148638

HLA B*4601 1:133-141 9 DWDQAYRKP 0.647933 -0.108321 -4.426806
0.539612 -3.887193 26718.105580

HLA B*7301 1:17-25 9 CSGVATAAP 0.698375 -0.030411 -4.555172
0.667964 -3.887208 35906.421464

HLA A*0211 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.453785
0.566374 -3.887411 28430.519664

HLA A*2402 1:17-25 9 CSGVATAAP 0.698375 -0.030411 -4.555407
0.667964 -3.887443 35925.851695

HLA A*6802 1:91-99 9 YELNITSAT 0.787532 -0.429583 -4.245510
0.357949 -3.887561 17599.891925

HLA B*3901 1:115-123 9 KVYQNAGGT 0.678003 -0.098284 -4.467318
0.579719 -3.887599 29330.389584

HLA A*3201 1:88-96 9 EAPYELNIT 1.024679 -0.321774 -4.590743
0.702905 -3.887838 38971.159477

HLA B*4402 1:74-82 9 RDKFLSAAT 0.783794 -0.331173 -4.340850
0.452621 -3.888229 21920.464508

HLA B*0801 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.360910
0.472542 -3.888367 22956.710411

HLA A*2301 1:41-49 9 CQIQMSDPA 0.720301 -0.119784 -4.488905
0.600517 -3.888388 30825.128789

HLA B*4801 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.426235
0.537766 -3.888469 26683.004953

HLA A*6801 1:90-98 9 PYELNITSA 1.095994 -0.320723 -4.663815
0.775271 -3.888544 46112.074442

HLA A*2602 1:41-49 9 CQIQMSDPA 0.720301 -0.119784 -4.489137
0.600517 -3.888620 30841.642503

HLA A*8001 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.426632
0.537766 -3.888866 26707.411613

HLA B*5401	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.551855	0.662917	-3.888937	35633.185724
HLA A*0219	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.454140	0.564800	-3.889339	28453.753853
HLA A*0212	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.429150	0.539612	-3.889538	26862.748603
HLA A*0203	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.409283	0.519628	-3.889655	25661.568767
HLA B*3801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.482660	0.592876	-3.889784	30385.050931
HLA A*0216	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.456412	0.566374	-3.890038	28602.995791
HLA B*5401	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.483196	0.592876	-3.890320	30422.552639
HLA B*5301	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.524556	0.634040	-3.890516	33462.315157
HLA A*2602	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.558548	0.667964	-3.890584	36186.646193
HLA B*0801	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.410275	0.519628	-3.890647	25720.220365
HLA A*0250	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.588504	0.697746	-3.890758	38770.755865
HLA A*3002	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.455178	0.564331	-3.890847	28521.873053
HLA A*3301	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.594164	0.702905	-3.891259	39279.339594
HLA A*3201	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.491830	0.600517	-3.891313	31033.446403
HLA B*7301	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.558116	0.666762	-3.891354	36150.643218
HLA A*0216	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.249427	0.357949	-3.891477	17759.330622

HLA B*3901	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.472912	0.581216	-3.891696	29710.636462
HLA A*3101	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.315654	0.423714	-3.891940	20684.921435
HLA A*3201	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.600108	0.707999	-3.892109	39820.652714
HLA A*2602	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.594911	0.702788	-3.892124	39346.971758
HLA B*3801	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.457006	0.564331	-3.892675	28642.171571
HLA B*1517	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.473983	0.581216	-3.892767	29784.020390
HLA A*3201	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.514857	0.621958	-3.892899	32723.316368
HLA B*3801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.556077	0.662917	-3.893159	35981.285558
HLA B*7301	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.596077	0.702905	-3.893171	39452.693463
HLA B*4403	1:90-98	9	PYELNITSA	1.095994	-0.320723	-4.668497	0.775271	-3.893226	46611.940548
HLA B*5101	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.507017	0.613638	-3.893379	32137.869259
HLA B*0803	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.486335	0.592876	-3.893459	30643.231573
HLA A*2603	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.541851	0.648272	-3.893578	34821.746078
HLA B*0702	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.413489	0.519628	-3.893861	25911.274828
HLA A*0250	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.581500	0.687624	-3.893876	38150.519239
HLA A*2501	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.472019	0.578083	-3.893936	29649.621325

HLA A*6901	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.366497	0.472542	-3.893955	23253.949831
HLA B*2705	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.464198	0.570132	-3.894065	29120.425434
HLA B*5301	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.591946	0.697746	-3.894200	39079.253894
HLA B*5801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.341216	0.446632	-3.894584	21938.971933
HLA B*1517	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.487476	0.592876	-3.894601	30723.904952
HLA B*0702	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.456191	0.561410	-3.894780	28588.454019
HLA B*4403	1:78-86	9	LSAATSSTP	0.733359	0.025119	-4.653291	0.758478	-3.894813	45008.166034
HLA B*4403	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.602855	0.707999	-3.894856	40073.282904
HLA B*4801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.434667	0.539612	-3.895055	27206.146887
HLA B*1502	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.597926	0.702788	-3.895138	39621.024659
HLA B*1509	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.482467	0.587095	-3.895372	30371.574780
HLA A*3201	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.620810	0.725355	-3.895455	41764.730831
HLA A*2603	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.462170	0.566374	-3.895796	28984.786781
HLA A*2501	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.433624	0.537766	-3.895858	27140.876394
HLA A*2603	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.563896	0.667964	-3.895931	36634.963407
HLA B*5801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.187374	0.291433	-3.895941	15394.810383

HLA B*0803	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.518266	0.621958	-3.896308	32981.197017
HLA B*5101	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.489335	0.592876	-3.896459	30855.661077
HLA A*0301	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.343143	0.446632	-3.896511	22036.511795
HLA A*3101	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.434324	0.537766	-3.896558	27184.666764
HLA B*0803	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.477933	0.581216	-3.896716	30056.112306
HLA B*3801	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.564770	0.667964	-3.896805	36708.764729
HLA A*2301	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.545222	0.648415	-3.896807	35093.125965
HLA B*1509	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.475179	0.578083	-3.897097	29866.147691
HLA A*6901	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.331600	0.434427	-3.897173	21458.523220
HLA A*3201	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.531285	0.634040	-3.897245	33984.815009
HLA B*4501	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.169561	0.271476	-3.898084	14776.124741
HLA A*2902	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.462999	0.564800	-3.898199	29040.191649
HLA A*3301	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.546620	0.648272	-3.898348	35206.268667
HLA B*1509	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.478205	0.579719	-3.898487	30074.979853
HLA A*0219	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.285980	0.387379	-3.898601	19318.788155
HLA B*4403	1:161-169	9	IVQGELSKQ	0.821593	-0.054238	-4.666246	0.767355	-3.898892	46370.990986

HLA B*3501	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.463700	0.564800	-3.898899	29087.046464
HLA A*2603	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.624270	0.725355	-3.898916	42098.873813
HLA B*2705	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.460464	0.561410	-3.899054	28871.169991
HLA B*4002	1:31-39	9	ELKGTDTGQ	0.941370	-0.200769	-4.639944	0.740601	-3.899343	43645.944153
HLA B*1801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.480747	0.581216	-3.899531	30251.539992
HLA B*1502	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.548081	0.648272	-3.899809	35324.935580
HLA B*0702	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.470034	0.570132	-3.899901	29514.391668
HLA B*3801	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.548500	0.648272	-3.900227	35358.968473
HLA B*1502	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.534332	0.634040	-3.900292	34224.112301
HLA A*3002	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.466707	0.566374	-3.900333	29289.163304
HLA B*4501	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.623509	0.723137	-3.900373	42025.147368
HLA A*2602	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.608094	0.707433	-3.900661	40559.657027
HLA B*4403	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.626087	0.725355	-3.900732	42275.293371
HLA A*6802	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.440435	0.539612	-3.900823	27569.889419
HLA B*0702	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.478960	0.578083	-3.900877	30127.252668
HLA A*1101	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.471232	0.570132	-3.901100	29595.935597

HLA B*4402	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.373825	0.472542	-3.901283	23649.653107
HLA A*0212	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.325132	0.423714	-3.901418	21141.300449
HLA B*4402	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.439263	0.537766	-3.901497	27495.563914
HLA B*0802	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.488625	0.587095	-3.901530	30805.290672
HLA B*5801	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.325533	0.423714	-3.901820	21160.867125
HLA A*2603	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.603990	0.701666	-3.902324	40178.130371
HLA A*3001	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.232715	0.330347	-3.902367	17088.923501
HLA B*4403	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.645146	0.742712	-3.902433	44171.856480
HLA B*4402	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.442145	0.539612	-3.902533	27678.684751
HLA A*6901	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.349219	0.446632	-3.902587	22346.968584
HLA B*1801	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.489892	0.587095	-3.902796	30895.247842
HLA A*2501	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.473243	0.570132	-3.903111	29733.308214
HLA A*3101	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.442785	0.539612	-3.903172	27719.443636
HLA A*6801	1:149-157	9	QADTDPLPV	0.679726	0.062986	-4.646194	0.742712	-3.903481	44278.563482
HLA A*3201	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.551942	0.648415	-3.903527	35640.318986
HLA A*0202	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.287775	0.384238	-3.903537	19398.800945

HLA B*4002	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.592141	0.688457	-3.903684	39096.805232
HLA A*8001	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.468486	0.564800	-3.903685	29409.356752
HLA A*2402	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.574863	0.671022	-3.903841	37571.900026
HLA A*6901	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.356645	0.452621	-3.904024	22732.402683
HLA B*5701	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.423784	0.519628	-3.904156	26532.869683
HLA A*0206	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.482326	0.578083	-3.904244	30361.717969
HLA A*0212	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.305911	0.401614	-3.904296	20226.026011
HLA A*3001	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.248879	0.344471	-3.904408	17736.959014
HLA A*2902	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.424513	0.519628	-3.904885	26577.404380
HLA A*1101	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.471448	0.566374	-3.905074	29610.669450
HLA B*4501	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.602897	0.697746	-3.905151	40077.185350
HLA B*5301	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.592783	0.687624	-3.905158	39154.589954
HLA A*3001	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.191199	0.286028	-3.905172	15530.995922
HLA A*0301	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.357940	0.452621	-3.905319	22800.265635
HLA B*1801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.485219	0.579719	-3.905500	30564.588829
HLA A*2501	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.466935	0.561410	-3.905525	29304.537096

HLA B*4501	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.613005	0.707433	-3.905571	41020.854003
HLA B*5101	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.493538	0.587095	-3.906443	31155.740953
HLA A*1101	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.487700	0.581216	-3.906483	30739.699237
HLA A*0250	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.525933	0.619394	-3.906539	33568.565551
HLA B*1801	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.520411	0.613638	-3.906773	33144.501663
HLA B*4501	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.613872	0.706847	-3.907025	41102.823634
HLA A*0211	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.065074	0.157927	-3.907148	11616.472049
HLA A*3301	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.595752	0.688457	-3.907295	39423.250467
HLA B*4002	1:135-143	9	DQAYRKPIT	1.136670	-0.428671	-4.615328	0.707999	-3.907329	41240.919366
HLA A*0212	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.341848	0.434427	-3.907421	21970.922087
HLA B*1502	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.610453	0.702905	-3.907548	40780.557338
HLA A*3301	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.578683	0.671022	-3.907661	37903.858376
HLA A*2603	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.556152	0.648415	-3.907737	35987.515050
HLA A*2602	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.614894	0.706847	-3.908047	41199.664885
HLA A*2403	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.427708	0.519628	-3.908080	26773.667396
HLA B*5801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.329412	0.421102	-3.908311	21350.716794

HLA B*5101 1:195-203 9 DGVIFFFNP 0.675455 -0.114045 -4.470121
0.561410 -3.908711 29520.300034

HLA A*3201 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.615615
0.706847 -3.908768 41268.147624

HLA A*2603 1:129-137 9 YKAFDWDQA 0.955276 -0.207214 -4.657029
0.748062 -3.908968 45397.229291

HLA A*2402 1:53-61 9 NISLPSYYP 0.515820 0.118220 -4.543018
0.634040 -3.908978 34915.497805

HLA A*2301 1:53-61 9 NISLPSYYP 0.515820 0.118220 -4.543058
0.634040 -3.909018 34918.709066

HLA A*2603 1:170-178 9 TGQQVSIAP 0.814303 -0.116557 -4.606922
0.697746 -3.909176 40450.312482

HLA A*6801 1:49-57 9 AYNINISLP 0.584960 0.117828 -4.612006
0.702788 -3.909219 40926.647079

HLA B*4403 1:31-39 9 ELKGTDTGQ 0.941370 -0.200769 -4.649892
0.740601 -3.909291 44657.212621

HLA B*0802 1:152-160 9 TDPLPVVFP 0.730366 -0.165566 -4.474282
0.564800 -3.909481 29804.490709

HLA B*5301 1:162-170 9 VQGELSKQT 0.977010 -0.314093 -4.572408
0.662917 -3.909491 37360.092793

HLA B*1501 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.215300
0.305553 -3.909748 16417.246643

HLA A*6801 1:16-24 9 CCSGVATAA 0.892838 -0.221816 -4.581129
0.671022 -3.910107 38117.923539

HLA A*0219 1:164-172 9 GELSKQTGQ 0.717063 -0.197435 -4.429926
0.519628 -3.910298 26910.748518

HLA B*5801 1:74-82 9 RDKFLSAAT 0.783794 -0.331173 -4.363128
0.452621 -3.910507 23074.248722

HLA B*1517 1:11-19 9 AVVLLCCSG 0.891360 -0.444728 -4.357298
0.446632 -3.910667 22766.616783

HLA B*4403 1:177-185 9 APNAGLDPV 0.672482 0.029184 -4.612368
0.701666 -3.910702 40960.758214

HLA A*2301	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.532730	0.621958	-3.910772	34098.073575
HLA B*0802	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.481067	0.570132	-3.910935	30273.805599
HLA A*0203	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.345445	0.434427	-3.911018	22153.652827
HLA B*5401	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.559655	0.648415	-3.911240	36278.969431
HLA A*0202	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.489337	0.578083	-3.911255	30855.828003
HLA B*0702	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.476413	0.564800	-3.911612	29951.093853
HLA B*4601	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.384428	0.472542	-3.911886	24234.161664
HLA A*3301	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.625666	0.713674	-3.911992	42234.375054
HLA A*6801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.473570	0.561410	-3.912160	29755.675315
HLA B*5301	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.608397	0.696230	-3.912167	40587.972505
HLA A*3201	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.620204	0.707433	-3.912770	41706.478312
HLA B*4002	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.635915	0.723137	-3.912778	43242.871571
HLA B*1517	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.333898	0.421102	-3.912796	21572.358389
HLA B*3801	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.546874	0.634040	-3.912834	35226.844575
HLA A*3301	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.561358	0.648415	-3.912944	36421.541115
HLA A*0211	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.314895	0.401614	-3.913281	20648.808285

HLA A*3101 1:11-19 9 AVVLLCCSG 0.891360 -0.444728 -4.359986 0.446632 -3.913354 22907.954309

HLA B*5101 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.479850 0.566374 -3.913476 30189.087389

HLA B*0803 1:74-82 9 RDKFLSAAT 0.783794 -0.331173 -4.366393 0.452621 -3.913772 23248.415233

HLA A*2603 1:135-143 9 DQAYRKPIT 1.136670 -0.428671 -4.622179 0.707999 -3.914180 41896.663291

HLA A*2902 1:77-85 9 FLSAATSST 0.627583 -0.297236 -4.244537 0.330347 -3.914190 17560.517661

HLA A*3301 1:55-63 9 SLPSYYPDQ 0.698032 -0.017956 -4.594404 0.680076 -3.914327 39301.020257

HLA A*2603 1:32-40 9 LKGTDTGQA 1.058870 -0.351437 -4.622013 0.707433 -3.914579 41880.573784

HLA A*0206 1:203-211 9 PGELLPEAA 1.144110 -0.557015 -4.501700 0.587095 -3.914605 31746.817477

HLA A*0203 1:133-141 9 DWDQAYRKP 0.647933 -0.108321 -4.454819 0.539612 -3.915206 28498.274895

HLA A*0101 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.388103 0.472542 -3.915560 24440.078429

HLA A*2601 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.388417 0.472542 -3.915875 24457.802080

HLA A*3301 1:148-156 9 WQADTDPLP 0.614046 0.092801 -4.622788 0.706847 -3.915941 41955.408420

HLA A*2602 1:119-127 9 NAGGTHPTT 1.008013 -0.359741 -4.564267 0.648272 -3.915994 36666.290986

HLA B*1503 1:195-203 9 DGVIFFFNP 0.675455 -0.114045 -4.477557 0.561410 -3.916147 30030.107524

HLA B*2705 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.454196 0.537766 -3.916430 28457.448452

HLA A*3001 1:91-99 9 YELNITSAT 0.787532 -0.429583 -4.274470 0.357949 -3.916520 18813.506731

HLA A*2501	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.481748	0.564800	-3.916948	30321.338476
HLA A*2301	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.536393	0.619394	-3.916999	34386.873472
HLA A*2501	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.504339	0.587095	-3.917243	31940.276158
HLA A*6801	1:202-210	9	NPGELLPEA	1.188654	-0.463299	-4.642716	0.725355	-3.917361	43925.456630
HLA B*5101	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.498688	0.581216	-3.917472	31527.399889
HLA B*0802	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.478938	0.561410	-3.917528	30125.785838
HLA A*2603	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.631246	0.713674	-3.917572	42780.523941
HLA B*5301	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.585546	0.667964	-3.917582	38507.583549
HLA B*4002	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.537142	0.619394	-3.917748	34446.268014
HLA A*0250	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.551960	0.634040	-3.917921	35641.861501
HLA B*0803	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.505175	0.587095	-3.918080	32001.849865
HLA A*0211	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.531969	0.613638	-3.918330	34038.358682
HLA A*2402	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.519028	0.600517	-3.918510	33039.057288
HLA A*3001	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.305894	0.387379	-3.918515	20225.260082
HLA B*5101	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.483459	0.564800	-3.918658	30440.991480
HLA B*7301	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.598924	0.680076	-3.918848	39712.226238

HLA A*0250	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.511810	0.592876	-3.918934	32494.512742
HLA B*1509	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.438884	0.519628	-3.919257	27471.625920
HLA A*0206	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.480691	0.561410	-3.919281	30247.612468
HLA B*5801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.351317	0.432006	-3.919310	22455.188679
HLA B*2705	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.484206	0.564800	-3.919406	30493.405552
HLA A*2402	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.568106	0.648415	-3.919691	36991.848964
HLA B*2705	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.459842	0.539612	-3.920230	28829.809341
HLA A*0203	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-3.875494	-0.044895	-3.920389	7507.482127
HLA A*0216	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.344343	0.423714	-3.920630	22097.514985
HLA A*0202	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.485000	0.564331	-3.920669	30549.215050
HLA A*0201	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.393445	0.472542	-3.920903	24742.599427
HLA A*2601	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.367768	0.446632	-3.921136	23322.108021
HLA B*1517	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.373895	0.452621	-3.921274	23653.491678
HLA B*3901	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.486081	0.564800	-3.921280	30625.332941
HLA A*2902	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.393842	0.472542	-3.921300	24765.231219
HLA B*4002	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.634989	0.713674	-3.921315	43150.797712

HLA B*3901	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.508857	0.587095	-3.921761	32274.292184
HLA A*6801	1:208-216	9	PEAAGPTQV	0.855949	-0.104037	-4.673859	0.751912	-3.921947	47190.948743
HLA B*1517	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.486894	0.564800	-3.922093	30682.711787
HLA B*1502	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.593332	0.671022	-3.922310	39204.187686
HLA B*4001	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.374969	0.452621	-3.922348	23712.043012
HLA A*3301	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.590337	0.667964	-3.922373	38934.703010
HLA A*2602	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.620258	0.697746	-3.922512	41711.668065
HLA A*0203	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.080487	0.157927	-3.922560	12036.130099
HLA B*4403	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.625408	0.702788	-3.922620	42209.249369
HLA A*0301	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.343768	0.421102	-3.922666	22068.245835
HLA A*0250	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.176961	0.253787	-3.923174	15030.084650
HLA A*0211	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.358227	0.434427	-3.923800	22815.318925
HLA A*0250	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.545819	0.621958	-3.923861	35141.380992
HLA A*2501	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.463474	0.539612	-3.923862	29071.944048
HLA B*0702	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.463530	0.539612	-3.923918	29075.718917
HLA B*5101	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.488677	0.564331	-3.924346	30808.957261

HLA B*2705	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.377152	0.452621	-3.924531	23831.514658
HLA A*0211	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.511845	0.587095	-3.924750	32497.149724
HLA B*1502	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.491362	0.566374	-3.924989	31000.054767
HLA A*0201	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.371677	0.446632	-3.925045	23533.002752
HLA A*0206	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.269590	0.344471	-3.925119	18603.294994
HLA B*4501	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.628032	0.702905	-3.925127	42465.085581
HLA A*2301	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.486750	0.561410	-3.925340	30672.588064
HLA B*5301	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.503469	0.578083	-3.925387	31876.406561
HLA A*0250	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.525959	0.600517	-3.925441	33570.563235
HLA A*2602	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.613223	0.687624	-3.925599	41041.497595
HLA A*2501	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.256050	0.330347	-3.925702	18032.244639
HLA A*2301	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.539365	0.613638	-3.925726	34623.007448
HLA B*4403	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.622149	0.696230	-3.925919	41893.716863
HLA A*6901	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.347055	0.421102	-3.925953	22235.901563
HLA B*2705	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.445625	0.519628	-3.925997	27901.338406
HLA B*5301	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.606140	0.680076	-3.926063	40377.507123

HLA B*5701	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.398640	0.472542	-3.926098	25040.329276
HLA B*5301	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.527124	0.600517	-3.926607	33660.764260
HLA A*3301	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.488090	0.561410	-3.926679	30767.317165
HLA A*0201	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.361123	0.434427	-3.926696	22968.014780
HLA B*0803	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.311094	0.384238	-3.926856	20468.853861
HLA A*3301	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.624665	0.697746	-3.926919	42137.153246
HLA B*3901	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.497161	0.570132	-3.927029	31416.730754
HLA A*3301	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.628807	0.701666	-3.927142	42540.964657
HLA A*0250	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.595245	0.667964	-3.927281	39377.209883
HLA B*4002	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.635264	0.707433	-3.927830	43178.118958
HLA A*3002	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.315262	0.387379	-3.927883	20666.242052
HLA A*0211	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.492384	0.564331	-3.928054	31073.093158
HLA A*2603	1:148-156	9	WQADTDPLP	0.614046	0.092801	-4.634944	0.706847	-3.928097	43146.362560
HLA A*0101	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.380786	0.452621	-3.928165	24031.799886
HLA A*3002	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.550130	0.621958	-3.928172	35491.971936
HLA B*3901	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.466162	0.537766	-3.928396	29252.425702

HLA B*4403	1:19-27	9	GVATAAPKT	1.007855	-0.294181	-4.642115	0.713674	-3.928441	43864.664982
HLA B*3801	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.542194	0.613638	-3.928555	34849.260684
HLA A*0206	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.493482	0.564800	-3.928681	31151.696037
HLA A*2501	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.448548	0.519628	-3.928920	28089.744950
HLA A*0206	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.448599	0.519628	-3.928972	28093.088321
HLA B*1517	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.490385	0.561410	-3.928975	30930.367159
HLA B*1501	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.350602	0.421102	-3.929501	22418.289086
HLA B*4002	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.627428	0.697746	-3.929682	42406.085634
HLA A*6802	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.449436	0.519628	-3.929808	28147.245512
HLA A*2301	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.494212	0.564331	-3.929882	31204.152119
HLA A*2403	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.402646	0.472542	-3.930104	25272.366286
HLA A*2602	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.601264	0.671022	-3.930242	39926.783149
HLA A*2501	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.265640	0.335272	-3.930369	18434.883121
HLA B*5301	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.208872	0.278445	-3.930427	16176.037009
HLA B*3901	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.496978	0.566374	-3.930604	31403.476590
HLA A*2603	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.531369	0.600517	-3.930852	33991.434400

HLA B*4002	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.634018	0.702905	-3.931113	43054.494190
HLA B*3501	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.471194	0.539612	-3.931582	29593.373936
HLA A*6801	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.629411	0.697746	-3.931665	42600.152262
HLA A*0101	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.378496	0.446632	-3.931864	23905.374465
HLA B*0802	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.469665	0.537766	-3.931899	29489.334185
HLA A*3001	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.092389	0.160477	-3.931913	12370.560124
HLA B*1801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.510299	0.578083	-3.932217	32381.675041
HLA B*0802	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.472003	0.539612	-3.932391	29648.498538
HLA B*5401	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.210954	0.278445	-3.932509	16253.757485
HLA B*0702	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.211175	0.278445	-3.932730	16262.025104
HLA B*4403	1:169-177	9	QTGQQVSIA	0.950594	-0.262137	-4.621933	0.688457	-3.933476	41872.871137
HLA B*3901	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.317764	0.384238	-3.933526	20785.654936
HLA A*0219	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.473694	0.539612	-3.934082	29764.208208
HLA B*1509	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.473737	0.539612	-3.934124	29767.106728
HLA A*2902	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.368553	0.434427	-3.934126	23364.286903
HLA A*0201	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.386766	0.452621	-3.934145	24364.961994

HLA A*3301	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.641995	0.707433	-3.934562	43852.564200
HLA B*4001	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.407368	0.472542	-3.934826	25548.674441
HLA A*3301	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.516293	0.581216	-3.935076	32831.660364
HLA B*1801	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.258872	0.323743	-3.935129	18149.786562
HLA B*1517	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.522434	0.587095	-3.935339	33299.246032
HLA B*3901	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.335939	0.400567	-3.935372	21674.012985
HLA A*0219	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.280078	0.344471	-3.935607	19058.028577
HLA B*4403	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.623237	0.687624	-3.935612	41998.782880
HLA A*8001	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.475391	0.539612	-3.935778	29880.692761
HLA A*1101	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.408397	0.472542	-3.935855	25609.284609
HLA A*2601	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.388671	0.452621	-3.936050	24472.096167
HLA A*0301	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.368226	0.432006	-3.936220	23346.724157
HLA B*4403	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.643731	0.707433	-3.936298	44028.233642
HLA B*1502	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.585093	0.648415	-3.936678	38467.398432
HLA B*4601	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.389383	0.452621	-3.936762	24512.243635
HLA A*2402	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.506972	0.570132	-3.936840	32134.566045

HLA B*1502	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.605134	0.667964	-3.937170	40284.123881
HLA A*3101	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.338277	0.400567	-3.937710	21790.995289
HLA B*1501	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.369718	0.432006	-3.937712	23427.064599
HLA B*5701	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.359094	0.421102	-3.937992	22860.909475
HLA B*1503	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.502823	0.564800	-3.938023	31829.018667
HLA A*0206	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.551829	0.613638	-3.938190	35631.065300
HLA A*6802	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.391801	0.452621	-3.939180	24649.078314
HLA B*1801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.504313	0.564800	-3.939512	31938.375487
HLA B*4501	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.607528	0.667964	-3.939564	40506.810482
HLA B*5801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.327216	0.387379	-3.939837	21242.992287
HLA B*5401	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.562011	0.621958	-3.940054	36476.358473
HLA B*4402	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.003950	0.063696	-3.940254	10091.368143
HLA B*5301	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.589033	0.648415	-3.940618	38817.977334
HLA B*1503	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.393708	0.452621	-3.941087	24757.595699
HLA A*3002	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.099057	0.157927	-3.941131	12561.954119
HLA A*3201	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.608014	0.666762	-3.941252	40552.197322

HLA B*3801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.563283	0.621958	-3.941325	36583.272034
HLA B*1503	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.528426	0.587095	-3.941330	33761.799545
HLA A*2301	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.528588	0.587095	-3.941492	33774.404582
HLA A*6901	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.329185	0.387379	-3.941806	21339.515747
HLA B*0802	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.461587	0.519628	-3.941960	28945.925344
HLA A*0202	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.508429	0.566374	-3.942055	32242.530560
HLA B*1801	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.479916	0.537766	-3.942150	30193.660685
HLA A*0216	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.481948	0.539612	-3.942336	30335.284664
HLA A*0101	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.329788	0.387379	-3.942410	21369.205596
HLA B*0803	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.520877	0.578083	-3.942794	33180.023684
HLA A*2301	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.535782	0.592876	-3.942906	34338.539888
HLA A*0216	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.229430	0.286028	-3.943403	16960.167053
HLA B*4002	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.109921	0.166493	-3.943428	12880.158919
HLA B*4403	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.666690	0.723137	-3.943554	46418.428137
HLA A*0201	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.288489	0.344471	-3.944018	19430.730584
HLA A*0250	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.345795	0.401614	-3.944181	22171.517499

HLA A*0202	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.557876	0.613638	-3.944238	36130.700481
HLA A*3001	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.279521	0.335272	-3.944249	19033.609103
HLA B*0702	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.397092	0.452621	-3.944471	24951.216517
HLA B*0801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.378909	0.434427	-3.944482	23928.146579
HLA A*2603	1:49-57	9	AYNINISLP	0.584960	0.117828	-4.647310	0.702788	-3.944522	44392.492308
HLA A*0301	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.346178	0.401614	-3.944564	22191.077230
HLA A*2402	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.566588	0.621958	-3.944630	36862.795917
HLA A*2902	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.345659	0.400567	-3.945092	22164.561754
HLA A*2402	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.564622	0.619394	-3.945228	36696.255669
HLA A*6901	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.377568	0.432006	-3.945561	23854.345463
HLA A*2603	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.616588	0.671022	-3.945566	41360.679234
HLA B*0803	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.511991	0.566374	-3.945617	32508.051523
HLA B*1517	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.465316	0.519628	-3.945688	29195.510286
HLA B*5401	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.303874	0.357949	-3.945924	20131.380522
HLA A*0219	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-3.986634	0.040514	-3.946120	9696.931897
HLA A*0206	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.333580	0.387379	-3.946202	21556.609092

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HLA B*4501	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.642542
	0.696230	-3.946312	43907.875393

HLA A*3101	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.290836
	0.344471	-3.946365	19536.027846

HLA A*2601	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.378895
	0.432006	-3.946889	23927.369900

HLA A*1101	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.486793
	0.539612	-3.947181	30675.575044

HLA B*1509	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.560907
	0.613638	-3.947269	36383.729748

HLA B*5701	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.393965
	0.446632	-3.947333	24772.199011

HLA A*0206	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.382022
	0.434427	-3.947595	24100.282207

HLA B*4002	1:36-44	9	DTGQACQIQ	0.956574	-0.260344	-4.643891
	0.696230	-3.947661	44044.433396

HLA A*0201	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.371381
	0.423714	-3.947667	23516.967040

HLA A*0301	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.335098
	0.387379	-3.947720	21632.076674

HLA B*1801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.517982
	0.570132	-3.947850	32959.614703

HLA A*0211	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.040405
	0.092119	-3.948286	10975.003294

HLA B*3801	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.528115
	0.579719	-3.948397	33737.698669

HLA A*0216	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.382957
	0.434427	-3.948530	24152.229294

HLA A*0203	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.421080
	0.472542	-3.948538	26368.168588

HLA A*2602	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.562263
	0.613638	-3.948624	36497.479222
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HLA A*3002	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.240200	0.291433	-3.948767	17386.019599
HLA A*2402	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.488395	0.539612	-3.948783	30788.962987
HLA A*2902	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.109451	0.160477	-3.948975	12866.230409
HLA B*3801	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.549533	0.600517	-3.949016	35443.235490
HLA B*3901	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.510461	0.561410	-3.949051	32393.764805
HLA B*4601	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.333397	0.384238	-3.949159	21547.514739
HLA B*0803	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.487065	0.537766	-3.949299	30694.831455
HLA B*0803	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.468939	0.519628	-3.949311	29440.079350
HLA A*2602	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.583399	0.634040	-3.949359	38317.647432
HLA A*8001	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.370688	0.421102	-3.949586	23479.465838
HLA A*2301	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.529363	0.579719	-3.949644	33834.754645
HLA B*4801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.179438	0.229395	-3.950042	15116.031343
HLA B*5401	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.563701	0.613638	-3.950062	36618.517239
HLA A*2403	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.402759	0.452621	-3.950138	25278.929732
HLA A*3201	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.516563	0.566374	-3.950189	32852.092518
HLA A*0212	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.236899	0.286028	-3.950872	17254.371259

HLA B*3801	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.532152	0.581216	-3.950936	34052.724925
HLA B*4002	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.638645	0.687624	-3.951020	43515.565071
HLA B*5301	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.573129	0.621958	-3.951171	37422.193334
HLA B*5801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.351968	0.400567	-3.951400	22488.863887
HLA A*2403	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.385908	0.434427	-3.951481	24316.898177
HLA B*4002	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.622609	0.671022	-3.951587	41938.161934
HLA A*8001	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.386063	0.434427	-3.951636	24325.582141
HLA B*5301	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.513055	0.561410	-3.951645	32587.816046
HLA A*3201	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.309721	0.357949	-3.951772	20404.287119
HLA B*4001	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.386343	0.434427	-3.951916	24341.247428
HLA B*5701	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-3.755906	-0.196092	-3.951998	5700.402480
HLA A*0101	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.386531	0.434427	-3.952104	24351.784384
HLA B*7301	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.600581	0.648415	-3.952166	39863.976753
HLA A*6802	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.376014	0.423714	-3.952301	23769.196168
HLA A*0301	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.282684	0.330347	-3.952336	19172.712179
HLA B*1502	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.545438	0.592876	-3.952562	35110.596505

HLA A*6801	1:32-40	9	LKGTDTGQA	1.058870	-0.351437	-4.660037	0.707433	-3.952603	45712.680518
HLA B*4002	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.517421	0.564800	-3.952620	32917.026662
HLA A*2603	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.615716	0.662917	-3.952799	41277.748753
HLA A*8001	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.405665	0.452621	-3.953044	25448.664462
HLA B*0803	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.517984	0.564800	-3.953184	32959.793011
HLA B*0803	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.523713	0.570132	-3.953580	33397.389383
HLA B*3501	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.406913	0.452621	-3.954292	25521.874700
HLA B*4402	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.401046	0.446632	-3.954414	25179.430788
HLA B*5101	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.492309	0.537766	-3.954543	31067.714360
HLA B*7301	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.389087	0.434427	-3.954660	24495.540655
HLA B*4002	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.621498	0.666762	-3.954736	41830.984497
HLA A*0206	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.536033	0.581216	-3.954817	34358.422785
HLA A*2601	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.285202	0.330347	-3.954855	19284.225471
HLA B*3501	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.474533	0.519628	-3.954905	29821.748275
HLA B*4601	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.378629	0.423714	-3.954916	23912.747151
HLA B*5401	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.535129	0.579719	-3.955410	34286.935284

HLA B*4403	1:88-96	9	EAPYELNIT	1.024679	-0.321774	-4.658512	0.702905	-3.955606	45552.463898
HLA B*4501	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.577802	0.621958	-3.955844	37827.040446
HLA B*5701	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.408541	0.452621	-3.955920	25617.737150
HLA A*0211	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.526076	0.570132	-3.955944	33579.645114
HLA A*6802	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.428598	0.472542	-3.956056	26828.619046
HLA A*6801	1:105-113	9	PPRGTQAVV	0.903475	-0.180338	-4.679310	0.723137	-3.956173	47786.972145
HLA A*3001	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.280254	0.323743	-3.956511	19065.762782
HLA A*0202	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.521323	0.564800	-3.956523	33214.146265
HLA A*0101	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.358196	0.401614	-3.956582	22813.714413
HLA B*3901	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.476291	0.519628	-3.956663	29942.669369
HLA B*3501	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.403651	0.446632	-3.957020	25330.950543
HLA B*0803	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.496686	0.539612	-3.957074	31382.417378
HLA A*0211	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.535265	0.578083	-3.957182	34297.695306
HLA A*0101	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.389214	0.432006	-3.957208	24502.697681
HLA A*8001	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.315294	0.357949	-3.957345	20667.807340
HLA A*3002	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.518781	0.561410	-3.957371	33020.295166

HLA A*3201	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.535817	0.578083	-3.957734	34341.326516
HLA B*4002	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.637909	0.680076	-3.957833	43441.942719
HLA A*2602	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.524232	0.566374	-3.957858	33437.342697
HLA A*2602	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.620854	0.662917	-3.957937	41769.023960
HLA A*2603	1:186-194	9	NYQNFAVTN	1.119422	-0.431798	-4.645594	0.687624	-3.957970	44217.522355
HLA B*4601	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.404857	0.446632	-3.958225	25401.348491
HLA A*2301	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.539445	0.581216	-3.958228	34629.376459
HLA B*4601	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.288964	0.330347	-3.958616	19451.976046
HLA A*1101	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.496571	0.537766	-3.958805	31374.099486
HLA A*6802	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.393866	0.434427	-3.959439	24766.571027
HLA B*4601	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.361288	0.401614	-3.959674	22976.714236
HLA A*3201	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.540953	0.581216	-3.959737	34749.858542
HLA B*5401	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.524476	0.564331	-3.960146	33456.160791
HLA A*0101	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.384188	0.423714	-3.960474	24220.792732
HLA A*0201	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.392506	0.432006	-3.960499	24689.115429
HLA B*4403	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.579987	0.619394	-3.960594	38017.835295

HLA A*3101	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.348070	0.387379	-3.960691	22287.929241
HLA A*2902	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.384642	0.423714	-3.960928	24246.095077
HLA A*8001	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.433542	0.472542	-3.960999	27135.737861
HLA B*4601	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.382175	0.421102	-3.961073	24108.758388
HLA A*6901	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.362063	0.400567	-3.961496	23017.770361
HLA B*1502	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.583563	0.621958	-3.961605	38332.160776
HLA A*0212	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.414248	0.452621	-3.961627	25956.591621
HLA B*5801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.363285	0.401614	-3.961671	23082.613790
HLA A*2403	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.319625	0.357949	-3.961675	20874.904887
HLA A*6801	1:177-185	9	APNAGLDPV	0.672482	0.029184	-4.663566	0.701666	-3.961900	46085.639134
HLA A*3301	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.581294	0.619394	-3.961900	38132.361235
HLA B*0803	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.523428	0.561410	-3.962018	33375.534720
HLA A*2601	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.385763	0.423714	-3.962049	24308.743338
HLA A*6802	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.054403	0.092119	-3.962284	11334.513678
HLA B*1801	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.528940	0.566374	-3.962566	33801.823073
HLA B*4002	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.630823	0.667964	-3.962859	42738.885397

HLA A*2601	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.384303	0.421102	-3.963202	24227.214141
HLA A*2902	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.409838	0.446632	-3.963206	25694.352683
HLA B*4501	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.643322	0.680076	-3.963246	43986.808454
HLA A*0101	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.384780	0.421102	-3.963678	24253.835264
HLA B*4403	1:170-178	9	TGQQVSIAP	0.814303	-0.116557	-4.661458	0.697746	-3.963712	45862.542455
HLA B*0702	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.410387	0.446632	-3.963755	25726.900123
HLA A*1101	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.483499	0.519628	-3.963871	30443.791209
HLA A*2601	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.398330	0.434427	-3.963903	25022.454226
HLA B*4001	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.410618	0.446632	-3.963986	25740.543347
HLA A*2603	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.528416	0.564331	-3.964086	33761.068963
HLA A*0301	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.364918	0.400567	-3.964351	23169.564845
HLA A*2301	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.534586	0.570132	-3.964453	34244.114198
HLA B*3801	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.542539	0.578083	-3.964456	34876.985710
HLA B*0802	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.348946	0.384238	-3.964708	22332.949208
HLA B*4801	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.437451	0.472542	-3.964909	27381.118086
HLA A*3002	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.535150	0.570132	-3.965017	34288.604721

HLA A*3301	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.627938	0.662917	-3.965021	42455.897319
HLA B*5801	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.349425	0.384238	-3.965188	22357.609844
HLA A*2902	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.397435	0.432006	-3.965428	24970.931866
HLA A*0206	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.389750	0.423714	-3.966036	24532.939296
HLA A*0250	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.579938	0.613638	-3.966300	38013.516423
HLA A*0201	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.324328	0.357949	-3.966379	21102.221356
HLA A*3201	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.353880	0.387379	-3.966501	22588.115341
HLA B*2705	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.324476	0.357949	-3.966527	21109.414705
HLA A*0201	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.387727	0.421102	-3.966625	24418.932684
HLA A*0211	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.531684	0.564800	-3.966884	34016.084579
HLA A*0211	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.486988	0.519628	-3.967360	30689.352108
HLA B*1502	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.505448	0.537766	-3.967682	32021.938837
HLA B*5301	1:98-106	9	ATYQSAIPP	0.417465	0.201929	-4.587170	0.619394	-3.967776	38651.803280
HLA A*2602	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.634669	0.666762	-3.967907	43119.061408
HLA A*0206	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.369631	0.401614	-3.968017	23422.375769
HLA A*2301	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.546145	0.578083	-3.968063	35167.816355

HLA A*6901 1:138-146 9 YRKPITYDT 0.544186 -0.159948 -4.352459 0.384238 -3.968221 22514.305680

HLA B*4001 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.213496 0.245175 -3.968321 16349.177855

HLA B*0702 1:178-186 9 PNAGLDPVN 1.201582 -0.769576 -4.400470 0.432006 -3.968464 25146.079502

HLA B*1509 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.506317 0.537766 -3.968551 32086.100032

HLA B*5401 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.535030 0.566374 -3.968656 34279.145651

HLA A*0219 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.441398 0.472542 -3.968856 27631.108806

HLA A*0206 1:138-146 9 YRKPITYDT 0.544186 -0.159948 -4.353161 0.384238 -3.968923 22550.753320

HLA A*0219 1:43-51 9 IQMSDPAYN 0.678035 -0.520108 -4.127002 0.157927 -3.969075 13396.827874

HLA B*0702 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.441936 0.472542 -3.969394 27665.361222

HLA A*2402 1:40-48 9 ACQIQMSDP 0.533748 0.079890 -4.583213 0.613638 -3.969575 38301.274687

HLA A*0201 1:138-146 9 YRKPITYDT 0.544186 -0.159948 -4.353925 0.384238 -3.969687 22590.437246

HLA B*1503 1:89-97 9 APYELNITS 1.361001 -1.037258 -4.293750 0.323743 -3.970007 19667.521203

HLA B*7301 1:67-75 9 ENYIAQTRD 1.094922 -0.841398 -4.223871 0.253524 -3.970347 16744.463770

HLA A*0206 1:118-126 9 QNAGGTHPT 0.654006 -0.382530 -4.242087 0.271476 -3.970611 17461.711208

HLA A*0212 1:94-102 9 NITSATYQS 1.243610 -0.899139 -4.315264 0.344471 -3.970793 20666.353854

HLA B*4501 1:200-208 9 FFNPGELLP 0.676947 -0.010185 -4.637630 0.666762 -3.970867 43413.984804

HLA A*2402	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.550762	0.579719	-3.971043	35543.659590
HLA A*0219	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.355849	0.384238	-3.971611	22690.750743
HLA A*3201	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.585255	0.613638	-3.971617	38481.760314
HLA B*4601	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.406196	0.434427	-3.971769	25479.797917
HLA B*4002	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.620697	0.648272	-3.972424	41753.886996
HLA B*1517	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.512125	0.539612	-3.972513	32518.077371
HLA A*8001	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.356869	0.384238	-3.972631	22744.088764
HLA B*3901	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.512341	0.539612	-3.972729	32534.265965
HLA B*3801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.542868	0.570132	-3.972735	34903.411004
HLA A*6901	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.396589	0.423714	-3.972875	24922.346802
HLA B*3501	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.407375	0.434427	-3.972948	25549.089091
HLA B*3801	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.539614	0.566374	-3.973240	34642.867645
HLA A*0212	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.358017	0.384238	-3.973780	22804.336446
HLA A*0216	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.420420	0.446632	-3.973788	26328.114708
HLA B*3801	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.560900	0.587095	-3.973805	36383.139257
HLA A*2603	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.640595	0.666762	-3.973832	43711.398346

HLA A*0101	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.374433	0.400567	-3.973866	23682.813311
HLA A*2603	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.567082	0.592876	-3.974206	36904.698680
HLA A*3002	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.305131	0.330347	-3.974783	20189.730990
HLA B*4001	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.376426	0.401614	-3.974812	23791.709849
HLA A*0216	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.447545	0.472542	-3.975002	28024.931891
HLA A*0212	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.447812	0.472542	-3.975270	28042.220964
HLA B*5301	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.545527	0.570132	-3.975395	35117.815136
HLA B*0801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.320362	0.344471	-3.975891	20910.395332
HLA B*3901	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.254349	0.278445	-3.975904	17961.754805
HLA A*2402	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.557179	0.581216	-3.975962	36072.694558
HLA B*5401	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.540883	0.564800	-3.976082	34744.219214
HLA B*5101	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.515814	0.539612	-3.976201	32795.446760
HLA A*0211	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.537730	0.561410	-3.976319	34492.887156
HLA A*2402	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.537896	0.561410	-3.976486	34506.138492
HLA B*4001	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.400240	0.423714	-3.976526	25132.751361
HLA B*4403	1:55-63	9	SLPSYYPDQ	0.698032	-0.017956	-4.656630	0.680076	-3.976554	45355.497508

HLA A*2902	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.335164	0.357949	-3.977215	21635.353682
HLA A*0203	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.398504	0.421102	-3.977402	25032.473515
HLA B*4801	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.069505	0.091985	-3.977521	11735.602217
HLA B*0802	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.450559	0.472542	-3.978017	28220.126426
HLA B*5701	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.401927	0.423714	-3.978213	25230.564361
HLA A*2403	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.365632	0.387379	-3.978253	23207.701008
HLA A*2602	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.571346	0.592876	-3.978470	37268.848887
HLA A*6901	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.284768	0.305553	-3.979215	19264.934904
HLA B*1501	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.366647	0.387379	-3.979268	23262.002507
HLA A*8001	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.403217	0.423714	-3.979503	25305.611263
HLA A*0203	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.251156	0.271476	-3.979680	17830.183528
HLA A*0202	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.400945	0.421102	-3.979843	25173.574098
HLA A*2402	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.544205	0.564331	-3.979874	35011.017156
HLA A*6801	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.517778	0.537766	-3.980012	32944.105569
HLA A*2301	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.546728	0.566374	-3.980354	35215.031010
HLA A*0206	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.520179	0.539612	-3.980567	33126.754916

HLA A*0203	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.856440	-0.124403	-3.980843	7185.218569
HLA A*0301	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.365322	0.384238	-3.981084	23191.134180
HLA B*5301	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.594754	0.613638	-3.981116	39332.712538
HLA A*6901	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.272623	0.291433	-3.981190	18733.678290
HLA A*2301	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.546371	0.564800	-3.981571	35186.085482
HLA A*2403	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.428464	0.446632	-3.981832	26820.347350
HLA A*6802	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.383563	0.401614	-3.981949	24185.963338
HLA A*3201	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.434730	0.452621	-3.982109	27210.121098
HLA A*2501	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.340079	0.357949	-3.982130	21881.602369
HLA B*4501	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.630546	0.648415	-3.982131	42711.611013
HLA B*0803	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.312642	0.330347	-3.982294	20541.957953
HLA A*0212	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.428934	0.446632	-3.982302	26849.382076
HLA B*5101	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.501996	0.519628	-3.982368	31768.464947
HLA A*2301	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.522136	0.539612	-3.982524	33276.375446
HLA A*0211	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.143669	0.160477	-3.983193	13920.961234
HLA B*1509	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.544618	0.561410	-3.983208	35044.368438

HLA A*3002	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.404403	0.421102	-3.983301	25374.840566
HLA A*0219	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.429966	0.446632	-3.983334	26913.223563
HLA B*5401	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.564619	0.581216	-3.983403	36696.057147
HLA B*5701	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.416209	0.432006	-3.984203	26074.109457
HLA B*1517	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.275656	0.291433	-3.984223	18864.975392
HLA B*1503	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.407944	0.423714	-3.984230	25582.559689
HLA A*3201	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.522019	0.537766	-3.984253	33267.375588
HLA B*4403	1:200-208	9	FFNPGELLP	0.676947	-0.010185	-4.651501	0.666762	-3.984739	44823.009174
HLA B*4601	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.417074	0.432006	-3.985068	26126.070522
HLA B*0702	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.408809	0.423714	-3.985095	25633.541183
HLA A*3201	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.077226	0.092119	-3.985107	11946.090162
HLA B*0702	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.406212	0.421102	-3.985111	25480.762836
HLA B*4801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.419734	0.434427	-3.985307	26286.557343
HLA B*4402	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.406419	0.421102	-3.985317	25492.896357
HLA B*4801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.417375	0.432006	-3.985368	26144.168198
HLA B*0702	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.369866	0.384238	-3.985628	23435.050443

HLA B*4001	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.373019	0.387379	-3.985640	23605.809691
HLA B*0801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.264181	0.278445	-3.985736	18373.054289
HLA A*2902	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.438445	0.452621	-3.985824	27443.848322
HLA B*4403	1:16-24	9	CCSGVATAA	0.892838	-0.221816	-4.656987	0.671022	-3.985965	45392.808815
HLA A*2403	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.316333	0.330347	-3.985986	20717.286735
HLA A*0212	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.407234	0.421102	-3.986133	25540.797372
HLA B*4403	1:17-25	9	CSGVATAAP	0.698375	-0.030411	-4.654102	0.667964	-3.986138	45092.248246
HLA B*1502	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.564537	0.578083	-3.986454	36689.109549
HLA A*3002	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.321880	0.335272	-3.986608	20983.600582
HLA A*3002	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.085148	0.098300	-3.986848	12166.012312
HLA B*4403	1:119-127	9	NAGGTHPTT	1.008013	-0.359741	-4.635344	0.648272	-3.987071	43186.061709
HLA A*2602	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.609300	0.621958	-3.987342	40672.377496
HLA B*7301	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.609485	0.621958	-3.987527	40689.763822
HLA A*2403	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.389242	0.401614	-3.987628	24504.288415
HLA B*3501	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.411534	0.423714	-3.987820	25794.909539
HLA B*3801	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.525853	0.537766	-3.988087	33562.391643

HLA A*3002	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.525937	0.537766	-3.988172	33568.928757
HLA A*3002	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.507971	0.519628	-3.988343	32208.534934
HLA A*0219	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.440975	0.452621	-3.988354	27604.215280
HLA B*0802	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.409584	0.421102	-3.988482	25679.344679
HLA A*0203	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.375975	0.387379	-3.988596	23767.010260
HLA A*3001	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.087357	0.098300	-3.989057	12228.037658
HLA B*7301	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.602831	0.613638	-3.989193	40071.115042
HLA B*4801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.435945	0.446632	-3.989313	27286.331959
HLA A*2402	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.554434	0.564800	-3.989634	35845.478816
HLA A*6802	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.421705	0.432006	-3.989699	26406.140502
HLA A*2402	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.582757	0.592876	-3.989882	38261.097878
HLA A*2602	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.088334	0.098300	-3.990034	12255.588016
HLA A*3301	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.554416	0.564331	-3.990085	35843.927489
HLA B*4402	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.422175	0.432006	-3.990168	26434.726822
HLA B*4002	1:34-42	9	GTDTGQACQ	0.815488	-0.167073	-4.638609	0.648415	-3.990195	43512.033998
HLA A*6802	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.226014	0.235698	-3.990316	16827.282059

HLA A*6801	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.590875	0.600517	-3.990358	38982.967726
HLA A*1101	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.378120	0.387379	-3.990741	23884.691349
HLA A*2602	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.463610	0.472542	-3.991068	29081.067487
HLA B*1801	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.443752	0.452621	-3.991132	27781.295696
HLA A*0201	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.392776	0.401614	-3.991162	24704.480226
HLA B*0702	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.425734	0.434427	-3.991307	26652.275664
HLA A*2601	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.393053	0.401614	-3.991439	24720.255784
HLA A*2301	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.326783	0.335272	-3.991512	21221.857117
HLA B*4001	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.392184	0.400567	-3.991617	24670.823751
HLA A*2602	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.529997	0.537766	-3.992231	33884.212170
HLA A*6901	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.393906	0.401614	-3.992292	24768.848867
HLA A*0201	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.392877	0.400567	-3.992310	24710.227780
HLA A*0219	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.416184	0.423714	-3.992470	26072.557865
HLA B*5301	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.579814	0.587095	-3.992718	38002.618593
HLA B*7301	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.554225	0.561410	-3.992815	35828.224084
HLA B*0802	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.445580	0.452621	-3.992959	27898.470634

HLA A*1101	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.439834	0.446632	-3.993202	27531.733435
HLA B*4001	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.425831	0.432006	-3.993824	26658.187940
HLA A*0219	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.415063	0.421102	-3.993961	26005.363917
HLA B*7301	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.572272	0.578083	-3.994189	37348.372022
HLA B*1509	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.558997	0.564800	-3.994197	36224.056774
HLA A*0202	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.447075	0.452621	-3.994454	27994.625934
HLA A*1101	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.447138	0.452621	-3.994517	27998.715324
HLA A*0212	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.152597	0.157927	-3.994671	14210.104349
HLA B*2705	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.224130	0.229395	-3.994734	16754.431161
HLA A*3201	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.071075	0.076178	-3.994896	11778.089130
HLA B*1502	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.608675	0.613638	-3.995036	40613.890796
HLA A*2402	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.573416	0.578083	-3.995333	37446.900377
HLA A*2603	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.629421	0.634040	-3.995381	42601.074120
HLA A*3101	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.427393	0.432006	-3.995387	26754.265524
HLA A*2601	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.396582	0.400567	-3.996015	24921.942324
HLA A*3002	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.430478	0.434427	-3.996051	26944.982554

HLA A*2301 1:205-213 9 ELLPEAAGP 0.578973 -0.041207 -4.533890
0.537766 -3.996125 34189.322049

HLA A*3001 1:196-204 9 GVIFFFNPG 0.529052 -0.653455 -3.871735
-0.124403 -3.996138 7442.779126

HLA A*3001 1:187-195 9 YQNFAVTND 0.973541 -0.744146 -4.225798
0.229395 -3.996402 16818.909039

HLA B*5801 1:91-99 9 YELNITSAT 0.787532 -0.429583 -4.354359
0.357949 -3.996410 22613.057739

HLA B*1509 1:176-184 9 IAPNAGLDP 0.476515 0.093617 -4.566685
0.570132 -3.996552 36870.973194

HLA A*3201 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.589536
0.592876 -3.996660 38862.943563

HLA A*2501 1:11-19 9 AVVLLCCSG 0.891360 -0.444728 -4.443508
0.446632 -3.996876 27765.669545

HLA B*4801 1:216-224 9 VLVPRSAID 1.164467 -0.740753 -4.420699
0.423714 -3.996985 26345.069594

HLA B*5301 1:73-81 9 TRDKFLSAA 0.841706 -0.248830 -4.589888
0.592876 -3.997012 38894.492994

HLA B*4001 1:22-30 9 TAAPKTYCE 1.011561 -0.590459 -4.418242
0.421102 -3.997140 26196.410597

HLA A*3101 1:138-146 9 YRKPITYDT 0.544186 -0.159948 -4.381414
0.384238 -3.997176 24066.537471

HLA A*2403 1:178-186 9 PNAGLDPVN 1.201582 -0.769576 -4.429595
0.432006 -3.997588 26890.228978

HLA B*4402 1:26-34 9 KTYCEELKG 0.984658 -0.550231 -4.432282
0.434427 -3.997855 27057.166318

HLA A*0250 1:203-211 9 PGELLPEAA 1.144110 -0.557015 -4.585459
0.587095 -3.998364 38499.876415

HLA B*4403 1:34-42 9 GTDTGQACQ 0.815488 -0.167073 -4.647293
0.648415 -3.998878 44390.811230

HLA A*0212 1:178-186 9 PNAGLDPVN 1.201582 -0.769576 -4.431211
0.432006 -3.999205 26990.501001

HLA A*0203	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.431502	0.432006	-3.999496	27008.613012
HLA B*1517	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.091732	0.092119	-3.999613	12351.835769
HLA A*0250	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.577821	0.578083	-3.999738	37828.677602
HLA B*4402	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.384033	0.384238	-3.999796	24212.146176
HLA B*3501	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.431834	0.432006	-3.999827	27029.222890
HLA A*3001	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.271502	0.271476	-4.000026	18685.398033
HLA A*0219	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.432111	0.432006	-4.000104	27046.482960
HLA B*3801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.539952	0.539612	-4.000340	34669.865786
HLA B*3801	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.561774	0.561410	-4.000364	36456.433278
HLA A*0101	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.384644	0.384238	-4.000406	24246.226246
HLA B*0801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.432524	0.432006	-4.000518	27072.247275
HLA A*2902	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.272172	0.271476	-4.000696	18714.229745
HLA B*2705	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.473361	0.472542	-4.000819	29741.351997
HLA B*1502	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.424914	0.423714	-4.001200	26602.002275
HLA B*1503	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.541164	0.539612	-4.001552	34766.782021
HLA B*5301	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.581273	0.579719	-4.001554	38130.504653

HLA B*3901	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.454203	0.452621	-4.001582	28457.910311
HLA B*1502	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.571727	0.570132	-4.001594	37301.525699
HLA B*2705	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.389209	0.387379	-4.001831	24502.432569
HLA A*2402	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.588979	0.587095	-4.001884	38813.147613
HLA A*0301	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.346503	0.344471	-4.002031	22207.650491
HLA A*0101	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.332716	0.330347	-4.002368	21513.736040
HLA B*4601	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.402998	0.400567	-4.002431	25292.882714
HLA A*0250	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.567079	0.564331	-4.002749	36904.499030
HLA A*6901	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.281882	0.278445	-4.003437	19137.375497
HLA A*0219	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.437928	0.434427	-4.003501	27411.204753
HLA A*6901	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.080186	0.076178	-4.004008	12027.798375
HLA B*4402	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.404622	0.400567	-4.004055	25387.610360
HLA A*2403	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.427886	0.423714	-4.004173	26784.677694
HLA B*1509	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.257723	0.253524	-4.004198	18101.835920
HLA B*1501	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.349064	0.344471	-4.004592	22338.990964
HLA A*0250	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.574908	0.570132	-4.004775	37575.762161

HLA A*0206	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.457462	0.452621	-4.004841	28672.247840
HLA A*2602	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.582931	0.578083	-4.004849	38276.418078
HLA A*0202	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.575136	0.570132	-4.005003	37595.485564
HLA A*2601	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.392600	0.387379	-4.005221	24694.458622
HLA B*0801	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.329044	0.323743	-4.005301	21332.590206
HLA A*3002	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.429143	0.423714	-4.005430	26862.312633
HLA A*3002	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.389792	0.384238	-4.005554	24535.328381
HLA B*2705	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.452338	0.446632	-4.005706	28335.932885
HLA B*3501	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-3.640142	-0.365615	-4.005757	4366.582755
HLA B*5101	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.478377	0.472542	-4.005835	30086.859467
HLA B*5801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.350732	0.344471	-4.006261	22424.960503
HLA B*1501	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.277891	0.271476	-4.006415	18962.282101
HLA A*0301	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.364845	0.357949	-4.006896	23165.679483
HLA A*6801	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.573341	0.566374	-4.006967	37440.418263
HLA B*0702	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.365007	0.357949	-4.007058	23174.328436
HLA B*3901	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.394439	0.387379	-4.007060	24799.284808

HLA B*5301	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.588356	0.581216	-4.007140	38757.544151
HLA A*0219	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.293174	0.286028	-4.007146	19641.470689
HLA B*3801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.572006	0.564800	-4.007206	37325.547287
HLA B*5701	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.394947	0.387379	-4.007568	24828.280605
HLA B*0702	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.279075	0.271476	-4.007599	19014.054908
HLA B*1801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.408207	0.400567	-4.007640	25598.065053
HLA A*3101	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.342929	0.335272	-4.007657	22025.665892
HLA A*2602	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.572044	0.564331	-4.007713	37328.778260
HLA A*0202	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.442378	0.434427	-4.007951	27693.512845
HLA B*1509	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.392322	0.384238	-4.008085	24678.699527
HLA A*6801	1:162-170	9	VQGELSKQT	0.977010	-0.314093	-4.671068	0.662917	-4.008150	46888.627497
HLA B*7301	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.589634	0.581216	-4.008418	38871.774823
HLA A*8001	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.455216	0.446632	-4.008584	28524.341963
HLA B*5801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.339278	0.330347	-4.008931	21841.273008
HLA B*5701	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.410597	0.401614	-4.008982	25739.290096
HLA A*2501	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.481629	0.472542	-4.009086	30312.973841

HLA B*4002	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.631119	0.621958	-4.009161	42768.028120
HLA A*2402	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.575660	0.566374	-4.009286	37640.868326
HLA B*3501	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.411083	0.401614	-4.009469	25768.130310
HLA B*1501	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.393981	0.384238	-4.009743	24773.137133
HLA A*0206	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.333606	0.323743	-4.009864	21557.891937
HLA A*2601	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.345201	0.335272	-4.009929	22141.192057
HLA A*0101	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.368167	0.357949	-4.010218	23343.566791
HLA A*0211	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.550231	0.539612	-4.010619	35500.229225
HLA A*0216	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.463357	0.452621	-4.010736	29064.081311
HLA A*6802	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.051424	0.040514	-4.010909	11257.027938
HLA A*2501	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.463775	0.452621	-4.011154	29092.082347
HLA B*4801	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.395400	0.384238	-4.011162	24854.217564
HLA B*4501	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.645282	0.634040	-4.011242	44185.718616
HLA A*0216	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.355969	0.344471	-4.011498	22697.012084
HLA A*2403	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.395748	0.384238	-4.011510	24874.125400
HLA A*0211	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.265328	0.253787	-4.011541	18421.623712

HLA B*2705	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.444084	0.432006	-4.012077	27802.495197
HLA A*3101	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.370225	0.357949	-4.012276	23454.455970
HLA B*1509	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.283997	0.271476	-4.012521	19230.780674
HLA B*4002	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.646746	0.634040	-4.012706	44334.891678
HLA B*0803	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.447253	0.434427	-4.012826	28006.138335
HLA A*8001	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.445066	0.432006	-4.013060	27865.437054
HLA A*2403	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.299266	0.286028	-4.013239	19918.939743
HLA B*3901	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.485963	0.472542	-4.013421	30617.050079
HLA B*1509	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.445846	0.432006	-4.013840	27915.530670
HLA B*0802	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.415523	0.401614	-4.013909	26032.953024
HLA A*3002	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.601020	0.587095	-4.013925	39904.325522
HLA A*2403	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.305436	0.291433	-4.014003	20203.935131
HLA B*5701	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.398527	0.384238	-4.014290	25033.827781
HLA A*2603	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.575749	0.561410	-4.014339	37648.607173
HLA B*0801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.320078	0.305553	-4.014525	20896.711937
HLA B*2705	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.449356	0.434427	-4.014929	28142.068690

HLA A*3301	1:41-49	9	CQIQMSDPA	0.720301	-0.119784	-4.616247	0.600517	-4.015730	41328.247236
HLA B*0702	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.417661	0.401614	-4.016047	26161.429214
HLA B*5701	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.416698	0.400567	-4.016131	26103.466043
HLA A*0211	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.340037	0.323743	-4.016294	21879.471686
HLA B*1801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.246006	0.229395	-4.016610	17619.993437
HLA A*3201	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.581263	0.564331	-4.016933	38129.679535
HLA A*0212	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.246337	0.229395	-4.016942	17633.438996
HLA A*2403	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.438262	0.421102	-4.017160	27432.270247
HLA A*0212	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.340948	0.323743	-4.017206	21925.445740
HLA A*2601	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.361760	0.344471	-4.017289	23001.712422
HLA B*7301	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.375528	0.357949	-4.017579	23742.593202
HLA A*3201	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.587905	0.570132	-4.017773	38717.307640
HLA A*0206	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.490601	0.472542	-4.018059	30945.765338
HLA A*2902	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.419724	0.401614	-4.018110	26285.988520
HLA B*4501	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.631864	0.613638	-4.018226	42841.435428
HLA B*3801	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.537861	0.519628	-4.018233	34503.338490

HLA B*4002	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.631920	0.613638	-4.018282	42846.998207
HLA B*4001	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.402557	0.384238	-4.018319	25267.171433
HLA B*4402	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.442106	0.423714	-4.018392	27676.139312
HLA A*0250	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.585088	0.566374	-4.018714	38466.982226
HLA B*4501	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.585229	0.566374	-4.018855	38479.470379
HLA B*5801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.354150	0.335272	-4.018878	22602.172622
HLA A*2602	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.583732	0.564800	-4.018932	38347.094521
HLA A*3301	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.641053	0.621958	-4.019095	43757.535072
HLA B*4801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.440207	0.421102	-4.019105	27555.425660
HLA A*2501	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.440259	0.421102	-4.019157	27558.705435
HLA A*0101	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.364229	0.344471	-4.019758	23132.867917
HLA A*2601	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.404413	0.384238	-4.020175	25375.389672
HLA B*1501	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.274106	0.253787	-4.020318	18797.737600
HLA A*0216	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.441777	0.421102	-4.020675	27655.185769
HLA B*7301	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.587073	0.566374	-4.020700	38643.231049
HLA A*2301	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.540457	0.519628	-4.020829	34710.214675

HLA B*5401	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.558931	0.537766	-4.021165	36218.570082
HLA B*1503	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.275459	0.253787	-4.021672	18856.404516
HLA B*1501	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.422480	0.400567	-4.021913	26453.324524
HLA A*3101	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-3.825864	-0.196092	-4.021956	6696.745365
HLA B*3501	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.422711	0.400567	-4.022143	26467.352978
HLA A*2603	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.644516	0.621958	-4.022558	44107.860305
HLA A*8001	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.423209	0.400567	-4.022642	26497.725707
HLA A*3301	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.636819	0.613638	-4.023181	43333.032001
HLA B*4501	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.097666	0.073876	-4.023791	12521.786877
HLA A*3201	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.611005	0.587095	-4.023910	40832.435607
HLA B*7301	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.594174	0.570132	-4.024041	39280.189591
HLA B*3901	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.445275	0.421102	-4.024173	27878.856939
HLA A*2601	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.382175	0.357949	-4.024225	24108.758388
HLA A*0203	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.329784	0.305553	-4.024231	21368.974387
HLA A*3001	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.302729	0.278445	-4.024284	20078.411871
HLA A*6802	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.424997	0.400567	-4.024429	26607.039737

HLA B*4403	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.646541	0.621958	-4.024583	44314.029912
HLA A*0211	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.369575	0.344471	-4.025103	23419.334868
HLA B*4501	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.604828	0.579719	-4.025110	40255.802598
HLA B*5301	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.589475	0.564331	-4.025144	38857.477597
HLA B*1517	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.355496	0.330347	-4.025149	22672.345045
HLA A*0216	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.425805	0.400567	-4.025238	26656.601591
HLA B*5801	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.349677	0.323743	-4.025934	22370.555475
HLA B*1503	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.317482	0.291433	-4.026049	20772.165544
HLA A*0216	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.410355	0.384238	-4.026117	25724.951681
HLA B*5101	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.472905	0.446632	-4.026273	29710.154272
HLA B*0802	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.460730	0.434427	-4.026303	28888.824838
HLA B*4002	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.606217	0.579719	-4.026498	40384.716215
HLA A*0216	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.428474	0.401614	-4.026860	26820.927737
HLA B*5401	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.473530	0.446632	-4.026898	29752.938867
HLA B*4801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.427710	0.400567	-4.027143	26773.812239
HLA A*0301	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.187633	0.160477	-4.027156	15403.974373

HLA B*4001	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.357616	0.330347	-4.027268	22783.250114
HLA B*1502	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.614384	0.587095	-4.027289	41151.327085
HLA A*3101	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.357691	0.330347	-4.027344	22787.194611
HLA A*3301	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.620434	0.592876	-4.027558	41728.595662
HLA A*0212	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.119587	0.091985	-4.027602	13170.037234
HLA B*5301	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.594070	0.566374	-4.027696	39270.840639
HLA B*7301	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.547412	0.519628	-4.027784	35270.512910
HLA A*2501	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.451539	0.423714	-4.027825	28283.860743
HLA A*6802	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.351627	0.323743	-4.027884	22471.229777
HLA A*3001	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.263780	0.235698	-4.028081	18356.065400
HLA B*4601	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.415575	0.387379	-4.028196	26036.051587
HLA A*6901	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.314275	0.286028	-4.028247	20619.338485
HLA A*0211	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.474933	0.446632	-4.028301	29849.187391
HLA A*0202	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.547964	0.519628	-4.028336	35315.381673
HLA A*3002	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.481492	0.452621	-4.028871	30303.463923
HLA B*5401	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.568543	0.539612	-4.028931	37029.090353

HLA A*8001	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.416318	0.387379	-4.028939	26080.598934
HLA A*6802	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.320473	0.291433	-4.029039	20915.712785
HLA B*3501	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.282860	0.253787	-4.029072	19180.492926
HLA B*5401	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.320541	0.291433	-4.029108	20918.994441
HLA A*0250	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.501794	0.472542	-4.029252	31753.688091
HLA B*3501	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.413515	0.384238	-4.029277	25912.816823
HLA A*2501	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.461573	0.432006	-4.029567	28944.985794
HLA B*1801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.476211	0.446632	-4.029579	29937.162334
HLA B*7301	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.594643	0.564800	-4.029843	39322.712886
HLA B*1517	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.353638	0.323743	-4.029895	22575.532330
HLA A*0250	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.414147	0.384238	-4.029909	25950.554165
HLA A*0250	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.594822	0.564800	-4.030022	39338.883805
HLA A*2603	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.567819	0.537766	-4.030053	36967.442159
HLA A*0212	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.431096	0.400567	-4.030529	26983.347184
HLA A*0211	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.503103	0.472542	-4.030561	31849.516049
HLA A*2402	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.568458	0.537766	-4.030692	37021.879417

HLA A*8001	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.432433	0.401614	-4.030819	27066.536021
HLA B*0801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.431556	0.400567	-4.030989	27011.973834
HLA B*0803	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.477794	0.446632	-4.031162	30046.520423
HLA B*1501	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-3.986324	-0.044895	-4.031219	9690.009738
HLA A*2501	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.465828	0.434427	-4.031401	29229.962493
HLA A*0101	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.310048	0.278445	-4.031603	20419.636395
HLA B*7301	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.569544	0.537766	-4.031778	37114.526478
HLA A*3301	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.610167	0.578083	-4.032084	40753.650786
HLA A*1101	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.455855	0.423714	-4.032141	28566.346139
HLA A*0301	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.367570	0.335272	-4.032299	23311.512148
HLA B*0702	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.432879	0.400567	-4.032312	27094.371447
HLA A*0250	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.593744	0.561410	-4.032333	39241.321065
HLA A*0201	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.190494	0.157927	-4.032568	15505.810076
HLA B*1801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.464576	0.432006	-4.032570	29145.800145
HLA A*0301	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.356967	0.323743	-4.033225	22749.257157
HLA A*3301	1:115-123	9	KVYQNAGGT	0.678003	-0.098284	-4.613308	0.579719	-4.033589	41049.491451

HLA B*0702	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.421472	0.387379	-4.034094	26392.001713
HLA B*5301	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.599688	0.564800	-4.034887	39782.110247
HLA B*0802	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.481687	0.446632	-4.035055	30317.073864
HLA B*7301	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.622534	0.587095	-4.035439	41930.902376
HLA A*3101	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.193897	0.157927	-4.035970	15627.752135
HLA B*7301	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.467990	0.432006	-4.035983	29375.805518
HLA B*0801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.322296	0.286028	-4.036268	21003.703060
HLA B*2705	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.460060	0.423714	-4.036346	28844.317835
HLA B*0801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.423761	0.387379	-4.036382	26531.434323
HLA A*3301	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.574410	0.537766	-4.036644	37532.691355
HLA A*2403	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.381754	0.344471	-4.037283	24085.423486
HLA B*4001	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.328891	0.291433	-4.037458	21325.090073
HLA B*2705	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.439126	0.401614	-4.037512	27486.937886
HLA A*3101	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.361295	0.323743	-4.037552	22977.087144
HLA A*0203	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.361572	0.323743	-4.037830	22991.759639
HLA B*5701	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.329558	0.291433	-4.038125	21357.879305

HLA B*4801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.439744	0.401614	-4.038130	27526.074159
HLA A*0250	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.557855	0.519628	-4.038227	36128.941356
HLA A*3201	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.599935	0.561410	-4.038524	39804.714431
HLA A*0216	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.471319	0.432006	-4.039313	29601.860287
HLA B*4403	1:53-61	9	NISLPSYYP	0.515820	0.118220	-4.673814	0.634040	-4.039774	47186.098334
HLA A*2902	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.325827	0.286028	-4.039800	21175.181708
HLA A*0219	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.441429	0.401614	-4.039815	27633.052131
HLA B*4402	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.441596	0.401614	-4.039982	27643.668084
HLA B*4801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.427447	0.387379	-4.040068	26757.594696
HLA B*0803	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.513025	0.472542	-4.040483	32585.524273
HLA B*1501	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.364742	0.323743	-4.040999	23160.165894
HLA B*2705	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.199916	0.157927	-4.041989	15845.862936
HLA A*2602	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.629117	0.587095	-4.042022	42571.354237
HLA B*5101	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.320766	0.278445	-4.042321	20929.861529
HLA A*2603	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.656332	0.613638	-4.042693	45324.346447
HLA A*3301	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.463843	0.421102	-4.042741	29096.646868

HLA B*1517	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.444375	0.401614	-4.042761	27821.152097
HLA A*3002	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.607688	0.564800	-4.042887	40521.714563
HLA B*5401	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.563005	0.519628	-4.043377	36559.925936
HLA A*2501	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.427666	0.384238	-4.043428	26771.060356
HLA A*2403	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.008536	-0.035101	-4.043637	10198.498696
HLA B*1502	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.445317	0.401614	-4.043703	27881.571859
HLA A*0101	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.367700	0.323743	-4.043957	23318.449378
HLA B*4501	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.631176	0.587095	-4.044080	42773.581367
HLA B*4501	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.622201	0.578083	-4.044118	41898.703248
HLA A*3001	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.278436	0.234162	-4.044274	18986.096495
HLA A*1101	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.476330	0.432006	-4.044324	29945.423267
HLA B*3901	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.491167	0.446632	-4.044535	30986.138222
HLA B*5801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.350920	0.305553	-4.045367	22434.667928
HLA B*1509	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.331473	0.286028	-4.045445	21452.255371
HLA A*0201	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.369657	0.323743	-4.045914	23423.769648
HLA A*0301	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.351519	0.305553	-4.045966	22465.638397

HLA B*4403	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.639068	0.592876	-4.046192	43557.960298
HLA B*1502	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.565839	0.519628	-4.046211	36799.234638
HLA A*3002	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.586112	0.539612	-4.046500	38557.821836
HLA B*4601	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.381930	0.335272	-4.046659	24095.197929
HLA B*5101	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.468180	0.421102	-4.047078	29388.680846
HLA A*6901	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.382436	0.335272	-4.047164	24123.239989
HLA A*0202	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.353027	0.305553	-4.047475	22543.800559
HLA A*2501	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.449109	0.401614	-4.047495	28126.087454
HLA B*1501	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.338991	0.291433	-4.047558	21826.862382
HLA B*4501	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.611964	0.564331	-4.047633	40922.661917
HLA B*4402	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.435193	0.387379	-4.047815	27239.135693
HLA B*0802	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.406116	0.357949	-4.048167	25475.111690
HLA A*0250	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.406492	0.357949	-4.048543	25497.172041
HLA A*3201	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.613345	0.564800	-4.048545	41053.044776
HLA B*7301	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.613139	0.564331	-4.048808	41033.505295
HLA A*6801	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.613959	0.564800	-4.049158	41111.051841

HLA A*3301	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.384456	0.335272	-4.049184	24235.734964
HLA B*5101	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.502041	0.452621	-4.049420	31771.730528
HLA B*7301	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.589115	0.539612	-4.049503	38825.328064
HLA A*0202	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.004655	-0.044895	-4.049550	10107.759396
HLA A*2603	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.614497	0.564800	-4.049696	41162.014430
HLA B*0802	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.473464	0.423714	-4.049750	29748.432326
HLA A*8001	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.380260	0.330347	-4.049913	24002.695425
HLA B*1801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.394954	0.344471	-4.050483	24828.683563
HLA B*4601	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.395078	0.344471	-4.050607	24835.803566
HLA A*2603	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.590379	0.539612	-4.050767	38938.494578
HLA B*1502	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.615763	0.564800	-4.050963	41282.215156
HLA A*6801	1:120-128	9	AGGTHPTTT	0.991249	-0.369291	-4.673217	0.621958	-4.051259	47121.303885
HLA A*3001	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.305084	0.253787	-4.051296	20187.546624
HLA B*0803	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.472776	0.421102	-4.051674	29701.315512
HLA B*4601	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.375589	0.323743	-4.051847	23745.933002
HLA B*3501	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.439829	0.387379	-4.052450	27531.435550

HLA A*6802	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.439899	0.387379	-4.052521	27535.904173
HLA A*0101	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.387802	0.335272	-4.052530	24423.160369
HLA A*2602	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.614114	0.561410	-4.052703	41125.733273
HLA A*2602	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.622912	0.570132	-4.052780	41967.439773
HLA B*0803	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.476812	0.423714	-4.053098	29978.651980
HLA A*3301	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.640315	0.587095	-4.053220	43683.267017
HLA A*3001	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.306855	0.253524	-4.053331	20270.060941
HLA A*6801	1:73-81	9	TRDKFLSAA	0.841706	-0.248830	-4.646377	0.592876	-4.053501	44297.251710
HLA A*0211	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.438165	0.384238	-4.053928	27426.186295
HLA B*1502	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.615549	0.561410	-4.054139	41261.896927
HLA B*4002	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.641699	0.587095	-4.054604	43822.682459
HLA A*6802	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.088132	0.033425	-4.054707	12249.887425
HLA A*2902	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.346371	0.291433	-4.054938	22200.923618
HLA B*1509	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.412962	0.357949	-4.055013	25879.894170
HLA B*5301	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.592877	0.537766	-4.055111	39163.063750
HLA B*1503	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.476291	0.421102	-4.055189	29942.669369

HLA B*3901	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.479448	0.423714	-4.055734	30161.172649
HLA A*3001	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.300967	0.245175	-4.055793	19997.110432
HLA B*1501	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.290047	0.234162	-4.055885	19500.549019
HLA B*4501	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.617671	0.561410	-4.056261	41463.959803
HLA B*5801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.342313	0.286028	-4.056286	21994.469026
HLA A*0101	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.361983	0.305553	-4.056431	23013.536948
HLA B*5101	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.490895	0.434427	-4.056468	30966.699060
HLA A*2301	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.529431	0.472542	-4.056889	33840.063287
HLA B*4402	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.380678	0.323743	-4.056936	24025.820199
HLA B*4403	1:40-48	9	ACQIQMSDP	0.533748	0.079890	-4.670809	0.613638	-4.057171	46860.732947
HLA B*3501	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.343596	0.286028	-4.057569	22059.532322
HLA B*4001	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.402068	0.344471	-4.057597	25238.755364
HLA A*0202	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.597219	0.539612	-4.057606	39556.559209
HLA B*5101	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.481577	0.423714	-4.057863	30309.366279
HLA B*5401	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.530803	0.472542	-4.058261	33947.145814
HLA A*1101	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.403083	0.344471	-4.058612	25297.809135

HLA A*0301	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.350071	0.291433	-4.058638	22390.896451
HLA A*0203	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.459534	0.400567	-4.058967	28809.385024
HLA B*3901	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.491203	0.432006	-4.059196	30988.652798
HLA A*3001	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.236039	0.176828	-4.059211	17220.241070
HLA A*8001	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.337704	0.278445	-4.059259	21762.249869
HLA A*6901	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.156272	0.096880	-4.059392	14330.847074
HLA A*3301	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.625772	0.566374	-4.059398	42244.658053
HLA A*0211	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.512059	0.452621	-4.059438	32513.152007
HLA B*1503	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-3.863460	-0.196092	-4.059553	7302.309646
HLA A*2902	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.338033	0.278445	-4.059588	21778.738503
HLA A*3301	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.624900	0.564800	-4.060100	42159.955146
HLA A*6802	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.228904	0.168569	-4.060335	16939.626913
HLA A*3101	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.351895	0.291433	-4.060461	22485.092674
HLA A*6801	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.631056	0.570132	-4.060923	42761.781578
HLA B*5701	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.418935	0.357949	-4.060985	26238.251280
HLA B*2705	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.391563	0.330347	-4.061216	24635.613766

HLA B*4002	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.639368	0.578083	-4.061286	43588.133142
HLA A*6901	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.315259	0.253524	-4.061735	20666.130250
HLA A*0250	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.601408	0.539612	-4.061795	39939.961291
HLA A*6901	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.297814	0.235698	-4.062116	19852.455723
HLA B*4001	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.386698	0.323743	-4.062955	24361.139753
HLA B*5701	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.393370	0.330347	-4.063023	24738.316447
HLA A*0219	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.386972	0.323743	-4.063230	24376.564189
HLA B*3801	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.535796	0.472542	-4.063254	34339.654512
HLA B*0801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.334755	0.271476	-4.063279	21614.997457
HLA A*0201	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.398558	0.335272	-4.063286	25035.588436
HLA B*1509	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.281899	0.218305	-4.063593	19138.100228
HLA A*0216	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.293256	0.229395	-4.063861	19645.190077
HLA A*2601	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.387983	0.323743	-4.064240	24433.336236
HLA B*4002	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.645968	0.581216	-4.064752	44255.573409
HLA A*0101	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.351091	0.286028	-4.065064	22443.529619
HLA A*2902	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.233711	0.168569	-4.065142	17128.166945

HLA B*4801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.059370	-0.005967	-4.065337	11464.884983
HLA A*3301	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.635628	0.570132	-4.065495	43214.340412
HLA B*5401	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.396091	0.330347	-4.065744	24893.779835
HLA B*4002	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.635915	0.570132	-4.065782	43242.871571
HLA B*0802	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.396258	0.330347	-4.065910	24903.343425
HLA B*5701	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.410484	0.344471	-4.066013	25732.607122
HLA B*4501	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.647488	0.581216	-4.066272	44410.748103
HLA B*1801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.487664	0.421102	-4.066562	30737.204863
HLA B*2705	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.487937	0.421102	-4.066835	30756.499962
HLA B*5101	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.498857	0.432006	-4.066851	31539.682583
HLA B*4501	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.631711	0.564800	-4.066911	42826.373195
HLA B*5801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.338402	0.271476	-4.066926	21797.244189
HLA B*0802	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.498965	0.432006	-4.066959	31547.532364
HLA B*1801	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.539708	0.472542	-4.067166	34650.365019
HLA A*3201	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.586963	0.519628	-4.067335	38633.406686
HLA A*2603	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.637637	0.570132	-4.067504	43414.689404

HLA B*1517 1:178-186 9 PNAGLDPVN 1.201582 -0.769576 -4.499790
0.432006 -4.067784 31607.493973

HLA B*5401 1:22-30 9 TAAPKTYCE 1.011561 -0.590459 -4.489436
0.421102 -4.068334 30862.839717

HLA A*2501 1:143-151 9 TYDTLWQAD 1.156171 -0.755604 -4.469148
0.400567 -4.068581 29454.257577

HLA B*3901 1:94-102 9 NITSATYQS 1.243610 -0.899139 -4.413061
0.344471 -4.068590 25885.775147

HLA A*0202 1:80-88 9 AATSSTPRE 1.057554 -0.585012 -4.541555
0.472542 -4.069012 34798.018061

HLA B*4002 1:101-109 9 QSAIPPRGT 0.865514 -0.299140 -4.635470
0.566374 -4.069097 43198.679670

HLA B*2705 1:143-151 9 TYDTLWQAD 1.156171 -0.755604 -4.469820
0.400567 -4.069253 29499.865311

HLA A*6802 1:100-108 9 YQSAIPPRG 0.865176 -0.579148 -4.355684
0.286028 -4.069657 22682.159559

HLA A*2403 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.375606
0.305553 -4.070053 23746.832259

HLA B*1801 1:216-224 9 VLVPRSAID 1.164467 -0.740753 -4.493787
0.423714 -4.070073 31173.612282

HLA B*4501 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.163466
0.093374 -4.070092 14570.215818

HLA B*4002 1:195-203 9 DGVIFFFNP 0.675455 -0.114045 -4.631596
0.561410 -4.070186 42815.022089

HLA A*6801 1:40-48 9 ACQIQMSDP 0.533748 0.079890 -4.683907
0.613638 -4.070269 48295.587778

HLA A*0219 1:118-126 9 QNAGGTHPT 0.654006 -0.382530 -4.341808
0.271476 -4.070332 21968.901556

HLA B*4403 1:115-123 9 KVYQNAGGT 0.678003 -0.098284 -4.650098
0.579719 -4.070380 44678.477652

HLA B*3901 1:45-53 9 MSDPAYNIN 0.920513 -0.629080 -4.361861
0.291433 -4.070428 23007.063823

HLA B*4002	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.634775	0.564331	-4.070444	43129.559806
HLA A*2603	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.657553	0.587095	-4.070458	45452.029797
HLA A*2603	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.590302	0.519628	-4.070674	38931.543652
HLA A*3002	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.415171	0.344471	-4.070700	26011.836285
HLA A*0301	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.357094	0.286028	-4.071067	22755.903960
HLA A*3101	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.357205	0.286028	-4.071177	22761.690721
HLA A*2501	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.342835	0.271476	-4.071359	22020.900151
HLA B*3901	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.505788	0.434427	-4.071361	32047.067787
HLA A*3001	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.290002	0.218305	-4.071697	19498.544702
HLA A*6801	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.170045	0.098300	-4.071745	14792.600983
HLA A*0212	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.377351	0.305553	-4.071799	23842.475875
HLA B*5301	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.544362	0.472542	-4.071820	35023.709640
HLA A*0206	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.163898	0.091985	-4.071913	14584.726517
HLA A*0203	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.407359	0.335272	-4.072087	25548.121585
HLA A*1101	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.232919	0.160477	-4.072443	17096.968473
HLA A*0203	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.164664	0.092119	-4.072546	14610.471184

HLA B*5301	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.612342	0.539612	-4.072730	40958.320762
HLA B*1509	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.525533	0.452621	-4.072912	33537.707366
HLA A*0219	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.473817	0.400567	-4.073249	29772.582481
HLA B*7301	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.327298	0.253787	-4.073511	21247.014946
HLA B*1509	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.546105	0.472542	-4.073563	35164.582186
HLA B*5801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.352482	0.278445	-4.074037	22515.523712
HLA A*2301	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.508471	0.434427	-4.074044	32245.670427
HLA A*1101	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.475689	0.401614	-4.074075	29901.229522
HLA A*2402	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.593774	0.519628	-4.074146	39244.080948
HLA A*3201	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.397923	0.323743	-4.074181	24999.046396
HLA B*4001	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.352740	0.278445	-4.074296	22528.926413
HLA A*0206	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.495606	0.421102	-4.074504	31304.417787
HLA B*1509	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.476408	0.401614	-4.074794	29950.769791
HLA A*2501	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.380554	0.305553	-4.075001	24018.932404
HLA B*4001	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.410409	0.335272	-4.075137	25728.152770
HLA A*6801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.366656	0.291433	-4.075223	23262.505892

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HLA B*0801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.252328
	0.176828	-4.075500	17878.381754

HLA B*1509	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.496867
	0.421102	-4.075765	31395.492806

HLA B*4801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.406299
	0.330347	-4.075952	25485.863726

HLA A*3001	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.244612
	0.168569	-4.076043	17563.557939

HLA B*4403	1:152-160	9	TDPLPVVFP	0.730366	-0.165566	-4.641177
	0.564800	-4.076377	43770.083211

HLA A*8001	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.421150
	0.344471	-4.076679	26372.448401

HLA B*5401	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.508993
	0.432006	-4.076987	32284.420593

HLA A*3301	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.616684
	0.539612	-4.077072	41369.854276

HLA B*5701	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.400879
	0.323743	-4.077136	25169.761172

HLA B*1509	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.511751
	0.434427	-4.077324	32490.118246

HLA A*2501	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.421806
	0.344471	-4.077335	26412.283951

HLA A*2501	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.464776
	0.387379	-4.077397	29159.205648

HLA B*4403	1:195-203	9	DGVIFFFNP	0.675455	-0.114045	-4.638844
	0.561410	-4.077434	43535.579895

HLA B*1517	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.464834
	0.387379	-4.077456	29163.149617

HLA A*3001	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.235492
	0.157927	-4.077565	17198.548558

HLA A*1101	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.369114
	0.291433	-4.077681	23394.515611
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HLA A*2301	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.478410	0.400567	-4.077843	30089.138285
HLA B*4402	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.422429	0.344471	-4.077957	26450.176301
HLA A*2601	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.383702	0.305553	-4.078149	24193.684330
HLA B*0802	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.478734	0.400567	-4.078167	30111.610161
HLA B*5401	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.462414	0.384238	-4.078177	29001.099035
HLA B*1801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.349658	0.271476	-4.078182	22369.587318
HLA B*0802	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.402051	0.323743	-4.078309	25237.799610
HLA B*4801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.413693	0.335272	-4.078421	25923.473109
HLA B*4001	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.349966	0.271476	-4.078490	22385.446162
HLA B*3801	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.462757	0.384238	-4.078520	29024.014423
HLA B*5101	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.436558	0.357949	-4.078609	27324.886956
HLA B*3901	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.480736	0.401614	-4.079122	30250.721716
HLA A*2301	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.463547	0.384238	-4.079309	29076.820012
HLA B*4801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.423787	0.344471	-4.079315	26533.013223
HLA A*3101	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.172808	0.093374	-4.079433	14887.011953
HLA B*4801	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.403461	0.323743	-4.079718	25319.852927

HLA A*1101	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.464141	0.384238	-4.079904	29116.644761
HLA A*3301	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.503749	0.423714	-4.080035	31896.934459
HLA B*1501	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.416019	0.335272	-4.080747	26062.686259
HLA B*4001	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.386315	0.305553	-4.080762	24339.667278
HLA A*6901	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.241239	0.160477	-4.080762	17427.642289
HLA B*4403	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.658921	0.578083	-4.080838	45595.363563
HLA A*2601	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.372699	0.291433	-4.081266	23588.448223
HLA A*2602	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.527939	0.446632	-4.081307	33724.012655
HLA B*4403	1:18-26	9	SGVATAAPK	0.424227	0.140104	-4.645757	0.564331	-4.081426	44234.031057
HLA B*4403	1:165-173	9	ELSKQTGQQ	0.723302	-0.142086	-4.662898	0.581216	-4.081682	46014.887132
HLA A*0250	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.528421	0.446632	-4.081789	33761.434252
HLA A*8001	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.417199	0.335272	-4.081927	26133.562571
HLA B*0801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.417408	0.335272	-4.082136	26146.148392
HLA B*3901	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.210193	0.127871	-4.082321	16225.292787
HLA B*1502	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.621987	0.539612	-4.082375	41878.081596
HLA A*2402	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.503646	0.421102	-4.082544	31889.342772

HLA B*0803	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.483351	0.400567	-4.082784	30433.417033
HLA A*3201	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.622750	0.539612	-4.083138	41951.776992
HLA B*1509	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.407204	0.323743	-4.083461	25539.001188
HLA B*4403	1:101-109	9	QSAIPPRGT	0.865514	-0.299140	-4.649870	0.566374	-4.083497	44655.038359
HLA B*5301	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.603254	0.519628	-4.083627	40110.154499
HLA B*0802	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.471070	0.387379	-4.083691	29584.890018
HLA A*3101	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.389259	0.305553	-4.083706	24505.216391
HLA A*3001	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.174697	0.090830	-4.083867	14951.904794
HLA B*3801	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.536498	0.452621	-4.083877	34395.245804
HLA B*5101	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.468349	0.384238	-4.084112	29400.130321
HLA A*1101	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.408022	0.323743	-4.084279	25587.127257
HLA A*2603	1:97-105	9	SATYQSAIP	0.500068	0.078015	-4.662372	0.578083	-4.084289	45959.159366
HLA B*1517	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.468946	0.384238	-4.084708	29440.557157
HLA A*0206	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.261691	0.176828	-4.084863	18267.995846
HLA B*4403	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.672186	0.587095	-4.085091	47009.526338
HLA A*2403	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.408971	0.323743	-4.085228	25643.111517

HLA A*0201	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.390856	0.305553	-4.085304	24595.530352
HLA A*6901	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.339341	0.253787	-4.085554	21844.463530
HLA B*4601	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.391653	0.305553	-4.086100	24640.678772
HLA A*2602	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.606104	0.519628	-4.086476	40374.230688
HLA A*0301	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.365169	0.278445	-4.086724	23182.980619
HLA A*0201	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.358473	0.271476	-4.086997	22828.282583
HLA B*3501	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.422302	0.335272	-4.087030	26442.450433
HLA A*6802	1:50-58	9	YNINISLPS	0.643875	-0.954020	-3.776910	-0.310145	-4.087055	5982.874821
HLA B*1801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.521699	0.434427	-4.087272	33242.908287
HLA B*5401	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.539978	0.452621	-4.087357	34671.929009
HLA A*2603	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.358967	0.271476	-4.087491	22854.232001
HLA B*4501	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.560327	0.472542	-4.087785	36335.144725
HLA B*0802	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.432266	0.344471	-4.087795	27056.141704
HLA A*2301	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.508913	0.421102	-4.087811	32278.482864
HLA A*1101	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.488416	0.400567	-4.087849	30790.462107
HLA A*0250	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.432350	0.344471	-4.087879	27061.411563

HLA B*4601	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.373916	0.286028	-4.087889	23654.643371
HLA A*2301	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.540706	0.452621	-4.088085	34730.124895
HLA B*4402	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.374405	0.286028	-4.088378	23681.275904
HLA B*1509	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.512193	0.423714	-4.088479	32523.179428
HLA A*0216	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.423763	0.335272	-4.088491	26531.577855
HLA A*3101	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.180509	0.091985	-4.088524	15153.367257
HLA B*4601	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.360139	0.271476	-4.088663	22916.011143
HLA A*0206	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.342581	0.253787	-4.088794	22008.037801
HLA B*1801	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.473053	0.384238	-4.088815	29720.281902
HLA A*3101	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.053759	-0.035101	-4.088860	11317.724866
HLA B*1509	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.216851	0.127871	-4.088980	16475.969636
HLA B*1501	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.324753	0.235698	-4.089055	21122.894559
HLA B*4501	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.659466	0.570132	-4.089333	45652.625971
HLA B*1502	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.477075	0.387379	-4.089697	29996.821777
HLA A*6802	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.319195	0.229395	-4.089799	20854.248755
HLA A*6802	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.425831	0.335272	-4.090559	26658.187940

HLA B*0702	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.435081	0.344471	-4.090609	27232.063297
HLA B*4402	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.421017	0.330347	-4.090669	26364.317350
HLA B*1517	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.448632	0.357949	-4.090683	28095.216129
HLA A*0201	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.382567	0.291433	-4.091134	24130.549323
HLA B*5701	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.427024	0.335272	-4.091752	26731.551367
HLA A*0301	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.345563	0.253787	-4.091775	22159.646078
HLA B*1509	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.538599	0.446632	-4.091967	34561.999299
HLA A*0301	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.363447	0.271476	-4.091971	23091.231730
HLA A*6802	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.252488	0.160477	-4.092011	17884.959928
HLA B*0803	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.450040	0.357949	-4.092090	28186.407013
HLA A*0212	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.427445	0.335272	-4.092173	26757.449941
HLA B*1801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.493912	0.401614	-4.092298	31182.551790
HLA B*4501	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.630485	0.537766	-4.092719	42705.603743
HLA B*5101	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.494447	0.401614	-4.092833	31221.037786
HLA A*2902	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.398617	0.305553	-4.093064	25038.974659
HLA A*3002	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.364627	0.271476	-4.093150	23154.027305

HLA B*2705	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.417027	0.323743	-4.093284	26123.243892
HLA A*3001	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.263354	0.169649	-4.093706	18338.100123
HLA A*2601	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.365468	0.271476	-4.093992	23198.914096
HLA A*2601	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.262765	0.168569	-4.094195	18313.216042
HLA B*7301	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.566943	0.472542	-4.094401	36892.921190
HLA B*0803	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.526539	0.432006	-4.094533	33615.451636
HLA A*2602	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.634209	0.539612	-4.094597	43073.364848
HLA A*3002	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.452551	0.357949	-4.094602	28349.886097
HLA A*6801	1:203-211	9	PGELLPEAA	1.144110	-0.557015	-4.681746	0.587095	-4.094651	48055.813090
HLA B*4403	1:176-184	9	IAPNAGLDP	0.476515	0.093617	-4.665029	0.570132	-4.094897	46241.226417
HLA A*6802	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.348906	0.253524	-4.095382	22330.895383
HLA B*2705	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.439869	0.344471	-4.095398	27533.967680
HLA B*5801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.349188	0.253787	-4.095401	22345.397010
HLA A*2403	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.374043	0.278445	-4.095598	23661.554707
HLA A*2301	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.520057	0.423714	-4.096343	33117.437198
HLA B*0702	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.431657	0.335272	-4.096386	27018.258232

HLA B*1503	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.528402	0.432006	-4.096396	33759.973119
HLA A*3101	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.326015	0.229395	-4.096620	21184.348122
HLA A*3301	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.616364	0.519628	-4.096737	41339.427810
HLA A*3001	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.188944	0.092119	-4.096825	15450.544886
HLA A*3201	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.441913	0.344471	-4.097442	27663.864597
HLA B*3901	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.315839	0.218305	-4.097534	20693.763672
HLA B*4001	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.383667	0.286028	-4.097639	24191.721132
HLA B*4403	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.343831	0.245175	-4.098657	22071.469513
HLA A*0216	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.370308	0.271476	-4.098832	23458.897400
HLA A*3002	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.385037	0.286028	-4.099009	24268.141433
HLA A*2902	1:50-58	9	YNINISLPS	0.643875	-0.954020	-3.789043	-0.310145	-4.099188	6152.372989
HLA A*6801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.276187	0.176828	-4.099359	18888.054476
HLA B*5701	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.405125	0.305553	-4.099572	25417.019030
HLA A*0203	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.391025	0.291433	-4.099592	24605.112473
HLA A*2301	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.546336	0.446632	-4.099704	35183.230305
HLA A*0301	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.341719	0.241980	-4.099740	21964.385746

HLA A*0250	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.192012	0.092119	-4.099894	15560.094401
HLA A*1101	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.458484	0.357949	-4.100534	28739.801748
HLA A*3001	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.224271	0.123229	-4.101042	16759.870421
HLA A*3001	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.223279	0.122021	-4.101259	16721.651728
HLA B*5801	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.354963	0.253524	-4.101439	22644.519478
HLA A*0203	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.278309	0.176828	-4.101481	18980.550820
HLA A*0211	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.522636	0.421102	-4.101535	33314.742127
HLA A*8001	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.373033	0.271476	-4.101557	23606.575932
HLA A*0216	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.425396	0.323743	-4.101653	26631.520986
HLA A*3201	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.355734	0.253787	-4.101946	22684.736573
HLA A*0101	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.373710	0.271476	-4.102234	23643.384779
HLA A*2902	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.425997	0.323743	-4.102255	26668.429374
HLA B*1517	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.502908	0.400567	-4.102341	31835.218164
HLA A*2601	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.380822	0.278445	-4.102377	24033.750106
HLA A*1101	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.432877	0.330347	-4.102529	27094.224870
HLA A*2402	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.526407	0.423714	-4.102693	33605.269250

HLA A*0206	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.534753	0.432006	-4.102746	34257.269962
HLA B*5101	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.433102	0.330347	-4.102755	27108.299893
HLA A*6802	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.337373	0.234162	-4.103211	21745.656077
HLA A*0202	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.263765	0.160477	-4.103289	18355.469584
HLA B*5101	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.503958	0.400567	-4.103391	31912.295897
HLA A*2402	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.576386	0.472542	-4.103843	37703.843522
HLA A*2403	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.194813	0.090830	-4.103983	15660.759261
HLA A*6901	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.333482	0.229395	-4.104086	21551.711656
HLA A*0219	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.382555	0.278445	-4.104111	24129.896614
HLA B*7301	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.556890	0.452621	-4.104269	36048.699181
HLA A*3101	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.227616	0.123229	-4.104387	16889.481737
HLA A*2902	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.196542	0.092119	-4.104423	15723.239674
HLA A*0211	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.536599	0.432006	-4.104593	34403.247937
HLA A*2601	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.391260	0.286028	-4.105233	24618.427167
HLA A*3101	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.282148	0.176828	-4.105320	19149.078085
HLA B*4402	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.440646	0.335272	-4.105375	27583.316191

HLA A*2602	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.526609	0.421102	-4.105508	33620.907755
HLA B*1509	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.506214	0.400567	-4.105646	32078.463322
HLA B*1503	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.196519	0.090830	-4.105689	15722.389088
HLA B*2705	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.377370	0.271476	-4.105894	23843.507779
HLA B*5801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.351089	0.245175	-4.105914	22443.408203
HLA B*1509	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.493435	0.387379	-4.106056	31148.325675
HLA A*3101	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.267123	0.160477	-4.106646	18497.920709
HLA A*0201	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.336409	0.229395	-4.107014	21697.476478
HLA A*0250	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.442550	0.335272	-4.107278	27704.451779
HLA A*0201	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.385831	0.278445	-4.107386	24312.557358
HLA A*0212	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.378914	0.271476	-4.107438	23928.405478
HLA A*2301	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.540001	0.432006	-4.107995	34673.804773
HLA B*1502	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.362167	0.253787	-4.108379	23023.250051
HLA A*0201	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.362423	0.253787	-4.108635	23036.830356
HLA B*4601	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.400165	0.291433	-4.108732	25128.400844
HLA A*3201	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.581305	0.472542	-4.108763	38133.392708

HLA A*2902	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.362578	0.253787	-4.108790	23045.057187
HLA B*4601	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.387264	0.278445	-4.108819	24392.922114
HLA A*0206	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.509442	0.400567	-4.108875	32317.796965
HLA B*5801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.350906	0.241980	-4.108926	22433.939725
HLA B*4002	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.646725	0.537766	-4.108959	44332.733109
HLA A*8001	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.432905	0.323743	-4.109162	27095.983848
HLA B*1801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.496689	0.387379	-4.109310	31382.587153
HLA B*1501	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.269806	0.160477	-4.109329	18612.556341
HLA A*3001	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.206245	0.096880	-4.109366	16078.495470
HLA B*1801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.439805	0.330347	-4.109458	27529.946170
HLA A*0301	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.345810	0.235698	-4.110111	22172.237183
HLA B*2705	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.445425	0.335272	-4.110154	27888.511188
HLA B*4002	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.649878	0.539612	-4.110265	44655.763101
HLA B*1503	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.352282	0.241980	-4.110303	22505.172541
HLA A*6901	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.150826	0.040514	-4.110311	14152.258590
HLA B*0801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.401908	0.291433	-4.110475	25229.472429

HLA A*2603	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.468563	0.357949	-4.110614	29414.607565
HLA A*3201	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.417485	0.305553	-4.111933	26150.816585
HLA B*1502	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.584787	0.472542	-4.112245	38440.354376
HLA A*2601	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.366548	0.253524	-4.113024	23256.717624
HLA A*0301	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.366671	0.253524	-4.113146	23263.260990
HLA B*5701	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.399209	0.286028	-4.113181	25073.133373
HLA B*1502	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.153824	0.040514	-4.113309	14250.289860
HLA B*4402	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.342910	0.229395	-4.113515	22024.712661
HLA A*6801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.331821	0.218305	-4.113515	21469.438289
HLA A*0219	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.449401	0.335272	-4.114129	28144.961502
HLA B*5801	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.350184	0.235698	-4.114486	22396.711555
HLA A*2602	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.459076	0.344471	-4.114605	28779.009211
HLA B*1501	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.207152	0.092119	-4.115034	16112.105942
HLA A*6802	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.333743	0.218305	-4.115437	21564.657295
HLA A*1101	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.273495	0.157927	-4.115568	18771.315831
HLA A*2602	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.212519	0.096880	-4.115639	16312.425175

HLA B*1503	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.460215	0.344471	-4.115744	28854.618615
HLA A*0212	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.407197	0.291433	-4.115764	25538.586702
HLA A*3002	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.547886	0.432006	-4.115880	35309.077510
HLA A*0211	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.516453	0.400567	-4.115886	32843.740450
HLA B*0803	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.503361	0.387379	-4.115983	31868.474948
HLA A*3002	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.285230	0.168569	-4.116661	19285.477418
HLA A*0212	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.395252	0.278445	-4.116807	24845.748118
HLA B*4002	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.180833	0.063696	-4.117138	15164.684450
HLA B*2705	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.395710	0.278445	-4.117265	24871.972433
HLA A*6901	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.351932	0.234162	-4.117770	22487.039027
HLA B*3501	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.336325	0.218305	-4.118019	21693.251176
HLA B*4403	1:205-213	9	ELLPEAAGP	0.578973	-0.041207	-4.656057	0.537766	-4.118291	45295.667161
HLA B*5401	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.542194	0.423714	-4.118480	34849.260684
HLA B*5401	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.520127	0.401614	-4.118513	33122.812485
HLA A*2402	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.565176	0.446632	-4.118544	36743.136942
HLA A*2402	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.553184	0.434427	-4.118757	35742.461657

HLA B*4501	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.658547	0.539612	-4.118935	45556.160554
HLA A*0212	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.353229	0.234162	-4.119067	22554.291513
HLA A*3201	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.449591	0.330347	-4.119244	28157.297356
HLA B*5801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.353513	0.234162	-4.119352	22569.060308
HLA A*3101	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.398654	0.278445	-4.120209	25041.142082
HLA B*5101	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.507628	0.387379	-4.120249	32183.105266
HLA A*0301	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.349728	0.229395	-4.120333	22373.218122
HLA B*4002	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.504764	0.384238	-4.120526	31971.567072
HLA B*5301	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.541834	0.421102	-4.120732	34820.427431
HLA B*1503	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.214238	0.093374	-4.120864	16377.151086
HLA B*1509	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.456273	0.335272	-4.121001	28593.867645
HLA A*3001	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.213050	0.091985	-4.121065	16332.381513
HLA A*2402	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.573886	0.452621	-4.121265	37487.439020
HLA A*3301	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.521946	0.400567	-4.121379	33261.796899
HLA B*5401	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.555912	0.434427	-4.121485	35967.662304
HLA A*3201	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-3.997108	-0.124403	-4.121511	9933.638462

HLA A*3002	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.568252	0.446632	-4.121620	37004.258596
HLA B*4402	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.375335	0.253524	-4.121811	23732.063065
HLA B*3801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.553934	0.432006	-4.121928	35804.197631
HLA A*3301	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.524121	0.401614	-4.122507	33428.841839
HLA A*2501	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.446318	0.323743	-4.122575	27945.902185
HLA A*0301	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.367782	0.245175	-4.122607	23322.865054
HLA A*6801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.457889	0.335272	-4.122618	28700.492433
HLA A*3101	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.394590	0.271476	-4.123113	24807.872623
HLA B*1801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.368381	0.245175	-4.123207	23355.061656
HLA B*5401	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.300286	0.176828	-4.123458	19965.762206
HLA B*5101	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-3.907974	-0.215742	-4.123715	8090.466941
HLA B*4801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.395339	0.271476	-4.123863	24850.721887
HLA B*3801	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.547748	0.423714	-4.124034	35297.809235
HLA A*8001	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.415476	0.291433	-4.124043	26030.136469
HLA A*2602	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.558558	0.434427	-4.124131	36187.429264
HLA A*2403	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.395647	0.271476	-4.124171	24868.339724

HLA B*5101	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.415629	0.291433	-4.124196	26039.291388
HLA B*5801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.353652	0.229395	-4.124257	22576.265129
HLA A*6801	1:164-172	9	GELSKQTGQ	0.717063	-0.197435	-4.644124	0.519628	-4.124496	44068.028989
HLA A*0301	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.283158	0.157927	-4.125232	19193.675525
HLA A*3201	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.548977	0.423714	-4.125263	35397.821288
HLA B*0702	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.431009	0.305553	-4.125456	26977.946579
HLA B*1501	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.166093	0.040514	-4.125578	14658.607252
HLA A*0101	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.379459	0.253787	-4.125671	23958.456737
HLA B*1503	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.431610	0.305553	-4.126058	27015.335074
HLA B*4801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.431718	0.305553	-4.126166	27022.058809
HLA A*8001	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.412201	0.286028	-4.126174	25834.571518
HLA A*0202	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.558205	0.432006	-4.126199	36158.075678
HLA A*2301	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.513814	0.387379	-4.126435	32644.809587
HLA A*0219	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.380610	0.253787	-4.126823	24022.051161
HLA A*0101	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.372159	0.245175	-4.126984	23559.115971
HLA A*3002	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.527859	0.400567	-4.127292	33717.810158

HLA B*2705	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.082442	-0.044895	-4.127336	12090.427159
HLA A*2402	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.511700	0.384238	-4.127462	32486.251581
HLA B*7301	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.361697	0.234162	-4.127535	22998.352876
HLA B*3501	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.304480	0.176828	-4.127651	20159.498542
HLA A*0203	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.288482	0.160477	-4.128006	19430.415232
HLA B*1517	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.414238	0.286028	-4.128211	25956.029938
HLA B*1517	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.472736	0.344471	-4.128265	29698.584063
HLA A*3001	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.294917	0.166493	-4.128424	19720.472714
HLA B*4403	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.668765	0.539612	-4.129153	46640.696274
HLA A*3001	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.194897	0.065526	-4.129372	15663.809585
HLA B*3501	1:50-58	9	YNINISLPS	0.643875	-0.954020	-3.819464	-0.310145	-4.129609	6598.782115
HLA A*0101	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.383155	0.253524	-4.129630	24163.207302
HLA A*3201	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.514150	0.384238	-4.129912	32670.073845
HLA A*2501	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.421641	0.291433	-4.130208	26402.283717
HLA A*0212	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.384249	0.253787	-4.130462	24224.199798
HLA B*3801	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.551685	0.421102	-4.130584	35619.308873

HLA B*4402	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.436220	0.305553	-4.130667	27303.608501
HLA B*1503	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.518182	0.387379	-4.130803	32974.774356
HLA B*3901	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.436450	0.305553	-4.130898	27318.087870
HLA A*6801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.565383	0.434427	-4.130956	36760.633420
HLA A*2601	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.384745	0.253787	-4.130958	24251.867186
HLA B*3801	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.565484	0.434427	-4.131057	36769.185866
HLA A*3002	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.436720	0.305553	-4.131168	27335.088758
HLA A*2301	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.489166	0.357949	-4.131216	30843.644767
HLA A*3301	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.476037	0.344471	-4.131566	29925.179935
HLA B*0802	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.410106	0.278445	-4.131661	25710.203981
HLA B*1501	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.410113	0.278445	-4.131668	25710.621253
HLA A*0301	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.223820	0.092119	-4.131701	16742.471003
HLA A*2602	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.584604	0.452621	-4.131983	38424.137070
HLA B*1517	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.437677	0.305553	-4.132124	27395.342146
HLA B*3801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.519911	0.387379	-4.132532	33106.331038
HLA B*1503	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.533329	0.400567	-4.132762	34145.145069

HLA B*4801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.424365	0.291433	-4.132931	26568.347732
HLA A*2601	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.369027	0.235698	-4.133329	23389.833296
HLA B*5301	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.580037	0.446632	-4.133405	38022.154658
HLA A*2301	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.535056	0.401614	-4.133442	34281.185622
HLA A*0203	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.387351	0.253787	-4.133563	24397.805234
HLA A*3001	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.261444	0.127871	-4.133573	18257.621871
HLA A*0250	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.586251	0.452621	-4.133630	38570.130819
HLA A*0301	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.367845	0.234162	-4.133684	23326.272004
HLA A*0219	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.363200	0.229395	-4.133805	23078.118750
HLA B*0801	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.387959	0.253524	-4.134435	24432.014455
HLA A*6901	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.352863	0.218305	-4.134557	22535.265012
HLA A*6901	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.311401	0.176828	-4.134573	20483.365186
HLA A*0206	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.426044	0.291433	-4.134611	26671.314995
HLA A*2402	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.566621	0.432006	-4.134615	36865.587954
HLA B*1502	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.587386	0.452621	-4.134765	38671.045449
HLA A*3201	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.556011	0.421102	-4.134909	35975.835638

HLA B*1517	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.470351	0.335272	-4.135079	29535.954935
HLA B*1501	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.377295	0.241980	-4.135315	23839.380433
HLA B*0802	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.470638	0.335272	-4.135366	29555.455291
HLA A*0250	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.556493	0.421102	-4.135391	36015.755953
HLA A*0101	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.364843	0.229395	-4.135447	23165.554159
HLA A*2301	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.480000	0.344471	-4.135529	30199.541655
HLA A*0211	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.471601	0.335272	-4.136329	29621.083660
HLA B*1517	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.415018	0.278445	-4.136573	26002.691018
HLA B*1502	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.228627	0.091985	-4.136642	16928.816667
HLA A*3301	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.583493	0.446632	-4.136861	38325.940098
HLA B*4403	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.609997	0.472542	-4.137455	40737.779841
HLA B*4402	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.304623	0.166493	-4.138130	20166.152340
HLA A*0211	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.367540	0.229395	-4.138144	23309.872740
HLA A*6801	1:133-141	9	DWDQAYRKP	0.647933	-0.108321	-4.677902	0.539612	-4.138290	47632.367969
HLA B*4403	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.591373	0.452621	-4.138752	39027.702804
HLA B*0803	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.474054	0.335272	-4.138782	29788.854630

HLA A*0216	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.430332	0.291433	-4.138899	26935.946369
HLA A*0201	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.392461	0.253524	-4.138936	24686.577817
HLA A*6801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.585610	0.446632	-4.138978	38513.208647
HLA B*1501	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.315807	0.176828	-4.138978	20692.196418
HLA A*3301	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.611689	0.472542	-4.139147	40896.767827
HLA B*5701	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.410947	0.271476	-4.139471	25760.046220
HLA B*1801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.203200	0.063696	-4.139505	15966.159925
HLA B*5301	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.574384	0.434427	-4.139957	37530.457896
HLA B*4001	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.394232	0.253787	-4.140445	24787.481416
HLA A*0206	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.476356	0.335272	-4.141085	29947.205335
HLA B*7301	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.588565	0.446632	-4.141933	38776.209632
HLA A*0203	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.376184	0.234162	-4.142022	23778.456359
HLA B*4501	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.465770	0.323743	-4.142027	29226.009489
HLA B*3801	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.589188	0.446632	-4.142556	38831.839872
HLA A*0203	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.421038	0.278445	-4.142593	26365.601033
HLA B*5101	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.478036	0.335272	-4.142764	30063.267568

HLA A*2402	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.428890	0.286028	-4.142862	26846.622426
HLA A*0203	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.311545	0.168569	-4.142975	20490.125879
HLA A*2902	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.309512	0.166493	-4.143019	20394.465225
HLA B*0802	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.434634	0.291433	-4.143201	27204.086414
HLA B*0802	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.414960	0.271476	-4.143484	25999.174464
HLA B*1503	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.108596	-0.035101	-4.143697	12840.919162
HLA A*6901	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.385732	0.241980	-4.143752	24307.033799
HLA B*0702	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.435557	0.291433	-4.144124	27261.986181
HLA B*7301	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.467936	0.323743	-4.144193	29372.150589
HLA B*1502	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.528527	0.384238	-4.144289	33769.654305
HLA A*0101	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.380150	0.235698	-4.144451	23996.593160
HLA A*6802	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.398372	0.253787	-4.144585	25024.890981
HLA B*5801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.363059	0.218305	-4.144754	23070.628961
HLA B*4601	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.386829	0.241980	-4.144850	24368.521171
HLA B*4601	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.398767	0.253787	-4.144980	25047.645477
HLA A*0250	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.579442	0.434427	-4.145015	37970.149259

HLA B*4402	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.363729	0.218305	-4.145424	23106.227118
HLA B*4001	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.374908	0.229395	-4.145512	23708.707979
HLA B*1509	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.303535	0.157927	-4.145609	20115.703799
HLA B*0801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.399507	0.253787	-4.145720	25090.365937
HLA A*1101	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.451602	0.305553	-4.146050	28287.992383
HLA A*0101	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.380352	0.234162	-4.146190	24007.760184
HLA A*3001	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.188582	0.042326	-4.146256	15437.678044
HLA A*0201	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.391573	0.245175	-4.146398	24636.146875
HLA A*2601	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.391737	0.245175	-4.146563	24645.478160
HLA B*4001	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.210296	0.063696	-4.146600	16229.155436
HLA A*0216	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.425067	0.278445	-4.146622	26611.358322
HLA A*0219	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.452631	0.305553	-4.147079	28355.101148
HLA A*8001	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.452892	0.305553	-4.147339	28372.133434
HLA B*1509	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.477820	0.330347	-4.147473	30048.308508
HLA B*4402	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.439411	0.291433	-4.147977	27504.936632
HLA A*3001	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.241415	0.093374	-4.148041	17434.714845

HLA B*5301	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.600801	0.452621	-4.148180	39884.253920
HLA A*2601	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.390269	0.241980	-4.148289	24562.288064
HLA A*0301	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.366645	0.218305	-4.148339	23261.876663
HLA B*5701	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.426864	0.278445	-4.148419	26721.719374
HLA A*0301	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.317007	0.168569	-4.148438	20749.478170
HLA B*1801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.427128	0.278445	-4.148683	26737.915172
HLA A*3201	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.420373	0.271476	-4.148897	26325.266218
HLA B*1517	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.325813	0.176828	-4.148985	21174.494387
HLA A*3201	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.550908	0.401614	-4.149294	35555.583400
HLA A*2602	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.581301	0.432006	-4.149294	38132.980115
HLA B*4801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.308107	0.157927	-4.150181	20328.593420
HLA A*0201	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.384811	0.234162	-4.150649	24255.541062
HLA A*2603	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.585633	0.434427	-4.151206	38515.292226
HLA B*1501	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.404883	0.253524	-4.151358	25402.860140
HLA B*3901	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.486706	0.335272	-4.151434	30669.435455
HLA B*7301	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.380857	0.229395	-4.151461	24035.700484

HLA A*3101	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.387630	0.235698	-4.151932	24413.517032
HLA A*2603	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.573221	0.421102	-4.152119	37430.089714
HLA A*6802	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.430626	0.278445	-4.152181	26954.167590
HLA A*2902	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.387985	0.235698	-4.152287	24433.468418
HLA B*4601	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.382203	0.229395	-4.152808	24110.323547
HLA B*0802	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.458477	0.305553	-4.152924	28739.335314
HLA A*6801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.321542	0.168569	-4.152973	20967.260219
HLA B*5701	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.406774	0.253787	-4.152987	25513.729840
HLA A*6901	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.321638	0.168569	-4.153069	20971.911387
HLA A*0216	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.458669	0.305553	-4.153117	28752.087225
HLA A*0202	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.488463	0.335272	-4.153191	30793.793747
HLA B*2705	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.444678	0.291433	-4.153245	27840.574580
HLA A*0216	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.313751	0.160477	-4.153274	20594.478205
HLA A*1101	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.424858	0.271476	-4.153382	26598.548566
HLA A*2601	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.382861	0.229395	-4.153465	24146.872792
HLA A*3101	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.245806	0.092119	-4.153687	17611.892912

HLA A*2601	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.387917	0.234162	-4.153755	24429.635430
HLA A*3101	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.407542	0.253524	-4.154018	25558.904435
HLA A*3101	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.408026	0.253787	-4.154239	25587.404106
HLA B*5401	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.554942	0.400567	-4.154375	35887.390033
HLA B*4501	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.601015	0.446632	-4.154383	39903.893768
HLA A*0219	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.446243	0.291433	-4.154810	27941.064709
HLA B*4002	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.627527	0.472542	-4.154985	42415.722042
HLA A*1101	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.490540	0.335272	-4.155268	30941.412902
HLA B*4402	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.433762	0.278445	-4.155318	27149.540696
HLA B*0801	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.324986	0.169649	-4.155337	21134.210568
HLA B*1502	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.479838	0.323743	-4.156096	30188.270802
HLA A*6901	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.401549	0.245175	-4.156374	25208.598305
HLA B*5301	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.588420	0.432006	-4.156413	38763.205763
HLA B*4801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.374915	0.218305	-4.156610	23709.092767
HLA B*4402	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.398602	0.241980	-4.156623	25038.161924
HLA B*7301	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.253686	0.096880	-4.156806	17934.373446

HLA A*3301	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.398847	0.241980	-4.156867	25052.253070
HLA B*5101	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.462447	0.305553	-4.156895	29003.295617
HLA B*1502	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.501472	0.344471	-4.157001	31730.162412
HLA B*1801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.448578	0.291433	-4.157145	28091.720530
HLA B*4002	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.603788	0.446632	-4.157156	40159.441825
HLA B*7301	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.581035	0.423714	-4.157321	38109.675882
HLA B*0702	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.410918	0.253524	-4.157394	25758.373966
HLA B*4801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.435950	0.278445	-4.157505	27286.627192
HLA A*0206	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.463244	0.305553	-4.157691	29056.535085
HLA A*0201	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.399688	0.241980	-4.157708	25100.819794
HLA B*4801	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.411240	0.253524	-4.157716	25777.471985
HLA B*0702	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.443804	0.286028	-4.157777	27784.602355
HLA B*0801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.376106	0.218305	-4.157801	23774.211657
HLA B*4402	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.429524	0.271476	-4.158048	26885.865137
HLA A*0203	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.393955	0.235698	-4.158257	24771.662958
HLA B*0801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.392538	0.234162	-4.158377	24690.985415

HLA B*0803	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.437209	0.278445	-4.158764	27365.865068
HLA A*2403	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.412627	0.253787	-4.158839	25859.880860
HLA A*1101	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.444951	0.286028	-4.158923	27858.051336
HLA B*5801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.335843	0.176828	-4.159015	21669.206104
HLA B*5401	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.546463	0.387379	-4.159084	35193.510025
HLA B*1503	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.430605	0.271476	-4.159129	26952.855250
HLA B*2705	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.464731	0.305553	-4.159178	29156.208589
HLA A*2603	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.489960	0.330347	-4.159612	30900.095278
HLA A*0211	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.431474	0.271476	-4.159998	27006.859706
HLA B*3801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.560663	0.400567	-4.160096	36363.264983
HLA A*0201	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.320755	0.160477	-4.160278	20929.295396
HLA A*0250	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.592458	0.432006	-4.160452	39125.369428
HLA B*0702	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.414292	0.253787	-4.160505	25959.259782
HLA B*5101	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.505121	0.344471	-4.160650	31997.868205
HLA B*1801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.496557	0.335272	-4.161285	31373.081120
HLA A*2603	1:80-88	9	AATSSTPRE	1.057554	-0.585012	-4.633946	0.472542	-4.161403	43047.274275

HLA B*4801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.395917	0.234162	-4.161755	24883.816058
HLA A*3301	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.614473	0.452621	-4.161852	41159.787671
HLA A*2402	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.563487	0.401614	-4.161873	36600.494383
HLA B*4601	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.416019	0.253524	-4.162495	26062.686259
HLA A*0101	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.404561	0.241980	-4.162581	25384.039663
HLA B*7301	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.584148	0.421102	-4.163046	38383.831382
HLA B*0803	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.449302	0.286028	-4.163274	28138.567262
HLA B*1509	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.455185	0.291433	-4.163752	28522.335958
HLA A*6802	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.286140	0.122021	-4.164119	19325.896312
HLA B*3801	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.487878	0.323743	-4.164135	30752.340512
HLA B*1501	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.409873	0.245175	-4.164698	25696.437822
HLA A*2902	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.406685	0.241980	-4.164705	25508.485374
HLA A*3101	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.410176	0.245175	-4.165001	25714.377000
HLA B*1503	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.500314	0.335272	-4.165042	31645.648430
HLA A*3301	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.552710	0.387379	-4.165331	35703.423714
HLA B*1502	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.597406	0.432006	-4.165400	39573.682642

HLA A*2601	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.383714	0.218305	-4.165408	24194.338764
HLA B*0803	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.489542	0.323743	-4.165799	30870.354036
HLA B*1801	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.242106	0.076178	-4.165927	17462.466952
HLA A*0203	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.411572	0.245175	-4.166397	25797.142397
HLA B*5701	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.420009	0.253524	-4.166484	26303.200871
HLA A*2602	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.438022	0.271476	-4.166546	27417.137058
HLA A*6802	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.232383	0.065526	-4.166858	17075.893137
HLA B*1801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.472447	0.305553	-4.166894	29678.828713
HLA A*2403	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.396295	0.229395	-4.166900	24905.499108
HLA B*1509	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.445456	0.278445	-4.167011	27890.472616
HLA A*0216	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.259339	0.092119	-4.167220	18169.336562
HLA A*0202	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.459238	0.291433	-4.167805	28789.753912
HLA B*7301	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.325841	0.157927	-4.167915	21175.869051
HLA A*8001	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.421775	0.253787	-4.167988	26410.426478
HLA A*2902	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.326027	0.157927	-4.168100	21184.921155
HLA A*0202	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.422029	0.253787	-4.168242	26425.861755

HLA B*4601	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.413439	0.245175	-4.168265	25908.331276
HLA B*4801	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.404114	0.235698	-4.168416	25357.961348
HLA B*5701	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.404145	0.235698	-4.168447	25359.744800
HLA B*5801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.326391	0.157927	-4.168464	21202.692857
HLA A*2602	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.404448	0.235698	-4.168750	25377.448926
HLA B*5301	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.499142	0.330347	-4.168794	31560.335110
HLA B*1502	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.615535	0.446632	-4.168903	41260.557615
HLA B*0802	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.455093	0.286028	-4.169066	28516.318788
HLA B*1517	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.440750	0.271476	-4.169274	27589.882771
HLA A*2501	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.447895	0.278445	-4.169450	28047.531152
HLA A*2501	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.455857	0.286028	-4.169829	28566.500681
HLA A*0201	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.405665	0.235698	-4.169967	25448.664462
HLA B*0702	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.415150	0.245175	-4.169975	26010.569826
HLA B*4601	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.404410	0.234162	-4.170249	25375.252394
HLA B*5701	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.415429	0.245175	-4.170255	26027.320218
HLA B*4801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.424308	0.253787	-4.170521	26564.898393

HLA B*4601	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.406619	0.235698	-4.170921	25504.621721
HLA A*6801	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.594658	0.423714	-4.170944	39323.989296
HLA B*1503	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.263105	0.092119	-4.170987	18327.587186
HLA B*3801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.572688	0.401614	-4.171073	37384.152098
HLA B*0803	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.515614	0.344471	-4.171143	32780.369550
HLA A*0206	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.268035	0.096880	-4.171155	18536.789308
HLA B*4001	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.424698	0.253524	-4.171174	26588.765492
HLA B*1502	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.592421	0.421102	-4.171319	39121.982952
HLA A*2501	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.425149	0.253787	-4.171362	26616.397556
HLA A*3201	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.571969	0.400567	-4.171401	37322.316594
HLA B*4402	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.425278	0.253787	-4.171491	26624.318282
HLA A*6801	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.555788	0.384238	-4.171550	35957.350986
HLA A*0211	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.450373	0.278445	-4.171928	28208.068250
HLA B*5101	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.458054	0.286028	-4.172026	28711.363145
HLA B*5401	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.477778	0.305553	-4.172225	30045.382606
HLA B*3501	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.213012	0.040514	-4.172497	16330.967872

HLA B*0803 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.478450 0.305553 -4.172897 30091.905654

HLA B*5701 1:137-145 9 AYRKPITYD 0.853411 -0.611431 -4.415072 0.241980 -4.173093 26005.926668

HLA A*6802 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.418439 0.245175 -4.173265 26208.317755

HLA A*2402 1:181-189 9 GLDPVNYQN 1.035268 -0.647889 -4.560703 0.387379 -4.173324 36366.609398

HLA B*5301 1:216-224 9 VLVPRSAID 1.164467 -0.740753 -4.597047 0.423714 -4.173333 39540.940542

HLA B*5701 1:114-122 9 LKVYQNAGG 0.762278 -0.528116 -4.407683 0.234162 -4.173521 25567.202032

HLA A*6901 1:144-152 9 YDTLWQADT 0.627145 -0.460652 -4.340032 0.166493 -4.173539 21879.234956

HLA A*0301 1:10-18 9 TAVVLLCCS 1.085894 -0.909066 -4.350555 0.176828 -4.173727 22415.863608

HLA B*5401 1:94-102 9 NITSATYQS 1.243610 -0.899139 -4.518405 0.344471 -4.173934 32991.725750

HLA A*0201 1:75-83 9 DKFLSAATS 1.204544 -0.986239 -4.392320 0.218305 -4.174015 24678.566018

HLA B*1502 1:100-108 9 YQSAIPPRG 0.865176 -0.579148 -4.460110 0.286028 -4.174082 28847.594957

HLA B*4402 1:114-122 9 LKVYQNAGG 0.762278 -0.528116 -4.408454 0.234162 -4.174292 25612.609866

HLA B*1517 1:187-195 9 YQNFAVTND 0.973541 -0.744146 -4.403689 0.229395 -4.174294 25333.143240

HLA B*1502 1:26-34 9 KTYCEELKG 0.984658 -0.550231 -4.608797 0.434427 -4.174370 40625.317668

HLA B*7301 1:143-151 9 TYDTLWQAD 1.156171 -0.755604 -4.575021 0.400567 -4.174453 37585.520902

HLA B*4402 1:43-51 9 IQMSDPAYN 0.678035 -0.520108 -4.332406 0.157927 -4.174479 21498.378450

HLA B*5701	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.404220	0.229395	-4.174825	25364.135369
HLA B*0801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.404274	0.229395	-4.174879	25367.291560
HLA B*1501	1:50-58	9	YNINISLPS	0.643875	-0.954020	-3.864870	-0.310145	-4.175015	7326.050968
HLA A*3201	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.140028	-0.035101	-4.175129	13804.717458
HLA B*3801	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.519721	0.344471	-4.175250	33091.826988
HLA A*0203	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.394056	0.218305	-4.175751	24777.426142
HLA A*0202	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.576564	0.400567	-4.175997	37719.348704
HLA A*6901	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.334231	0.157927	-4.176305	21588.936734
HLA B*0801	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.412051	0.235698	-4.176353	25825.628288
HLA B*7301	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.578827	0.401614	-4.177213	37916.368836
HLA B*3901	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.335399	0.157927	-4.177472	21647.061335
HLA B*0801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.423561	0.245175	-4.178387	26519.236897
HLA A*6802	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.345187	0.166493	-4.178694	22140.473380
HLA B*5801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.347273	0.168569	-4.178704	22247.091697
HLA B*1509	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.484528	0.305553	-4.178975	30516.014264
HLA A*2602	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.537293	0.357949	-4.179343	34458.196511

HLA B*4601	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.356629	0.176828	-4.179801	22731.541841
HLA A*0216	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.415695	0.235698	-4.179997	26043.236038
HLA A*0203	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.433584	0.253524	-4.180059	27138.380414
HLA A*3201	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.612302	0.432006	-4.180296	40954.554075
HLA A*6801	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.567784	0.387379	-4.180405	36964.442434
HLA A*0212	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.416259	0.235698	-4.180560	26077.071844
HLA A*0206	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.414727	0.234162	-4.180565	25985.253580
HLA A*2601	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.279176	0.098300	-4.180876	19018.478572
HLA A*8001	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.341630	0.160477	-4.181153	21959.870864
HLA A*3301	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.615617	0.434427	-4.181190	41268.370881
HLA A*0219	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.417067	0.235698	-4.181369	26125.646508
HLA B*4001	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.415538	0.234162	-4.181376	26033.798050
HLA A*8001	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.410839	0.229395	-4.181443	25753.636504
HLA A*2403	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.427464	0.245175	-4.182289	26758.608005
HLA B*1503	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.359227	0.176828	-4.182399	22867.960036
HLA B*3501	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.411917	0.229395	-4.182521	25817.665830

HLA B*1502	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.583131	0.400567	-4.182564	38294.023176
HLA B*1517	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.436131	0.253524	-4.182606	27297.996117
HLA A*0202	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.351310	0.168569	-4.182741	22454.824242
HLA B*2705	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.401208	0.218305	-4.182903	25188.831580
HLA B*1503	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.343415	0.160477	-4.182939	22050.345085
HLA A*2403	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.417105	0.234162	-4.182943	26127.907996
HLA B*0801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.425098	0.241980	-4.183118	26613.229926
HLA A*0212	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.401521	0.218305	-4.183215	25206.961850
HLA B*2705	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.417666	0.234162	-4.183504	26161.712276
HLA B*5301	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.541905	0.357949	-4.183955	34826.079129
HLA B*1509	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.528703	0.344471	-4.184232	33783.358842
HLA A*0212	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.344745	0.160477	-4.184269	22117.966657
HLA A*3002	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.426636	0.241980	-4.184657	26707.700583
HLA B*4001	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.403066	0.218305	-4.184761	25296.851145
HLA A*0212	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.140042	-0.044895	-4.184936	13805.165557
HLA B*1517	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.261599	0.076178	-4.185421	18264.141967

HLA B*3501	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.439054	0.253524	-4.185529	27482.328532
HLA B*0702	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.419720	0.234162	-4.185558	26285.704113
HLA B*4801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.427593	0.241980	-4.185613	26766.571050
HLA B*1502	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.343634	0.157927	-4.185707	22061.441839
HLA A*0101	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.404046	0.218305	-4.185741	25353.983331
HLA B*1501	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.404248	0.218305	-4.185943	25365.782028
HLA B*4601	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.404309	0.218305	-4.186004	25369.350157
HLA B*5301	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.570279	0.384238	-4.186042	37177.425570
HLA B*4501	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.607152	0.421102	-4.186050	40471.763675
HLA A*2603	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.638743	0.452621	-4.186122	43525.453598
HLA B*3801	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.544583	0.357949	-4.186634	35041.524762
HLA A*0212	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.431942	0.245175	-4.186767	27035.950081
HLA A*1101	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.283894	0.096880	-4.187014	19226.203618
HLA B*1501	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.355762	0.168569	-4.187193	22686.209283
HLA B*5801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.354016	0.166493	-4.187523	22595.204007
HLA A*3301	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.571825	0.384238	-4.187588	37310.002141

HLA A*2501	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.441530	0.253524	-4.188005	27639.481024
HLA A*0203	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.354660	0.166493	-4.188167	22628.721931
HLA A*2603	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.634827	0.446632	-4.188195	43134.693287
HLA A*3002	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.280374	0.092119	-4.188255	19071.023835
HLA B*5701	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.406671	0.218305	-4.188365	25507.657399
HLA A*2403	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.286910	0.098300	-4.188610	19360.219469
HLA B*1801	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.442792	0.253524	-4.189267	27719.893517
HLA B*3501	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.423448	0.234162	-4.189286	26512.351417
HLA A*1101	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.467741	0.278445	-4.189296	29358.964843
HLA A*3001	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.265495	0.076178	-4.189316	18428.700856
HLA A*0211	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.494880	0.305553	-4.189327	31252.131292
HLA B*4002	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.263223	0.073876	-4.189347	18332.545367
HLA B*1517	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.349825	0.160477	-4.189348	22378.181174
HLA B*0702	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.418855	0.229395	-4.189460	26233.425559
HLA B*1502	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.524760	0.335272	-4.189489	33478.068249
HLA A*0250	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.590184	0.400567	-4.189617	38921.014309

HLA A*3001	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.298146	0.108361	-4.189784	19867.604842
HLA B*4001	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.425506	0.235698	-4.189808	26638.293305
HLA A*0212	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.281993	0.092119	-4.189874	19142.242076
HLA A*3101	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.408184	0.218305	-4.189878	25596.680263
HLA B*5801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.350396	0.160477	-4.189919	22407.618945
HLA B*4501	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.621935	0.432006	-4.189929	41873.097666
HLA A*2602	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.591765	0.401614	-4.190151	39062.978373
HLA A*2602	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.613933	0.423714	-4.190219	41108.605445
HLA A*2301	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.521133	0.330347	-4.190785	33199.594981
HLA B*3501	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.357533	0.166493	-4.191040	22778.936602
HLA B*5801	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.360910	0.169649	-4.191261	22956.710411
HLA A*2403	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.445688	0.253524	-4.192164	27905.414169
HLA A*6901	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.290832	0.098300	-4.192532	19535.816472
HLA B*0801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.314660	0.122021	-4.192639	20637.640530
HLA B*1517	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.428356	0.235698	-4.192658	26813.673806
HLA B*4801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.437909	0.245175	-4.192735	27410.018446

HLA A*8001	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.438593	0.245175	-4.193419	27453.203412
HLA A*0101	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.359925	0.166493	-4.193432	22904.732369
HLA B*4002	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.625946	0.432006	-4.193939	42261.573319
HLA A*0212	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.447467	0.253524	-4.193943	28019.929149
HLA A*6802	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.435924	0.241980	-4.193944	27285.003447
HLA A*0101	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.362716	0.168569	-4.194147	23052.413962
HLA A*6901	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.364002	0.169649	-4.194353	23120.731915
HLA A*0203	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.286570	0.091985	-4.194585	19345.038611
HLA B*4002	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.629125	0.434427	-4.194698	42572.045162
HLA B*1501	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.364918	0.169649	-4.195269	23169.564845
HLA A*3301	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.525639	0.330347	-4.195292	33545.872947
HLA B*1801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.449133	0.253787	-4.195345	28127.609086
HLA A*3101	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.429778	0.234162	-4.195616	26901.578279
HLA B*7301	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.583157	0.387379	-4.195778	38296.302074
HLA A*6801	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.449481	0.253524	-4.195956	28150.138856
HLA A*2403	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.293035	0.096880	-4.196156	19635.202457

HLA A*2402	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.554199	0.357949	-4.196250	35826.092054
HLA B*5401	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.482961	0.286028	-4.196933	30406.098826
HLA B*4601	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.355168	0.157927	-4.197241	22655.179864
HLA B*4001	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.439444	0.241980	-4.197464	27507.019892
HLA A*0101	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.374720	0.176828	-4.197892	23698.449281
HLA A*6801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.469562	0.271476	-4.198086	29482.315523
HLA A*6801	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.556196	0.357949	-4.198247	35991.214321
HLA A*0201	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.375199	0.176828	-4.198371	23724.617739
HLA A*0219	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.432609	0.234162	-4.198447	27077.520272
HLA A*2403	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.434256	0.235698	-4.198558	27180.402184
HLA A*0301	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.368207	0.169649	-4.198559	23345.713753
HLA B*1801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.484589	0.286028	-4.198561	30520.306860
HLA A*2601	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.375469	0.176828	-4.198641	23739.382299
HLA B*3801	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.490089	0.291433	-4.198656	30909.290781
HLA A*0203	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.440914	0.241980	-4.198935	27600.332824
HLA B*3501	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.321213	0.122021	-4.199192	20951.385953

HLA B*4403	1:11-19	9	AVVLLCCSG	0.891360	-0.444728	-4.645869	0.446632	-4.199237	44245.519006
HLA A*0212	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.441664	0.241980	-4.199684	27648.005350
HLA A*2902	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.429240	0.229395	-4.199844	26868.271501
HLA B*4002	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.530474	0.330347	-4.200127	33921.444507
HLA B*3501	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.436239	0.235698	-4.200541	27304.790203
HLA A*0301	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.367380	0.166493	-4.200887	23301.299257
HLA B*4501	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.636004	0.434427	-4.201577	43251.762172
HLA A*0219	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.455296	0.253524	-4.201771	28529.589106
HLA B*4402	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.438093	0.235698	-4.202394	27421.587129
HLA B*0702	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.420791	0.218305	-4.202486	26350.628613
HLA A*0202	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.526483	0.323743	-4.202740	33611.087379
HLA A*0219	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.448054	0.245175	-4.202880	28057.850965
HLA A*2402	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.533686	0.330347	-4.203339	34173.234276
HLA B*5301	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.603922	0.400567	-4.203354	40171.827448
HLA B*4501	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.587853	0.384238	-4.203616	38712.699875
HLA A*2402	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.548133	0.344471	-4.203662	35329.140118

HLA A*0211	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.439392	0.235698	-4.203694	27503.746268
HLA A*2601	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.364436	0.160477	-4.203960	23143.883409
HLA A*8001	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.457488	0.253524	-4.203963	28673.954141
HLA B*4001	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.362153	0.157927	-4.204226	23022.502744
HLA A*3301	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.636286	0.432006	-4.204279	43279.849757
HLA A*0250	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.475832	0.271476	-4.204356	29911.098653
HLA A*2501	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.433911	0.229395	-4.204515	27158.795461
HLA A*2301	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.490747	0.286028	-4.204719	30956.146694
HLA B*1501	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.326852	0.122021	-4.204831	21225.186807
HLA B*5701	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.301933	0.096880	-4.205053	20041.622764
HLA A*0212	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.080844	-0.124403	-4.205247	12046.031517
HLA B*5301	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.607063	0.401614	-4.205449	40463.444515
HLA A*0202	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.382863	0.176828	-4.206035	24147.003424
HLA A*3101	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.302988	0.096880	-4.206108	20090.363845
HLA A*8001	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.440329	0.234162	-4.206168	27563.178484
HLA B*1517	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.424649	0.218305	-4.206343	26585.744975

HLA A*3301	1:91-99	9	YELNITSAT	0.787532	-0.429583	-4.564359	0.357949	-4.206409	36674.027864
HLA A*0211	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.498124	0.291433	-4.206691	31486.492115
HLA A*2301	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.498404	0.291433	-4.206971	31506.768914
HLA A*2403	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.375540	0.168569	-4.206971	23743.235435
HLA B*5701	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.384061	0.176828	-4.207233	24213.718048
HLA A*0201	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.374283	0.166493	-4.207790	23674.614961
HLA B*3501	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.283978	0.076178	-4.207800	19229.948401
HLA B*0803	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.499412	0.291433	-4.207979	31579.976079
HLA B*1517	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.442340	0.234162	-4.208179	27691.115847
HLA A*6801	1:74-82	9	RDKFLSAAT	0.783794	-0.331173	-4.660850	0.452621	-4.208229	45798.326635
HLA B*5101	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.480036	0.271476	-4.208560	30201.992397
HLA A*2902	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.462403	0.253524	-4.208878	29000.314582
HLA B*2705	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.462776	0.253787	-4.208989	29025.270583
HLA A*2301	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.532753	0.323743	-4.209011	34099.918293
HLA B*4403	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.641058	0.432006	-4.209051	43758.008521
HLA A*2902	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.454607	0.245175	-4.209433	28484.402747

HLA A*0250	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.495561	0.286028	-4.209533	31301.200237
HLA B*0802	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.463493	0.253787	-4.209705	29073.202283
HLA B*5801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.331755	0.122021	-4.209734	21466.186412
HLA A*1101	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.463843	0.253787	-4.210056	29096.646868
HLA A*6801	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.642399	0.432006	-4.210393	43893.388042
HLA B*0702	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.452624	0.241980	-4.210645	28354.640957
HLA B*2705	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.452979	0.241980	-4.210999	28377.813136
HLA A*6901	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.333059	0.122021	-4.211038	21530.735244
HLA B*5401	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.482599	0.271476	-4.211123	30380.777358
HLA A*2403	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.369250	0.157927	-4.211324	23401.857344
HLA B*0801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.339595	0.127871	-4.211724	21857.230281
HLA A*8001	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.453825	0.241980	-4.211845	28433.134486
HLA A*0101	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.381536	0.169649	-4.211887	24073.308683
HLA A*0301	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.308829	0.096880	-4.211949	20362.383932
HLA B*5301	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.600108	0.387379	-4.212730	39820.652714
HLA B*7301	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.557691	0.344471	-4.213220	36115.262197

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HLA B*4501	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.305340
	0.091985	-4.213355	20199.454285

HLA A*2602	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.614203
	0.400567	-4.213636	41134.188597

HLA A*0216	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.371924
	0.157927	-4.213997	23546.374198

HLA A*0101	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.374546
	0.160477	-4.214070	23688.963937

HLA A*2602	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.544860
	0.330347	-4.214513	35063.901253

HLA A*2603	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.598821
	0.384238	-4.214583	39702.774458

HLA B*4002	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.635987
	0.421102	-4.214885	43250.124293

HLA B*4002	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.538726
	0.323743	-4.214983	34572.097510

HLA A*0219	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.433412
	0.218305	-4.215107	27127.664989

HLA A*8001	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.383993
	0.168569	-4.215424	24209.919533

HLA A*0202	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.248886
	0.033425	-4.215461	17737.246881

HLA A*0216	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.460779
	0.245175	-4.215605	28892.107016

HLA A*1101	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.307743
	0.092119	-4.215625	20311.554372

HLA B*0801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.376125
	0.160477	-4.215648	23775.240606

HLA A*2902	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.434418
	0.218305	-4.216113	27190.550042

HLA B*0702	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.384898
	0.168569	-4.216329	24260.396680
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HLA B*3901	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.446123	0.229395	-4.216728	27933.356711
HLA A*1101	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.393690	0.176828	-4.216861	24756.524235
HLA A*2602	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.552155	0.335272	-4.216884	35657.869032
HLA A*3001	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.290890	0.073876	-4.217015	19538.458816
HLA B*1501	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.310516	0.093374	-4.217141	20441.631359
HLA A*2602	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.540887	0.323743	-4.217145	34744.595140
HLA A*0101	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.375676	0.157927	-4.217750	23750.686603
HLA B*3501	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.387593	0.169649	-4.217944	24411.403933
HLA B*4403	1:26-34	9	KTYCEELKG	0.984658	-0.550231	-4.652605	0.434427	-4.218178	44937.123318
HLA A*0216	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.460291	0.241980	-4.218311	28859.614257
HLA B*4002	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.212448	-0.005967	-4.218415	16309.777937
HLA A*6901	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.311051	0.092119	-4.218933	20466.860742
HLA B*0803	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.464238	0.245175	-4.219063	29123.103707
HLA A*0206	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.455204	0.235698	-4.219506	28523.570406
HLA A*0219	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.386317	0.166493	-4.219824	24339.798954
HLA A*2402	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.511331	0.291433	-4.219898	32458.671014

HLA B*0803	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.462508	0.241980	-4.220529	29007.375424
HLA B*3801	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.550920	0.330347	-4.220572	35556.545172
HLA B*5401	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.454755	0.234162	-4.220593	28494.112541
HLA B*5401	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.555865	0.335272	-4.220593	35963.770894
HLA A*3001	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.254083	0.033425	-4.220659	17950.777826
HLA A*6801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.342849	0.122021	-4.220829	22021.614946
HLA B*3801	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.556208	0.335272	-4.220936	35992.187877
HLA A*6901	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.329495	0.108361	-4.221134	21354.759852
HLA A*0101	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.344372	0.123229	-4.221142	22098.949573
HLA B*1517	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.318351	0.096880	-4.221471	20813.785977
HLA B*1801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.463538	0.241980	-4.221558	29076.190810
HLA B*1517	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.464108	0.241980	-4.222129	29114.439595
HLA A*1101	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.451555	0.229395	-4.222160	28284.931851
HLA B*3501	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.467945	0.245175	-4.222771	29372.786196
HLA B*5701	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.380869	0.157927	-4.222942	24036.350645
HLA B*1517	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.476735	0.253787	-4.222947	29973.300479

HLA A*2902	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.321333	0.098300	-4.223033	20957.167329
HLA A*0216	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.476878	0.253524	-4.223353	29983.193397
HLA A*2402	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.465347	0.241980	-4.223367	29197.563636
HLA B*5801	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.315701	0.092119	-4.223582	20687.159619
HLA B*0802	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.465643	0.241980	-4.223663	29217.472825
HLA B*0802	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.477235	0.253524	-4.223711	30007.858812
HLA A*0219	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.384228	0.160477	-4.223752	24223.020375
HLA B*0803	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.495263	0.271476	-4.223787	31279.701949
HLA B*4501	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.624418	0.400567	-4.223851	42113.224523
HLA A*0206	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.502356	0.278445	-4.223911	31794.771005
HLA B*4001	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.317294	0.093374	-4.223920	20763.177480
HLA B*5101	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.477599	0.253524	-4.224075	30033.031939
HLA B*2705	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.477646	0.253524	-4.224122	30036.281622
HLA A*8001	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.459931	0.235698	-4.224233	28835.736661
HLA B*4402	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.401142	0.176828	-4.224314	25185.016342
HLA A*2602	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.608700	0.384238	-4.224463	40616.307751

HLA B*4001	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.394730	0.169649	-4.225082	24815.926401
HLA A*3101	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.391756	0.166493	-4.225263	24646.544817
HLA B*1501	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.316373	0.090830	-4.225543	20719.192152
HLA B*4002	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.627198	0.401614	-4.225584	42383.609195
HLA B*4002	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.626303	0.400567	-4.225736	42296.339436
HLA A*2501	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.444124	0.218305	-4.225818	27805.052257
HLA A*2603	1:178-186	9	PNAGLDPVN	1.201582	-0.769576	-4.657892	0.432006	-4.225885	45487.451816
HLA B*2705	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.471479	0.245175	-4.226304	29612.751999
HLA A*0216	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.460622	0.234162	-4.226460	28881.636606
HLA B*4002	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.650383	0.423714	-4.226669	44707.733606
HLA B*1501	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.354676	0.127871	-4.226805	22629.578880
HLA A*2902	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.460995	0.234162	-4.226834	28906.490480
HLA B*2705	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.462739	0.235698	-4.227040	29022.758316
HLA B*0803	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.456543	0.229395	-4.227148	28611.662490
HLA A*3201	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.456545	0.229395	-4.227150	28611.817276
HLA A*3001	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.267762	0.040514	-4.227247	18525.160248

HLA B*0802	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.472581	0.245175	-4.227406	29687.981997
HLA B*4403	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.628166	0.400567	-4.227599	42478.182290
HLA B*0702	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.463418	0.235698	-4.227719	29068.169669
HLA A*3002	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.551465	0.323743	-4.227722	35601.200005
HLA B*0801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.396944	0.168569	-4.228375	24942.714017
HLA A*3002	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.482324	0.253787	-4.228537	30361.553716
HLA B*5801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.356420	0.127871	-4.228548	22720.599689
HLA A*0201	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.398426	0.169649	-4.228778	25028.004958
HLA B*4501	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.652514	0.423714	-4.228800	44927.643229
HLA B*4601	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.397395	0.168569	-4.228826	24968.635442
HLA B*4001	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.222866	-0.005967	-4.228833	16705.737944
HLA B*4403	1:22-30	9	TAAPKTYCE	1.011561	-0.590459	-4.649983	0.421102	-4.228881	44666.635647
HLA B*4501	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.630631	0.401614	-4.229016	42719.930166
HLA A*8001	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.447340	0.218305	-4.229035	28011.744770
HLA A*3101	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.398750	0.169649	-4.229102	25046.696960
HLA A*2501	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.471162	0.241980	-4.229182	29591.132665

HLA A*2601	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.398969	0.169649	-4.229320	25059.301617
HLA A*0211	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.184677	-0.044895	-4.229572	15299.496384
HLA B*2705	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.357912	0.127871	-4.230040	22798.785520
HLA A*2601	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.396913	0.166493	-4.230420	24940.959894
HLA B*0801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.388509	0.157927	-4.230582	24462.962870
HLA B*7301	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.294316	0.063696	-4.230620	19693.180112
HLA A*0201	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.399265	0.168569	-4.230696	25076.389013
HLA A*3101	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.321633	0.090830	-4.230804	20971.684477
HLA A*2603	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.654687	0.423714	-4.230973	45153.031248
HLA A*6901	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.294783	0.063696	-4.231088	19714.392574
HLA B*7301	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.391688	0.160477	-4.231211	24642.678403
HLA B*4001	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.391704	0.160477	-4.231228	24643.611620
HLA A*0202	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.465553	0.234162	-4.231392	29211.467037
HLA A*2601	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.389320	0.157927	-4.231393	24508.663467
HLA A*0219	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.473401	0.241980	-4.231421	29744.087379
HLA A*3101	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.400031	0.168569	-4.231462	25120.653353

HLA A*8001	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.323844	0.092119	-4.231726	21078.717356
HLA A*3201	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.517768	0.286028	-4.231741	32943.392681
HLA A*0216	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.398558	0.166493	-4.232065	25035.588436
HLA B*5301	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.576574	0.344471	-4.232102	37720.164942
HLA B*4601	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.392635	0.160477	-4.232158	24696.462617
HLA B*5701	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.324316	0.092119	-4.232198	21101.650560
HLA A*2301	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.538023	0.305553	-4.232471	34516.220381
HLA A*1101	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.325978	0.093374	-4.232603	21182.514522
HLA B*0803	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.486934	0.253787	-4.233146	30685.533748
HLA A*2301	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.487241	0.253787	-4.233454	30707.288155
HLA B*5401	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.109381	-0.124403	-4.233784	12864.142432
HLA A*2501	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.331081	0.096880	-4.234201	21432.883052
HLA B*4601	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.400837	0.166493	-4.234344	25167.310310
HLA B*3901	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.488400	0.253787	-4.234612	30789.296118
HLA A*0301	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.358022	0.123229	-4.234793	22804.583186
HLA A*2403	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.453212	0.218305	-4.234906	28393.015768

HLA B*3501	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.393029	0.157927	-4.235103	24718.918482
HLA A*3101	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.357195	0.122021	-4.235175	22761.198173
HLA A*2602	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.540782	0.305553	-4.235229	34736.137771
HLA B*1503	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.488865	0.253524	-4.235341	30822.293990
HLA A*0250	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.559147	0.323743	-4.235405	36236.600906
HLA B*1503	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.514171	0.278445	-4.235726	32671.664557
HLA A*0301	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.357956	0.122021	-4.235936	22801.129080
HLA B*5801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.332869	0.096880	-4.235989	21521.302521
HLA A*2603	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.637660	0.401614	-4.236046	43417.038154
HLA B*1502	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.465612	0.229395	-4.236217	29215.418074
HLA A*2603	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.636913	0.400567	-4.236346	43342.410092
HLA B*4402	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.330136	0.093374	-4.236762	21386.321992
HLA B*7301	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.572293	0.335272	-4.237021	37350.190522
HLA A*6901	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.360261	0.123229	-4.237032	22922.458650
HLA B*5801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.360271	0.123229	-4.237041	22922.954687
HLA A*0212	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.404065	0.166493	-4.237572	25355.080653

HLA B*4403	1:216-224	9	VLVPRSAID	1.164467	-0.740753	-4.661312	0.423714	-4.237599	45847.162136
HLA A*1101	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.482803	0.245175	-4.237629	30395.079751
HLA B*1501	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.404150	0.166493	-4.237656	25360.019188
HLA A*0216	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.456240	0.218305	-4.237935	28591.702072
HLA A*0301	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.366116	0.127871	-4.238245	23233.578950
HLA A*0101	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.360325	0.122021	-4.238304	22925.807109
HLA A*3001	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.303021	0.064686	-4.238334	20091.885515
HLA B*3801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.517174	0.278445	-4.238729	32898.333838
HLA B*4001	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.407538	0.168569	-4.238968	25558.627895
HLA B*4002	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.468420	0.229395	-4.239024	29404.902251
HLA B*5401	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.474921	0.235698	-4.239222	29848.379998
HLA A*0216	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.407939	0.168569	-4.239370	25582.282893
HLA A*2603	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.336257	0.096880	-4.239377	21689.848058
HLA B*1517	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.337847	0.098300	-4.239547	21769.432667
HLA B*5101	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.493388	0.253787	-4.239600	31144.955677
HLA A*0212	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.416459	0.176828	-4.239630	26089.065897

HLA B*4001	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.417161	0.176828	-4.240333	26131.300594
HLA B*5701	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.400997	0.160477	-4.240520	25176.570374
HLA B*4601	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.410359	0.169649	-4.240711	25725.230021
HLA B*3501	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.483095	0.241980	-4.241115	30415.476409
HLA B*1801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.315393	0.073876	-4.241517	20672.503917
HLA B*3501	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.402183	0.160477	-4.241707	25245.446656
HLA A*8001	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.408287	0.166493	-4.241794	25602.773897
HLA B*3901	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.333907	0.091985	-4.241922	21572.825210
HLA B*0802	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.476105	0.234162	-4.241943	29929.875168
HLA B*1509	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.495852	0.253787	-4.242065	31322.204949
HLA B*4403	1:138-146	9	YRKPITYDT	0.544186	-0.159948	-4.626528	0.384238	-4.242291	42318.311718
HLA A*2403	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.412133	0.169649	-4.242484	25830.518733
HLA B*0802	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.461136	0.218305	-4.242831	28915.874858
HLA A*6901	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.316850	0.073876	-4.242974	20741.958623
HLA A*1101	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.496639	0.253524	-4.243115	31379.022053
HLA A*0206	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.488444	0.245175	-4.243270	30792.461048

HLA B*5701	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.409896	0.166493	-4.243403	25697.828008
HLA B*0802	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.473159	0.229395	-4.243763	29727.518037
HLA A*2501	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.477942	0.234162	-4.243780	30056.762714
HLA B*5701	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.412380	0.168569	-4.243811	25845.195627
HLA B*5101	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.478097	0.234162	-4.243935	30067.496478
HLA A*6801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.549543	0.305553	-4.243990	35444.002474
HLA B*5101	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.489372	0.245175	-4.244198	30858.332004
HLA A*0216	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.421637	0.176828	-4.244808	26401.998052
HLA B*0803	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.498615	0.253524	-4.245091	31522.112981
HLA A*6801	1:113-121	9	VLKVYQNAG	0.952015	-0.550401	-4.646807	0.401614	-4.245193	44341.128135
HLA B*1502	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.550823	0.305553	-4.245271	35548.659411
HLA B*3901	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.499015	0.253524	-4.245490	31551.116609
HLA B*5801	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.353911	0.108361	-4.245549	22589.703987
HLA B*4402	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.373935	0.127871	-4.246064	23655.667145
HLA B*5101	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.482016	0.235698	-4.246318	30340.044243
HLA A*2601	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.369572	0.123229	-4.246343	23419.208172

HLA B*4403	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.570120	0.323743	-4.246377	37163.751534
HLA A*2601	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.343408	0.096880	-4.246529	22049.987218
HLA B*1502	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.525118	0.278445	-4.246673	33505.608692
HLA A*3001	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.310372	0.063696	-4.246676	20434.886667
HLA A*0201	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.338822	0.092119	-4.246703	21818.362213
HLA A*6802	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.320708	0.073876	-4.246832	20927.031015
HLA A*2403	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.374750	0.127871	-4.246879	23700.116017
HLA B*5101	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.476345	0.229395	-4.246949	29946.395291
HLA B*3901	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.481398	0.234162	-4.247237	30296.907097
HLA B*5101	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.424083	0.176828	-4.247254	26551.105512
HLA A*6802	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.405501	0.157927	-4.247574	25439.029075
HLA B*1517	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.416703	0.168569	-4.248134	26103.748479
HLA B*1509	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.414908	0.166493	-4.248415	25996.080290
HLA A*3201	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.484262	0.235698	-4.248564	30497.364992
HLA A*0301	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.347022	0.098300	-4.248722	22234.217514
HLA B*3801	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.554303	0.305553	-4.248750	35834.620937

HLA B*5701	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.418637	0.169649	-4.248988	26220.230326
HLA B*0702	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.409490	0.160477	-4.249013	25673.788384
HLA B*7301	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.520724	0.271476	-4.249248	33168.358219
HLA A*3101	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.377410	0.127871	-4.249539	23845.700722
HLA B*0702	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.416797	0.166493	-4.250304	26109.397825
HLA A*2501	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.410822	0.160477	-4.250346	25752.661252
HLA A*2501	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.495655	0.245175	-4.250480	31307.974411
HLA A*2301	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.521995	0.271476	-4.250519	33265.575909
HLA B*4002	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.638034	0.387379	-4.250655	43454.400358
HLA B*3801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.537337	0.286028	-4.251310	34461.738578
HLA A*2402	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.575272	0.323743	-4.251529	37607.283885
HLA A*1101	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.420206	0.168569	-4.251637	26315.156569
HLA A*1101	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.493660	0.241980	-4.251681	31164.506739
HLA A*2603	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.575439	0.323743	-4.251696	37621.731697
HLA A*1101	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.350041	0.098300	-4.251741	22389.321787
HLA A*2501	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.487594	0.235698	-4.251896	30732.216722

HLA B*3801	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.523513	0.271476	-4.252037	33382.035439
HLA B*4002	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.538155	0.286028	-4.252127	34526.678785
HLA B*4403	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.326182	0.073876	-4.252306	21192.486638
HLA A*2403	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.316128	0.063696	-4.252433	20707.538224
HLA A*0201	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.346124	0.093374	-4.252750	22188.316222
HLA A*3201	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.286177	0.033425	-4.252752	19327.569200
HLA B*3501	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.421336	0.168569	-4.252767	26383.721900
HLA A*0202	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.326856	0.073876	-4.252981	21225.416460
HLA B*1517	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.498277	0.245175	-4.253102	31497.566060
HLA B*0802	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.488898	0.235698	-4.253200	30824.628512
HLA A*8001	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.430765	0.176828	-4.253936	26962.772287
HLA A*2602	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.641497	0.387379	-4.254118	43802.298678
HLA A*1101	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.488419	0.234162	-4.254257	30790.628680
HLA A*0101	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.382215	0.127871	-4.254343	24110.975727
HLA A*6801	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.331003	0.076178	-4.254825	21429.057059
HLA B*0702	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.295427	0.040514	-4.254913	19743.637077

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HLA A*0211	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.497161
	0.241980	-4.255181	31416.730754

HLA A*3101	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.297537
	0.042326	-4.255211	19839.786617

HLA A*0219	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.432045
	0.176828	-4.255217	27042.386353

HLA A*0250	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.415704
	0.160477	-4.255228	26043.799608

HLA B*7301	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.585675
	0.330347	-4.255328	38519.042951

HLA B*5301	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.592061
	0.335272	-4.256790	39089.614574

HLA B*0702	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.384691
	0.127871	-4.256820	24248.849776

HLA A*6802	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.380382
	0.123229	-4.257153	24009.448674

HLA B*1509	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.502330
	0.245175	-4.257155	31792.878993

HLA A*0203	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.350577
	0.093374	-4.257202	22416.955040

HLA A*8001	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.415359
	0.157927	-4.257432	26023.096414

HLA A*6802	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.427344
	0.169649	-4.257695	26751.226207

HLA A*2603	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.602291
	0.344471	-4.257820	40021.286582

HLA B*0801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.424541
	0.166493	-4.258047	26579.129806

HLA A*2403	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.350062
	0.091985	-4.258077	22390.411927

HLA B*4801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.424625
	0.166493	-4.258132	26584.306755
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HLA A*0301	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.351662
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HLA B*3901	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.503610
	0.245175	-4.258436	31886.755110

HLA B*5801	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.350673
	0.091985	-4.258688	22421.927795

HLA A*2301	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.537147
	0.278445	-4.258702	34446.640717

HLA B*4501	1:181-189	9	GLDPVNYQN	1.035268	-0.647889	-4.646433
	0.387379	-4.259054	44303.003521

HLA B*5101	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.501179
	0.241980	-4.259199	31708.712582

HLA A*0206	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.425708
	0.166493	-4.259215	26650.689667

HLA B*5801	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.352712
	0.093374	-4.259338	22527.463913

HLA B*4801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.419903
	0.160477	-4.259426	26296.798268

HLA B*4402	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.429125
	0.169649	-4.259476	26861.150081

HLA A*2601	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.387609
	0.127871	-4.259738	24412.328391

HLA A*3101	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.333881
	0.073876	-4.260005	21571.541476

HLA B*5801	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.359117
	0.098300	-4.260817	22862.146258

HLA A*0301	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.369224
	0.108361	-4.260863	23400.464769

HLA B*4001	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.352863
	0.091985	-4.260878	22535.265012

HLA B*3901	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.502898
	0.241980	-4.260919	31834.529271
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HLA B*4801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.437834	0.176828	-4.261006	27405.273732
HLA B*4601	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.353290	0.092119	-4.261172	22557.464157
HLA A*6801	1:143-151	9	TYDTLWQAD	1.156171	-0.755604	-4.661768	0.400567	-4.261201	45895.304839
HLA B*1517	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.419189	0.157927	-4.261262	26253.585931
HLA B*3501	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.353680	0.092119	-4.261562	22577.730797
HLA A*0301	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.353568	0.091985	-4.261583	22571.868693
HLA B*4601	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.383742	0.122021	-4.261721	24195.909480
HLA A*2601	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.353929	0.092119	-4.261811	22590.681670
HLA B*0702	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.419929	0.157927	-4.262002	26298.363204
HLA B*4801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.430819	0.168569	-4.262249	26966.127405
HLA A*3301	1:89-97	9	APYELNITS	1.361001	-1.037258	-4.586042	0.323743	-4.262299	38551.564537
HLA B*1509	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.504280	0.241980	-4.262300	31935.956616
HLA A*2902	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.439258	0.176828	-4.262430	27495.266419
HLA A*2603	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.568071	0.305553	-4.262518	36988.847258
HLA A*2402	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.568562	0.305553	-4.263009	37030.692973
HLA B*4402	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.385267	0.122021	-4.263246	24281.011064

HLA B*5701	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.385455	0.122021	-4.263434	24291.521944
HLA A*3301	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.481854	0.218305	-4.263549	30328.720953
HLA A*1101	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.499271	0.235698	-4.263572	31569.727092
HLA A*2602	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.440705	0.176828	-4.263877	27587.047011
HLA B*4601	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.372918	0.108361	-4.264557	23600.319022
HLA A*2601	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.355466	0.090830	-4.264636	22670.750588
HLA A*2601	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.386998	0.122021	-4.264978	24378.014852
HLA A*0202	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.500838	0.235698	-4.265140	31683.848946
HLA A*6801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.423347	0.157927	-4.265421	26506.184692
HLA B*1503	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.501212	0.235698	-4.265513	31711.114242
HLA A*0201	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.357879	0.091985	-4.265894	22797.058841
HLA A*0216	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.364222	0.098300	-4.265923	23132.492481
HLA A*2501	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.423963	0.157927	-4.266036	26543.780957
HLA A*2902	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.388213	0.122021	-4.266192	24446.293471
HLA A*6901	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.394131	0.127871	-4.266260	24781.715893
HLA A*2403	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.443207	0.176828	-4.266379	27746.449423

HLA B*0801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.357383	0.090830	-4.266554	22771.051150
HLA B*4402	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.358732	0.091985	-4.266747	22841.871458
HLA B*4402	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.340728	0.073876	-4.266852	21914.298837
HLA A*1101	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.142494	-0.124403	-4.266897	13883.356687
HLA A*2603	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.602766	0.335272	-4.267494	40065.045654
HLA A*0201	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.395675	0.127871	-4.267804	24869.954196
HLA B*3901	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.503648	0.235698	-4.267950	31889.515290
HLA A*0101	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.376466	0.108361	-4.268104	23793.898028
HLA A*0301	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.333710	0.065526	-4.268184	21563.024084
HLA A*2403	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.434700	0.166493	-4.268207	27208.207516
HLA B*4001	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.434820	0.166493	-4.268326	27215.715415
HLA B*2705	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.434911	0.166493	-4.268418	27221.458147
HLA A*2403	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.309428	0.040514	-4.268913	20390.493667
HLA B*1801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.429804	0.160477	-4.269327	26903.179207
HLA A*0101	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.343263	0.073876	-4.269387	22042.592603
HLA B*4001	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.377770	0.108361	-4.269408	23865.446290

HLA A*0250 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.574964 0.305553 -4.269412 37580.641215

HLA A*6801 1:89-97 9 APYELNITS 1.361001 -1.037258 -4.593159 0.323743 -4.269416 39188.496144

HLA B*4601 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.397475 0.127871 -4.269603 24973.228501

HLA A*0206 1:75-83 9 DKFLSAATS 1.204544 -0.986239 -4.488151 0.218305 -4.269845 30771.645112

HLA A*0212 1:163-171 9 QGELSKQTG 0.927669 -0.758020 -4.439632 0.169649 -4.269983 27518.927263

HLA A*2403 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.392268 0.122021 -4.270248 24675.629010

HLA B*1509 1:114-122 9 LKVYQNAGG 0.762278 -0.528116 -4.504750 0.234162 -4.270588 31970.529313

HLA B*1501 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.367495 0.096880 -4.270616 23307.476891

HLA A*0301 1:23-31 9 AAPKTYCEE 0.685714 -0.594884 -4.361793 0.090830 -4.270964 23003.454602

HLA A*2501 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.439556 0.168569 -4.270987 27514.163696

HLA B*4801 1:163-171 9 QGELSKQTG 0.927669 -0.758020 -4.440740 0.169649 -4.271092 27589.285745

HLA B*4403 1:113-121 9 VLKVYQNAG 0.952015 -0.550401 -4.672902 0.401614 -4.271288 47087.156845

HLA A*0211 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.440066 0.168569 -4.271497 27546.482803

HLA A*2902 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.394799 0.123229 -4.271569 24819.819997

HLA A*3101 1:84-92 9 STPREAPYE 0.746095 -0.647795 -4.369936 0.098300 -4.271637 23438.854182

HLA B*2705 1:10-18 9 TAVVLLCCS 1.085894 -0.909066 -4.448543 0.176828 -4.271715 28089.441026

HLA A*0212 1:194-202 9 NDGVIFFFN 0.826929 -0.753053 -4.346009 0.073876 -4.272134 22182.435222

HLA A*2402 1:43-51 9 IQMSDPAYN 0.678035 -0.520108 -4.431122 0.157927 -4.273195 26984.952978

HLA A*0201 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.396424 0.123229 -4.273195 24912.910690

HLA A*3002 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.366607 0.093374 -4.273233 23259.863243

HLA A*2603 1:181-189 9 GLDPVNYQN 1.035268 -0.647889 -4.660779 0.387379 -4.273400 45790.894322

HLA A*0201 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.395440 0.122021 -4.273419 24856.503465

HLA A*2902 1:194-202 9 NDGVIFFFN 0.826929 -0.753053 -4.347433 0.073876 -4.273557 22255.277295

HLA A*0212 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.401455 0.127871 -4.273583 25203.143867

HLA B*5801 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.349782 0.076178 -4.273604 22376.002138

HLA B*1801 1:156-164 9 PVVFPIVQG 0.934938 -0.699240 -4.509324 0.235698 -4.273626 32309.056362

HLA B*1501 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.338044 0.063696 -4.274349 21779.327614

HLA A*0203 1:163-171 9 QGELSKQTG 0.927669 -0.758020 -4.444248 0.169649 -4.274600 27813.025780

HLA B*4403 1:181-189 9 GLDPVNYQN 1.035268 -0.647889 -4.662071 0.387379 -4.274693 45927.345236

HLA A*6901 1:171-179 9 GQQVSIAPN 0.716617 -0.624632 -4.367025 0.091985 -4.275041 23282.272355

HLA B*1501 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.398638 0.123229 -4.275409 25040.193811

HLA A*3002 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.403602 0.127871 -4.275731 25328.072917

HLA B*5801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.366814	0.090830	-4.275984	23270.939208
HLA B*5101	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.494325	0.218305	-4.276020	31212.256099
HLA B*0803	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.511728	0.235698	-4.276029	32488.360614
HLA A*3201	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.611348	0.335272	-4.276077	40864.699594
HLA B*5801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.350029	0.073876	-4.276153	22388.716176
HLA A*6901	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.318553	0.042326	-4.276227	20823.471853
HLA A*0219	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.368374	0.092119	-4.276255	23354.682614
HLA A*2301	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.518245	0.241980	-4.276266	32979.591235
HLA B*0702	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.446010	0.169649	-4.276362	27926.104067
HLA A*2403	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.437056	0.160477	-4.276580	27356.243751
HLA B*1503	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.521758	0.245175	-4.276583	33247.404603
HLA B*0803	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.443508	0.166493	-4.277015	27765.669545
HLA B*1509	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.506963	0.229395	-4.277568	32133.870675
HLA A*0212	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.371649	0.093374	-4.278275	23531.475070
HLA B*4402	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.439448	0.160477	-4.278972	27507.317513
HLA B*5401	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.532528	0.253524	-4.279003	34082.213120

HLA A*0219	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.447660	0.168569	-4.279091	28032.361852
HLA B*0801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.402810	0.123229	-4.279581	25281.938547
HLA B*0802	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.456560	0.176828	-4.279731	28612.746012
HLA B*4402	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.448357	0.168569	-4.279788	28077.438691
HLA A*8001	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.354510	0.073876	-4.280634	22620.888479
HLA B*5301	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.586289	0.305553	-4.280736	38573.469526
HLA A*0203	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.408696	0.127871	-4.280824	25626.885665
HLA B*3801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.535021	0.253787	-4.281233	34278.403874
HLA B*1501	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.379731	0.098300	-4.281432	23973.496517
HLA A*0101	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.374957	0.093374	-4.281583	23711.401623
HLA A*0301	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.355511	0.073876	-4.281635	22673.080987
HLA B*5301	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.573186	0.291433	-4.281752	37427.052448
HLA A*3201	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.573411	0.291433	-4.281978	37446.495212
HLA B*5401	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.511519	0.229395	-4.282123	32472.721879
HLA A*1101	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.374243	0.091985	-4.282258	23672.437752
HLA B*0803	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.500673	0.218305	-4.282368	31671.852790

HLA B*3901	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.459259	0.176828	-4.282431	28791.155691
HLA A*2301	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.536240	0.253524	-4.282716	34374.783702
HLA B*1501	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.316859	0.033425	-4.283434	20742.407475
HLA B*4801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.411320	0.127871	-4.283449	25782.213833
HLA B*4001	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.411330	0.127871	-4.283458	25782.771754
HLA A*2601	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.375563	0.091985	-4.283579	23744.519952
HLA A*0211	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.537347	0.253524	-4.283822	34462.484323
HLA A*1101	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.502226	0.218305	-4.283921	31785.312072
HLA B*4001	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.406617	0.122021	-4.284596	25504.483744
HLA A*2301	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.514237	0.229395	-4.284842	32676.613934
HLA A*0201	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.393321	0.108361	-4.284960	24735.506144
HLA A*2601	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.325677	0.040514	-4.285162	21167.851432
HLA B*0801	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.378773	0.093374	-4.285399	23920.639737
HLA B*1503	1:50-58	9	YNINISLPS	0.643875	-0.954020	-3.975300	-0.310145	-4.285445	9447.141708
HLA A*0101	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.382555	0.096880	-4.285676	24129.896614
HLA A*6901	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.319115	0.033425	-4.285690	20850.413256

HLA A*2601	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.394192	0.108361	-4.285831	24785.201863
HLA B*5801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.351538	0.065526	-4.286012	22466.610711
HLA A*6802	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.362221	0.076178	-4.286042	23026.114953
HLA A*1101	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.455730	0.169649	-4.286082	28558.156653
HLA B*4601	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.378145	0.091985	-4.286161	23886.112740
HLA A*0201	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.383291	0.096880	-4.286411	24170.790267
HLA A*3002	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.564887	0.278445	-4.286442	36718.695590
HLA A*0250	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.578115	0.291433	-4.286682	37854.267372
HLA A*2501	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.463526	0.176828	-4.286697	29075.404325
HLA B*1801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.520860	0.234162	-4.286698	33178.767206
HLA B*5301	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.572819	0.286028	-4.286792	37395.479484
HLA A*2301	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.522686	0.235698	-4.286987	33318.527152
HLA B*5801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.351855	0.064686	-4.287168	22483.024857
HLA A*8001	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.385955	0.098300	-4.287655	24319.529354
HLA A*3301	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.579130	0.291433	-4.287697	37942.838984
HLA B*0803	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.522190	0.234162	-4.288028	33280.516198

HLA A*0101	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.378911	0.090830	-4.288082	23928.276028
HLA B*0802	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.454769	0.166493	-4.288276	28495.037456
HLA B*7301	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.593981	0.305553	-4.288428	39262.768335
HLA B*5401	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.542248	0.253787	-4.288460	34853.597158
HLA A*0101	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.330829	0.042326	-4.288503	21420.480043
HLA B*4002	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.560104	0.271476	-4.288628	36316.475458
HLA A*3301	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.449377	0.160477	-4.288901	28143.438932
HLA B*4501	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.633431	0.344471	-4.288960	42996.303540
HLA A*0202	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.507337	0.218305	-4.289031	32161.523234
HLA A*0211	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.523292	0.234162	-4.289130	33365.064002
HLA B*1501	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.355344	0.065526	-4.289818	22664.373880
HLA B*1801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.466672	0.176828	-4.289843	29286.786633
HLA A*2402	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.561577	0.271476	-4.290101	36439.870120
HLA B*7301	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.532246	0.241980	-4.290266	34060.094581
HLA A*6901	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.381158	0.090830	-4.290328	24052.350149
HLA B*4403	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.519801	0.229395	-4.290405	33097.914334

HLA B*0802	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.448696	0.157927	-4.290769	28099.320213
HLA B*5801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.354580	0.063696	-4.290884	22624.560072
HLA A*6802	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.389505	0.098300	-4.291205	24519.140248
HLA B*4601	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.414715	0.123229	-4.291486	25984.550703
HLA B*1517	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.461247	0.169649	-4.291598	28923.228081
HLA B*5701	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.414868	0.123229	-4.291639	25993.689589
HLA A*2501	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.458279	0.166493	-4.291786	28726.278245
HLA A*2501	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.383991	0.092119	-4.291872	24209.788561
HLA A*0250	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.570930	0.278445	-4.292485	37233.179167
HLA A*0301	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.368693	0.076178	-4.292515	23371.872026
HLA B*2705	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.453047	0.160477	-4.292571	28382.265589
HLA B*0801	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.384733	0.092119	-4.292615	24251.211195
HLA A*8001	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.462440	0.169649	-4.292792	29002.824907
HLA B*4501	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.623204	0.330347	-4.292856	41995.602078
HLA A*0202	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.571416	0.278445	-4.292972	37274.897988
HLA B*1502	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.584407	0.291433	-4.292974	38406.679930

HLA B*0702	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.401424	0.108361	-4.293063	25201.371428
HLA A*0219	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.421113	0.127871	-4.293241	26370.165748
HLA B*4801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.415780	0.122021	-4.293759	26048.308609
HLA A*2902	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.463570	0.169649	-4.293922	29078.393079
HLA A*2602	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.580201	0.286028	-4.294174	38036.556080
HLA B*1801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.460873	0.166493	-4.294380	28898.359817
HLA A*0201	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.393039	0.098300	-4.294739	24719.453394
HLA A*0216	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.388316	0.093374	-4.294942	24452.113240
HLA B*4501	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.581167	0.286028	-4.295139	38121.223102
HLA A*0203	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.417264	0.122021	-4.295244	26137.521502
HLA B*1517	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.461792	0.166493	-4.295299	28959.552250
HLA B*0702	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.472289	0.176828	-4.295461	29668.073198
HLA A*0101	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.387682	0.092119	-4.295563	24416.422842
HLA B*4001	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.418984	0.123229	-4.295755	26241.232316
HLA A*0212	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.464470	0.168569	-4.295901	29138.705609
HLA B*3501	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.359836	0.063696	-4.296140	22900.024194

HLA B*5701	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.424198	0.127871	-4.296326	26558.144733
HLA B*4001	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.393229	0.096880	-4.296349	24730.287857
HLA B*1503	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.418707	0.122021	-4.296686	26224.486127
HLA A*0201	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.370599	0.073876	-4.296723	23474.639524
HLA A*8001	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.424668	0.127871	-4.296796	26586.895608
HLA A*2402	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.575284	0.278445	-4.296839	37608.301155
HLA A*6901	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.390631	0.093374	-4.297256	24582.759996
HLA A*0101	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.395663	0.098300	-4.297363	24869.281486
HLA A*2601	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.390967	0.093374	-4.297592	24601.784925
HLA A*2403	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.391204	0.093374	-4.297830	24615.230984
HLA B*5701	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.396143	0.098300	-4.297843	24896.742808
HLA B*4001	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.390182	0.092119	-4.298063	24557.372023
HLA B*3501	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.407133	0.108361	-4.298772	25534.856629
HLA B*0801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.364363	0.065526	-4.298838	23140.002353
HLA A*0101	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.390830	0.091985	-4.298845	24594.066746
HLA A*0211	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.465426	0.166493	-4.298933	29202.934620

HLA B*4002 1:94-102 9 NITSATYQS 1.243610 -0.899139 -4.643783
0.344471 -4.299312 44033.474086

HLA B*3901 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.468175
0.168569 -4.299606 29388.362869

HLA B*5101 1:43-51 9 IQMSDPAYN 0.678035 -0.520108 -4.457614
0.157927 -4.299688 28682.332002

HLA A*6802 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.427590
0.127871 -4.299719 26766.426246

HLA A*0216 1:171-179 9 GQQVSIAPN 0.716617 -0.624632 -4.392066
0.091985 -4.300081 24664.151333

HLA A*0206 1:67-75 9 ENYIAQTRD 1.094922 -0.841398 -4.553849
0.253524 -4.300325 35797.225227

HLA A*0206 1:137-145 9 AYRKPITYD 0.853411 -0.611431 -4.542374
0.241980 -4.300395 34863.780567

HLA A*3301 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.606093
0.305553 -4.300540 40373.138602

HLA B*5301 1:118-126 9 QNAGGTHPT 0.654006 -0.382530 -4.572053
0.271476 -4.300577 37329.586047

HLA B*0801 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.409441
0.108361 -4.301079 25670.871811

HLA B*4403 1:100-108 9 YQSAIPPRG 0.865176 -0.579148 -4.587167
0.286028 -4.301140 38651.594178

HLA A*2301 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.546510
0.245175 -4.301335 35197.318091

HLA A*0203 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.366889
0.065526 -4.301364 23274.968140

HLA B*0702 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.424715
0.123229 -4.301485 26589.772407

HLA A*6802 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.409899
0.108361 -4.301538 25697.967031

HLA B*1502 1:197-205 9 VIFFFNPGE 0.720374 -0.559897 -4.462367
0.160477 -4.301891 28997.961350

HLA A*2403	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.394176	0.092119	-4.302057	24784.263285
HLA A*0250	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.537882	0.235698	-4.302184	34505.018464
HLA A*8001	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.399068	0.096880	-4.302188	25064.996122
HLA A*6901	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.367801	0.065526	-4.302275	23323.874469
HLA B*4402	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.425622	0.123229	-4.302392	26645.355642
HLA A*2902	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.396248	0.093374	-4.302874	24902.804534
HLA B*0801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.178648	-0.124403	-4.303051	15088.579546
HLA B*4601	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.343686	0.040514	-4.303171	22064.067694
HLA B*1517	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.425330	0.122021	-4.303310	26627.487232
HLA B*4601	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.394143	0.090830	-4.303314	24782.386234
HLA B*0803	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.473107	0.169649	-4.303458	29723.980151
HLA A*8001	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.426738	0.123229	-4.303508	26713.914191
HLA A*0211	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.521993	0.218305	-4.303687	33265.395946
HLA B*4402	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.400980	0.096880	-4.304100	25175.616975
HLA B*4501	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.432198	0.127871	-4.304326	27051.897285
HLA A*0301	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.369053	0.064686	-4.304367	23391.225238

HLA A*1101 1:144-152 9 YDTLWQADT 0.627145 -0.460652 -4.470863 0.166493 -4.304370 29570.808884

HLA B*5701 1:171-179 9 GQQVSIAPN 0.716617 -0.624632 -4.396829 0.091985 -4.304844 24936.102965

HLA A*2601 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.381202 0.076178 -4.305024 24054.822566

HLA B*3901 1:144-152 9 YDTLWQADT 0.627145 -0.460652 -4.471566 0.166493 -4.305072 29618.680056

HLA A*0301 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.369025 0.063696 -4.305329 23389.706760

HLA B*4601 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.402376 0.096880 -4.305496 25256.648295

HLA A*2403 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.414081 0.108361 -4.305720 25946.623553

HLA A*0203 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.402691 0.096880 -4.305811 25274.964113

HLA A*3101 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.414365 0.108361 -4.306004 25963.613685

HLA B*2705 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.474705 0.168569 -4.306135 29833.527863

HLA A*0201 1:23-31 9 AAPKTYCEE 0.685714 -0.594884 -4.397061 0.090830 -4.306232 24949.461796

HLA A*0216 1:38-46 9 GQACQIQMS 0.965607 -1.010502 -4.261519 -0.044895 -4.306414 18260.782839

HLA A*0211 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.551772 0.245175 -4.306598 35626.439357

HLA A*3001 1:204-212 9 GELLPEAAG 0.791497 -0.797464 -4.300772 -0.005967 -4.306740 19988.133330

HLA A*0219 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.400412 0.093374 -4.307037 25142.678795

HLA A*2301 1:114-122 9 LKVYQNAGG 0.762278 -0.528116 -4.541369 0.234162 -4.307207 34783.149219

HLA B*4501	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.598741	0.291433	-4.307308	39695.472351
HLA B*1509	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.543096	0.235698	-4.307397	34921.731698
HLA A*0216	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.435572	0.127871	-4.307700	27262.871101
HLA B*7301	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.599206	0.291433	-4.307773	39738.015257
HLA B*4001	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.406144	0.098300	-4.307845	25476.765554
HLA B*3801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.549959	0.241980	-4.307979	35477.958146
HLA A*0219	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.477862	0.169649	-4.308214	30051.234695
HLA B*4002	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.643517	0.335272	-4.308246	44006.563880
HLA B*0801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.342006	0.033425	-4.308581	21978.887168
HLA B*4801	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.402066	0.093374	-4.308691	25238.618826
HLA A*0202	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.562352	0.253524	-4.308828	36504.982992
HLA A*2601	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.374393	0.065526	-4.308868	23680.635348
HLA B*2705	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.373764	0.064686	-4.309077	23646.326849
HLA A*3002	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.538566	0.229395	-4.309170	34559.381726
HLA B*5401	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.551533	0.241980	-4.309553	35606.785801
HLA B*2705	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.479223	0.169649	-4.309574	30145.512530

HLA B*7301 1:86-94 9 PREAPYELN 0.811488 -0.746802 -4.374262
0.064686 -4.309575 23673.462296

HLA B*5401 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.554881
0.245175 -4.309706 35882.342571

HLA B*1501 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.418091
0.108361 -4.309730 26187.342108

HLA A*0203 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.432973
0.123229 -4.309744 27100.235183

HLA A*8001 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.431852
0.122021 -4.309832 27030.392716

HLA B*3801 1:67-75 9 ENYIAQTRD 1.094922 -0.841398 -4.563463
0.253524 -4.309939 36598.514390

HLA B*5801 1:206-214 9 LLPEAAGPT 0.415766 -0.375252 -4.350476
0.040514 -4.309961 22411.740897

HLA A*0301 1:206-214 9 LLPEAAGPT 0.415766 -0.375252 -4.350821
0.040514 -4.310306 22429.571006

HLA B*0702 1:157-165 9 VVFPIVQGE 0.697577 -0.605458 -4.402648
0.092119 -4.310530 25272.503007

HLA A*2601 1:194-202 9 NDGVIFFFN 0.826929 -0.753053 -4.384708
0.073876 -4.310832 24249.768078

HLA A*0250 1:137-145 9 AYRKPITYD 0.853411 -0.611431 -4.552863
0.241980 -4.310883 35715.980774

HLA A*0216 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.407770
0.096880 -4.310890 25572.320226

HLA A*0101 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.376611
0.065526 -4.311086 23801.880152

HLA B*0801 1:84-92 9 STPREAPYE 0.746095 -0.647795 -4.409401
0.098300 -4.311101 25668.511018

HLA B*4403 1:204-212 9 GELLPEAAG 0.791497 -0.797464 -4.305246
-0.005967 -4.311213 20195.083685

HLA B*3501 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.376776
0.065526 -4.311250 23810.895447

HLA B*0702	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.403287	0.091985	-4.311302	25309.718613
HLA B*4402	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.402188	0.090830	-4.311358	25245.719807
HLA A*0202	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.553415	0.241980	-4.311435	35761.416231
HLA B*0801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.408327	0.096880	-4.311447	25605.128644
HLA A*0219	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.403604	0.091985	-4.311620	25328.209939
HLA A*3301	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.488771	0.176828	-4.311943	30815.624904
HLA B*0802	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.480599	0.168569	-4.312030	30241.231328
HLA A*2501	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.434143	0.122021	-4.312123	27173.345038
HLA A*3201	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.434192	0.122021	-4.312172	27176.432314
HLA B*0802	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.472743	0.160477	-4.312266	29699.066065
HLA A*2301	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.470234	0.157927	-4.312307	29527.966703
HLA B*4601	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.410637	0.098300	-4.312337	25741.657399
HLA B*4403	1:94-102	9	NITSATYQS	1.243610	-0.899139	-4.657062	0.344471	-4.312591	45400.667737
HLA B*5101	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.479105	0.166493	-4.312612	30137.359439
HLA B*4601	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.406015	0.093374	-4.312641	25469.186226
HLA A*2501	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.410951	0.098300	-4.312652	25760.324939

HLA B*3501	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.440726	0.127871	-4.312855	27588.390229
HLA A*2602	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.554996	0.241980	-4.313016	35891.855687
HLA A*0250	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.481807	0.168569	-4.313238	30325.439630
HLA B*0802	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.483104	0.169649	-4.313455	30416.134593
HLA A*0211	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.411973	0.098300	-4.313674	25821.018145
HLA B*0801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.387856	0.073876	-4.313980	24426.199470
HLA A*3301	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.387915	0.073876	-4.314039	24429.503269
HLA B*7301	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.592494	0.278445	-4.314049	39128.544515
HLA B*5801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.118267	-0.196092	-4.314359	13130.056419
HLA A*0212	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.422781	0.108361	-4.314420	26471.648890
HLA A*0202	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.411480	0.096880	-4.314600	25791.700144
HLA B*1502	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.556659	0.241980	-4.314680	36029.592339
HLA A*6901	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.379518	0.064686	-4.314831	23961.697271
HLA A*0101	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.379738	0.064686	-4.315052	23973.885602
HLA A*0201	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.270215	-0.044895	-4.315109	18630.084974
HLA B*5701	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.423507	0.108361	-4.315146	26515.937381

HLA B*5701	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.408729	0.093374	-4.315355	25628.826679
HLA B*4402	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.407740	0.092119	-4.315621	25570.521825
HLA A*0219	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.389533	0.073876	-4.315658	24520.732050
HLA B*4402	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.414064	0.098300	-4.315765	25945.640994
HLA A*0212	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.379511	0.063696	-4.315815	23961.308384
HLA B*5801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.358337	0.042326	-4.316011	22821.120795
HLA A*2403	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.381891	0.065526	-4.316365	24092.982041
HLA A*3001	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.272022	-0.044895	-4.316916	18707.751384
HLA A*0203	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.425441	0.108361	-4.317079	26634.258525
HLA B*1801	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.425457	0.108361	-4.317096	26635.267163
HLA A*3301	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.440731	0.123229	-4.317502	27588.688731
HLA B*1801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.439530	0.122021	-4.317510	27512.526410
HLA A*0201	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.383180	0.065526	-4.317655	24164.645268
HLA B*4801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.441201	0.123229	-4.317972	27618.555235
HLA A*1101	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.440419	0.122021	-4.318398	27568.845388
HLA B*3901	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.488334	0.169649	-4.318685	30784.632604

HLA B*1501	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.392616	0.073876	-4.318740	24695.393800
HLA B*1509	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.488449	0.169649	-4.318800	30792.794217
HLA A*3301	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.572692	0.253524	-4.319168	37384.556588
HLA B*1801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.416108	0.096880	-4.319229	26068.044667
HLA A*2902	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.447176	0.127871	-4.319304	28001.138948
HLA A*0216	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.489053	0.169649	-4.319404	30835.636493
HLA A*0211	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.496259	0.176828	-4.319430	31351.533462
HLA B*4801	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.427823	0.108361	-4.319462	26780.765623
HLA B*7301	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.555233	0.235698	-4.319535	35911.472313
HLA A*0211	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.411560	0.091985	-4.319575	25796.444608
HLA A*2603	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.611421	0.291433	-4.319988	40871.553447
HLA A*0203	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.410846	0.090830	-4.320016	25754.054480
HLA A*0301	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.362439	0.042326	-4.320113	23037.702760
HLA A*2402	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.574104	0.253787	-4.320317	37506.304434
HLA B*3501	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.417316	0.096880	-4.320436	26140.632511
HLA A*2403	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.396779	0.076178	-4.320601	24933.270193

HLA A*2402 1:156-164 9 PVVFPIVQG 0.934938 -0.699240 -4.556601 0.235698 -4.320902 36024.719766

HLA A*0206 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.489572 0.168569 -4.321003 30872.525180

HLA A*0206 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.386575 0.065526 -4.321050 24354.287582

HLA A*6802 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.414579 0.093374 -4.321205 25976.398716

HLA A*2602 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.444648 0.123229 -4.321419 27838.616661

HLA A*3201 1:60-68 9 YPDQKSLEN 1.087218 -0.808773 -4.600033 0.278445 -4.321588 39813.759700

HLA A*0101 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.385518 0.063696 -4.321822 24295.070393

HLA B*1517 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.445094 0.123229 -4.321865 27867.246100

HLA A*2402 1:187-195 9 YQNFAVTND 0.973541 -0.744146 -4.551443 0.229395 -4.322048 35599.466661

HLA A*0219 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.444128 0.122021 -4.322108 27805.353104

HLA A*3001 1:201-209 9 FNPGELLPE 0.811387 -0.836977 -4.296766 -0.025590 -4.322357 19804.613249

HLA B*1503 1:188-196 9 QNFAVTNDG 0.673013 -0.639588 -4.355950 0.033425 -4.322525 22696.029798

HLA A*8001 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.416219 0.093374 -4.322845 26074.673695

HLA B*0801 1:171-179 9 GQQVSIAPN 0.716617 -0.624632 -4.415284 0.091985 -4.323299 26018.591777

HLA B*4001 1:194-202 9 NDGVIFFFN 0.826929 -0.753053 -4.397183 0.073876 -4.323308 24956.481422

HLA B*0702 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.445392 0.122021 -4.323372 27886.399036

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HLA B*5701	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.414370
	0.090830	-4.323540	25963.894607

HLA B*0702	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.420493
	0.096880	-4.323613	26332.530476

HLA A*2403	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.446941
	0.123229	-4.323712	27985.994739

HLA A*0250	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.553119
	0.229395	-4.323723	35737.047910

HLA A*3101	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.199390
	-0.124403	-4.323792	15826.672309

HLA B*5301	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.500643
	0.176828	-4.323815	31669.625432

HLA A*6801	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.559735
	0.235698	-4.324036	36285.643061

HLA B*0802	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.446097
	0.122021	-4.324077	27931.694480

HLA A*0219	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.447387
	0.123229	-4.324158	28014.775743

HLA A*6802	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.415068
	0.090830	-4.324238	26005.645291

HLA A*0219	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.387995
	0.063696	-4.324299	24433.997153

HLA A*8001	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.432783
	0.108361	-4.324422	27088.362434

HLA A*3002	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.558955
	0.234162	-4.324793	36220.529520

HLA B*1801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.482794
	0.157927	-4.324867	30394.422022

HLA B*5401	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.446929
	0.122021	-4.324908	27985.237744

HLA B*5401	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.421790
	0.096880	-4.324910	26411.283757
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HLA A*0212	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.448372
	0.123229	-4.325142	28078.350081

HLA A*2301	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.543570
	0.218305	-4.325265	34959.914942

HLA A*2602	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.578904
	0.253524	-4.325380	37923.138511

HLA B*5801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.358819
	0.033425	-4.325394	22846.444080

HLA B*1801	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.417549
	0.092119	-4.325430	26154.636635

HLA B*0801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.389369
	0.063696	-4.325673	24511.447997

HLA A*6801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.399629
	0.073876	-4.325753	25097.425207

HLA B*5401	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.544066
	0.218305	-4.325761	34999.844002

HLA B*4501	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.661099
	0.335272	-4.325827	45824.597137

HLA A*6801	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.612300
	0.286028	-4.326272	40954.332516

HLA B*1517	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.368752
	0.042326	-4.326426	23375.033221

HLA B*1517	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.417325
	0.090830	-4.326496	26141.198189

HLA A*0201	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.402775
	0.076178	-4.326597	25279.887043

HLA A*0202	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.420147
	0.093374	-4.326773	26311.597758

HLA B*0803	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.454781
	0.127871	-4.326910	28495.808241

HLA B*4801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.423834
	0.096880	-4.326954	26535.884191
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HLA A*3002	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.449300	0.122021	-4.327279	28138.415035
HLA B*1509	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.391068	0.063696	-4.327372	24607.508586
HLA A*2601	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.392160	0.064686	-4.327474	24669.489123
HLA A*0206	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.292551	-0.035101	-4.327653	19613.332446
HLA B*1517	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.419731	0.091985	-4.327747	26286.415136
HLA B*4501	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.581298	0.253524	-4.327774	38132.773820
HLA B*5101	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.488357	0.160477	-4.327881	30786.298064
HLA B*3801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.573096	0.245175	-4.327922	37419.359143
HLA B*5701	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.404345	0.076178	-4.328166	25371.408921
HLA B*0702	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.421674	0.093374	-4.328300	26404.283461
HLA B*4001	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.404711	0.076178	-4.328533	25392.829974
HLA A*2902	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.303058	-0.025590	-4.328649	20093.624709
HLA A*2902	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.425622	0.096880	-4.328742	26645.355642
HLA A*0101	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.405049	0.076178	-4.328871	25412.619306
HLA B*3901	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.489410	0.160477	-4.328934	30861.003162
HLA B*4601	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.394599	0.065526	-4.329073	24808.409460

HLA A*0203 1:84-92 9 STPREAPYE 0.746095 -0.647795 -4.427417
0.098300 -4.329117 26755.712940

HLA A*0202 1:29-37 9 CEELKGTDT 0.714161 -0.468986 -4.574320
0.245175 -4.329146 37524.976335

HLA A*2902 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.405808
0.076178 -4.329630 25457.063990

HLA B*5301 1:146-154 9 TLWQADTDP 0.196026 0.057761 -4.583490
0.253787 -4.329703 38325.732760

HLA A*0101 1:206-214 9 LLPEAAGPT 0.415766 -0.375252 -4.370416
0.040514 -4.329901 23464.735988

HLA A*0301 1:188-196 9 QNFAVTNDG 0.673013 -0.639588 -4.363600
0.033425 -4.330175 23099.353023

HLA A*2902 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.438560
0.108361 -4.330199 27451.124227

HLA B*0802 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.458136
0.127871 -4.330265 28716.800044

HLA B*5701 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.395877
0.065526 -4.330351 24881.527645

HLA B*1502 1:67-75 9 ENYIAQTRD 1.094922 -0.841398 -4.583923
0.253524 -4.330398 38363.901939

HLA A*0216 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.406711
0.076178 -4.330532 25510.003398

HLA B*1801 1:163-171 9 QGELSKQTG 0.927669 -0.758020 -4.500192
0.169649 -4.330543 31636.747311

HLA A*0201 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.394575
0.063696 -4.330880 24807.067389

HLA B*4501 1:173-181 9 QVSIAPNAG 0.868398 -0.562845 -4.636469
0.305553 -4.330916 43298.116468

HLA B*4801 1:157-165 9 VVFPIVQGE 0.697577 -0.605458 -4.423077
0.092119 -4.330958 26489.699336

HLA B*3801 1:156-164 9 PVVFPIVQG 0.934938 -0.699240 -4.566687
0.235698 -4.330989 36871.172662

HLA B*7301	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.458869	0.127871	-4.330998	28765.311642
HLA B*1801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.499760	0.168569	-4.331190	31605.271141
HLA A*2601	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.395123	0.063696	-4.331427	24838.356517
HLA B*4403	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.424804	0.093374	-4.331430	26595.239182
HLA A*2602	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.623004	0.291433	-4.331571	41976.295235
HLA B*4001	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.422551	0.090830	-4.331721	26457.618159
HLA A*2501	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.501442	0.169649	-4.331793	31727.930954
HLA A*2902	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.207392	-0.124403	-4.331795	16120.999195
HLA B*2705	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.453851	0.122021	-4.331830	28434.826557
HLA A*0201	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.396718	0.064686	-4.332032	24929.763398
HLA B*4403	1:59-67	9	YYPDQKSLE	0.890200	-0.554928	-4.667470	0.335272	-4.332199	46501.874411
HLA B*4403	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.623725	0.291433	-4.332292	42046.068902
HLA B*4801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.395992	0.063696	-4.332296	24888.124229
HLA B*1503	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.498808	0.166493	-4.332315	31536.099636
HLA B*5801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.297725	-0.035101	-4.332826	19848.374959
HLA A*0202	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.424893	0.091985	-4.332908	26600.707081

HLA B*1502	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.551587	0.218305	-4.333281	35611.216538
HLA B*4601	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.397071	0.063696	-4.333375	24950.001697
HLA B*5401	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.499962	0.166493	-4.333468	31619.978930
HLA B*2705	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.441901	0.108361	-4.333540	27663.116315
HLA B*1501	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.376513	0.042326	-4.334186	23796.472614
HLA B*0802	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.431307	0.096880	-4.334428	26996.488306
HLA A*2602	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.612984	0.278445	-4.334539	41018.856787
HLA B*3801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.568841	0.234162	-4.334680	37054.540150
HLA A*3101	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.400513	0.065526	-4.334987	25148.528297
HLA B*4403	1:77-85	9	FLSAATSST	0.627583	-0.297236	-4.665335	0.330347	-4.334987	46273.758644
HLA A*2402	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.588899	0.253524	-4.335375	38806.009125
HLA A*2501	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.411731	0.076178	-4.335553	25806.634201
HLA B*0803	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.494088	0.157927	-4.336161	31195.206418
HLA B*4402	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.444659	0.108361	-4.336298	27839.369691
HLA A*2403	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.369882	0.033425	-4.336458	23435.937927
HLA B*4002	1:45-53	9	MSDPAYNIN	0.920513	-0.629080	-4.628117	0.291433	-4.336683	42473.356717

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HLA A*8001	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.413080
	0.076178	-4.336902	25886.895485

HLA B*5101	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.505499
	0.168569	-4.336930	32025.750237

HLA B*4801	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.413256
	0.076178	-4.337078	25897.401009

HLA A*0212	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.459104
	0.122021	-4.337083	28780.877567

HLA B*7301	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.582393
	0.245175	-4.337219	38229.028139

HLA B*3801	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.555532
	0.218305	-4.337226	35936.153981

HLA A*3301	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.623300
	0.286028	-4.337273	42004.917965

HLA A*0211	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.430934
	0.093374	-4.337559	26973.276657

HLA A*3002	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.591333
	0.253524	-4.337809	39024.113665

HLA A*3301	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.591641
	0.253787	-4.337853	39051.779680

HLA A*2902	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.302863	-
0.035101	-4.337964	20084.604278

HLA B*0802	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.431535
	0.093374	-4.338161	27010.658680

HLA B*5101	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.507814
	0.169649	-4.338165	32196.862661

HLA A*0216	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.403929
	0.065526	-4.338403	25347.126147

HLA A*0216	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.429505
	0.090830	-4.338676	26884.701566

HLA A*3301	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.610169
	0.271476	-4.338693	40753.871260
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HLA B*5701	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.412753	0.073876	-4.338878	25867.436514
HLA B*5301	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.574840	0.235698	-4.339141	37569.867483
HLA B*3501	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.432531	0.093374	-4.339157	27072.686652
HLA A*0212	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.436131	0.096880	-4.339251	27297.996117
HLA A*0202	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.505950	0.166493	-4.339457	32059.032625
HLA B*5301	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.593039	0.253524	-4.339514	39177.685359
HLA B*4801	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.437867	0.098300	-4.339567	27407.349443
HLA A*6802	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.432038	0.091985	-4.340053	27041.947468
HLA A*2501	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.404267	0.063696	-4.340571	25366.879861
HLA B*0801	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.381207	0.040514	-4.340692	24055.082835
HLA B*4002	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.646670	0.305553	-4.341118	44327.217243
HLA A*2403	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.415018	0.073876	-4.341143	26002.691018
HLA B*1501	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.417455	0.076178	-4.341276	26148.977500
HLA A*2601	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.383695	0.042326	-4.341369	24193.291677
HLA B*3801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.570977	0.229395	-4.341582	37237.207932
HLA A*1101	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.469463	0.127871	-4.341591	29475.617450

HLA A*3101 1:86-94 9 PREAPYELN 0.811488 -0.746802 -4.406288 0.064686 -4.341601 25485.174357

HLA B*1501 1:204-212 9 GELLPEAAG 0.791497 -0.797464 -4.335707 -0.005967 -4.341674 21662.407947

HLA A*3201 1:43-51 9 IQMSDPAYN 0.678035 -0.520108 -4.499802 0.157927 -4.341875 31608.348949

HLA B*3901 1:39-47 9 QACQIQMSD 0.891798 -0.769777 -4.464123 0.122021 -4.342102 29115.384645

HLA A*0212 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.407770 0.065526 -4.342245 25572.320226

HLA A*6802 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.406010 0.063696 -4.342315 25468.910656

HLA A*8001 1:23-31 9 AAPKTYCEE 0.685714 -0.594884 -4.433441 0.090830 -4.342611 27129.426138

HLA A*2501 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.470506 0.127871 -4.342635 29546.502710

HLA A*0216 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.466145 0.123229 -4.342916 29251.317956

HLA B*4402 1:38-46 9 GQACQIQMS 0.965607 -1.010502 -4.298261 -0.044895 -4.343155 19872.872136

HLA A*3201 1:137-145 9 AYRKPITYD 0.853411 -0.611431 -4.585556 0.241980 -4.343576 38508.416845

HLA B*1517 1:167-175 9 SKQTGQQVS 1.053333 -0.925462 -4.471789 0.127871 -4.343917 29633.906177

HLA A*0250 1:67-75 9 ENYIAQTRD 1.094922 -0.841398 -4.597472 0.253524 -4.343948 39579.677595

HLA A*2301 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.440865 0.096880 -4.343985 27597.197393

HLA B*3501 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.467219 0.123229 -4.343990 29323.726026

HLA A*2501 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.452420 0.108361 -4.344059 28341.298692

HLA A*0212	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.338099	-0.005967	-4.344066	21782.037728
HLA A*0212	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.420251	0.076178	-4.344072	26317.861588
HLA B*1502	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.512797	0.168569	-4.344228	32568.429203
HLA B*4601	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.377763	0.033425	-4.344338	23865.058965
HLA B*4001	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.410155	0.065526	-4.344629	25713.125024
HLA B*5301	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.578893	0.234162	-4.344731	37922.112725
HLA A*2902	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.410301	0.065526	-4.344775	25721.750990
HLA B*4801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.435710	0.090830	-4.344881	27271.574348
HLA B*4402	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.421195	0.076178	-4.345017	26375.159309
HLA A*3301	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.437270	0.092119	-4.345152	27369.714543
HLA B*4001	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.385666	0.040514	-4.345152	24303.352124
HLA A*0216	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.453531	0.108361	-4.345170	28413.913472
HLA B*1801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.473123	0.127871	-4.345252	29725.105796
HLA A*3002	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.512054	0.166493	-4.345561	32512.800224
HLA A*0203	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.419494	0.073876	-4.345618	26272.056194
HLA B*7301	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.379508	0.033425	-4.346083	23961.178756

HLA B*0803	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.514965	0.168569	-4.346396	32731.460739
HLA B*4402	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.379870	0.033425	-4.346445	23981.149682
HLA B*5101	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.443398	0.096880	-4.346518	27758.610610
HLA B*4601	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.420443	0.073876	-4.346568	26329.539068
HLA B*4403	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.565230	0.218305	-4.346925	36747.709081
HLA A*3301	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.443814	0.096880	-4.346934	27785.203608
HLA A*2501	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.470278	0.123229	-4.347049	29531.001977
HLA A*0201	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.389400	0.042326	-4.347073	24513.171913
HLA A*2602	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.600971	0.253787	-4.347183	39899.792342
HLA A*2603	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.565660	0.218305	-4.347355	36784.107685
HLA A*6801	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.576837	0.229395	-4.347441	37743.026802
HLA A*0212	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.445759	0.098300	-4.347459	27909.943492
HLA A*3201	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.566036	0.218305	-4.347731	36815.961140
HLA A*0250	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.592917	0.245175	-4.347742	39166.665669
HLA A*3301	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.626322	0.278445	-4.347877	42298.170024
HLA B*4403	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.601471	0.253524	-4.347947	39945.795627

HLA A*0212	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.438950	0.090830	-4.348121	27475.787551
HLA B*0803	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.525172	0.176828	-4.348343	33509.777969
HLA A*3301	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.506293	0.157927	-4.348367	32084.364257
HLA B*4501	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.590393	0.241980	-4.348414	38939.758516
HLA B*3501	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.440893	0.091985	-4.348908	27598.989024
HLA B*5301	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.594167	0.245175	-4.348992	39279.552092
HLA A*0206	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.447359	0.098300	-4.349059	28012.957120
HLA A*3002	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.446046	0.096880	-4.349166	27928.370316
HLA A*3002	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.567775	0.218305	-4.349469	36963.642549
HLA A*0219	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.457849	0.108361	-4.349488	28697.853024
HLA B*1509	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.441614	0.092119	-4.349496	27644.864503
HLA A*3201	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.446400	0.096880	-4.349521	27951.194134
HLA B*3901	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.442958	0.093374	-4.349584	27730.542832
HLA A*0101	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.383493	0.033425	-4.350068	24182.038355
HLA B*5301	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.579677	0.229395	-4.350282	37990.696246
HLA A*3002	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.315525	-0.035101	-4.350626	20678.767679

HLA A*3002	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.473868	0.123229	-4.350639	29776.126152
HLA A*0219	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.449098	0.098300	-4.350798	28125.326670
HLA A*8001	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.416506	0.065526	-4.350980	26091.888829
HLA A*0203	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.384423	0.033425	-4.350999	24233.899457
HLA A*2402	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.596206	0.245175	-4.351031	39464.434118
HLA B*1502	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.585213	0.234162	-4.351051	38478.013219
HLA B*0803	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.511568	0.160477	-4.351092	32476.411239
HLA A*3101	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.384705	0.033425	-4.351280	24249.636890
HLA A*2602	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.580960	0.229395	-4.351565	38103.079041
HLA B*4601	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.427774	0.076178	-4.351595	26777.723295
HLA A*3301	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.587416	0.235698	-4.351718	38673.765224
HLA B*5101	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.443898	0.092119	-4.351780	27790.615471
HLA A*2902	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.394235	0.042326	-4.351909	24787.615514
HLA B*1517	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.417669	0.065526	-4.352143	26161.853809
HLA A*6802	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.394552	0.042326	-4.352226	24805.725391
HLA B*1503	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.521892	0.169649	-4.352243	33257.658475

HLA B*4001	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.417257	0.064686	-4.352571	26137.097302
HLA B*1503	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.449943	0.096880	-4.353064	28180.155808
HLA A*3002	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.598271	0.245175	-4.353097	39652.545957
HLA B*0702	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.429338	0.076178	-4.353160	26874.377078
HLA B*4002	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.631653	0.278445	-4.353208	42820.581438
HLA B*0803	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.445357	0.092119	-4.353239	27884.136192
HLA A*8001	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.445498	0.091985	-4.353513	27893.188667
HLA A*0201	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.386961	0.033425	-4.353536	24375.904825
HLA B*3501	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.444955	0.090830	-4.354126	27858.352756
HLA A*2601	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.387917	0.033425	-4.354492	24429.635430
HLA B*5101	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.476641	0.122021	-4.354620	29966.815091
HLA B*0802	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.477961	0.123229	-4.354732	30058.063572
HLA A*3101	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.418627	0.063696	-4.354931	26219.662938
HLA A*2603	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.633457	0.278445	-4.355012	42998.862273
HLA A*0301	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.320000	-0.035101	-4.355102	20892.981657
HLA B*4002	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.447136	0.091985	-4.355151	27998.563854

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HLA A*2603	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.609349
	0.253787	-4.355562	40676.998452

HLA B*1503	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.524197
	0.168569	-4.355627	33434.629422

HLA A*2301	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.532523
	0.176828	-4.355695	34081.844360

HLA A*0250	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.522289
	0.166493	-4.355795	33288.078901

HLA B*1509	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.516511
	0.160477	-4.356035	32848.182775

HLA A*1101	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.479317
	0.123229	-4.356088	30152.036591

HLA A*3201	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.609981
	0.253524	-4.356456	40736.237162

HLA A*0250	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.590908
	0.234162	-4.356746	38985.920348

HLA B*1509	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.525409
	0.168569	-4.356840	33528.092675

HLA A*2601	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.331353
	-0.025590	-4.356943	21446.337417

HLA A*0216	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.431140
	0.073876	-4.357265	26986.120888

HLA B*1509	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.534581
	0.176828	-4.357753	34243.743686

HLA B*4801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.422539
	0.064686	-4.357853	26456.902505

HLA A*0203	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.400240
	0.042326	-4.357914	25132.751361

HLA B*4403	1:118-126	9	QNAGGTHPT	0.654006	-0.382530	-4.629550
	0.271476	-4.358074	42613.751696

HLA A*0250	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.423676
	0.065526	-4.358151	26526.267670
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HLA B*0802	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.450465	0.092119	-4.358346	28214.020376
HLA B*4601	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.423051	0.064686	-4.358365	26488.123013
HLA A*2402	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.592724	0.234162	-4.358562	39149.294762
HLA A*3002	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.594618	0.235698	-4.358919	39320.372909
HLA A*0219	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.455855	0.096880	-4.358975	28566.346139
HLA B*1501	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.324161	-0.035101	-4.359262	21094.117504
HLA A*2603	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.604540	0.245175	-4.359365	40229.024638
HLA B*7301	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.452756	0.093374	-4.359382	28363.232405
HLA B*4002	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.613214	0.253524	-4.359689	41040.609484
HLA B*3901	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.423401	0.063696	-4.359705	26509.482994
HLA A*2902	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.452469	0.091985	-4.360484	28344.518664
HLA B*1502	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.605757	0.245175	-4.360582	40341.917449
HLA A*2301	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.527089	0.166493	-4.360595	33658.032856
HLA A*3101	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.437014	0.076178	-4.360836	27353.579984
HLA A*2403	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.403360	0.042326	-4.361034	25313.963575
HLA B*1503	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.426571	0.065526	-4.361045	26703.655290

HLA B*7301	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.437439	0.076178	-4.361261	27380.377452
HLA A*2301	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.521887	0.160477	-4.361410	33257.298637
HLA A*6801	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.615575	0.253787	-4.361788	41264.352445
HLA B*4801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.435969	0.073876	-4.362093	27287.808159
HLA A*2603	1:100-108	9	YQSAIPPRG	0.865176	-0.579148	-4.648132	0.286028	-4.362104	44476.627397
HLA B*5301	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.604330	0.241980	-4.362351	40209.659824
HLA B*1503	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.427179	0.064686	-4.362493	26741.097643
HLA B*4501	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.592043	0.229395	-4.362647	39087.922847
HLA B*3501	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.396161	0.033425	-4.362737	24897.820341
HLA A*0216	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.484798	0.122021	-4.362777	30535.005320
HLA B*5701	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.426538	0.063696	-4.362842	26701.632873
HLA A*2402	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.581298	0.218305	-4.362993	38132.773820
HLA B*0802	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.471382	0.108361	-4.363021	29606.184458
HLA B*4402	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.427837	0.064686	-4.363151	26781.634922
HLA A*8001	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.403715	0.040514	-4.363200	25334.650830
HLA B*0702	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.428864	0.065526	-4.363338	26845.024864

HLA B*4403	1:173-181	9	QVSIAPNAG	0.868398	-0.562845	-4.669087	0.305553	-4.363534	46675.277064
HLA B*5801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.357801	-0.005967	-4.363769	22792.989329
HLA A*6801	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.642371	0.278445	-4.363926	43890.538634
HLA B*5701	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.428655	0.064686	-4.363968	26832.102629
HLA B*4601	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.406323	0.042326	-4.363997	25487.242520
HLA B*4403	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.522197	0.157927	-4.364270	33281.056334
HLA A*0219	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.455281	0.090830	-4.364452	28528.663069
HLA B*0802	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.438485	0.073876	-4.364609	27446.372397
HLA B*1501	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.429454	0.064686	-4.364767	26881.502005
HLA B*0702	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.463394	0.098300	-4.365094	29066.597156
HLA B*0801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.407577	0.042326	-4.365251	25560.978582
HLA B*4402	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.431051	0.065526	-4.365526	26980.573765
HLA A*0219	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.431486	0.065526	-4.365960	27007.590236
HLA A*0219	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.442305	0.076178	-4.366127	27688.868850
HLA B*2705	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.459421	0.092119	-4.367303	28801.904927
HLA B*5701	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.409631	0.042326	-4.367305	25682.123278

HLA B*3801	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.525399	0.157927	-4.367473	33527.367149
HLA A*3301	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.597038	0.229395	-4.367642	39540.084902
HLA A*2902	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.458503	0.090830	-4.367673	28741.045608
HLA B*0702	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.441955	0.073876	-4.368079	27666.558580
HLA B*1801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.491334	0.123229	-4.368105	30998.042350
HLA A*2403	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.433076	0.064686	-4.368390	27106.686759
HLA B*1502	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.604279	0.235698	-4.368580	40204.874453
HLA B*1517	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.462255	0.093374	-4.368880	28990.432292
HLA A*2902	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.433614	0.064686	-4.368928	27140.289084
HLA A*1101	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.459760	0.090830	-4.368930	28824.351046
HLA B*3901	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.477468	0.108361	-4.369106	30023.934696
HLA B*4501	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.535740	0.166493	-4.369246	34335.196232
HLA A*2301	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.538918	0.169649	-4.369270	34587.437472
HLA B*5701	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.409990	0.040514	-4.369476	25703.389506
HLA B*1502	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.497765	0.127871	-4.369893	31460.441118
HLA A*2602	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.588243	0.218305	-4.369938	38747.481105

HLA A*0206	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.461139	0.090830	-4.370309	28916.031290
HLA A*0202	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.335404	-0.035101	-4.370505	21647.295552
HLA A*1101	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.444455	0.073876	-4.370579	27826.269886
HLA B*4801	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.411182	0.040514	-4.370667	25773.985890
HLA B*0802	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.462990	0.091985	-4.371005	29039.563239
HLA A*2602	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.605383	0.234162	-4.371221	40307.231366
HLA A*2902	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.404669	0.033425	-4.371244	25390.357392
HLA B*5101	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.436869	0.065526	-4.371343	27344.406773
HLA B*4801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.437019	0.065526	-4.371493	27353.875945
HLA A*0211	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.499642	0.127871	-4.371771	31596.723247
HLA A*8001	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.435644	0.063696	-4.371949	27267.443647
HLA B*4002	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.625948	0.253787	-4.372161	42261.801950
HLA A*6801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.495615	0.123229	-4.372386	31305.095208
HLA A*2602	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.530380	0.157927	-4.372454	33914.104851
HLA B*4501	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.650904	0.278445	-4.372459	44761.459644
HLA A*0250	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.590941	0.218305	-4.372635	38988.873193

HLA A*0211	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.469672	0.096880	-4.372792	29489.812791
HLA B*5401	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.533280	0.160477	-4.372803	34141.266139
HLA A*2501	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.463678	0.090830	-4.372849	29085.630280
HLA A*6802	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.437559	0.064686	-4.372873	27387.932860
HLA B*3501	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.471291	0.098300	-4.372991	29599.938636
HLA B*1503	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.204371	-0.168791	-4.373161	16009.232748
HLA B*2705	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.414008	0.040514	-4.373494	25942.272499
HLA B*2705	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.496933	0.123229	-4.373704	31400.248858
HLA B*3801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.501677	0.127871	-4.373805	31745.100056
HLA A*0212	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.407547	0.033425	-4.374122	25559.180978
HLA A*2501	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.414692	0.040514	-4.374177	25983.145005
HLA A*0301	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.368219	-0.005967	-4.374186	23346.345251
HLA B*3501	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.448193	0.073876	-4.374317	28066.807996
HLA A*3201	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.608769	0.234162	-4.374607	40622.680412
HLA A*6901	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.349320	-0.025590	-4.374910	22352.167658
HLA A*0211	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.544604	0.169649	-4.374955	35043.230940

HLA A*0211	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.483485	0.108361	-4.375124	30442.803040
HLA A*2301	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.543777	0.168569	-4.375208	34976.562280
HLA A*6901	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.369419	-0.005967	-4.375387	23410.974424
HLA B*1509	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.472440	0.096880	-4.375560	29678.347039
HLA B*5101	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.466853	0.090830	-4.376023	29298.988921
HLA B*1801	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.468077	0.091985	-4.376092	29381.686141
HLA B*5701	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.409610	0.033425	-4.376185	25680.872871
HLA A*3201	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.621423	0.245175	-4.376248	41823.743492
HLA B*0801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.350696	-0.025590	-4.376287	22423.140829
HLA B*0702	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.441046	0.064686	-4.376359	27608.695716
HLA B*5101	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.504329	0.127871	-4.376458	31939.584992
HLA A*0250	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.553316	0.176828	-4.376488	35753.291611
HLA B*5401	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.534461	0.157927	-4.376535	34234.296992
HLA A*6901	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.252138	-0.124403	-4.376541	17870.549145
HLA B*7301	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.468584	0.091985	-4.376599	29416.039768
HLA B*5801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.351030	-0.025590	-4.376620	22440.372999

HLA A*2402	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.545293	0.168569	-4.376723	35098.821925
HLA A*3301	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.452962	0.076178	-4.376784	28376.738510
HLA A*1101	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.442326	0.065526	-4.376801	27690.217026
HLA B*0802	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.467882	0.090830	-4.377052	29368.496114
HLA A*0212	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.442124	0.064686	-4.377438	27677.337136
HLA A*0216	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.441861	0.063696	-4.378165	27660.572307
HLA B*0801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.343150	-0.035101	-4.378251	22036.869443
HLA A*3002	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.470405	0.091985	-4.378420	29539.630247
HLA B*1509	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.443325	0.064686	-4.378638	27753.955699
HLA A*3002	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.555994	0.176828	-4.379166	35974.473287
HLA A*0202	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.501195	0.122021	-4.379174	31709.913389
HLA A*2603	1:67-75	9	ENYIAQTRD	1.094922	-0.841398	-4.632837	0.253524	-4.379312	42937.494670
HLA A*2402	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.556262	0.176828	-4.379434	35996.666571
HLA A*2902	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.420161	0.040514	-4.379647	26312.451829
HLA B*1509	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.473918	0.093374	-4.380543	29779.509141
HLA B*4403	1:60-68	9	YPDQKSLEN	1.087218	-0.808773	-4.659153	0.278445	-4.380708	45619.790024

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HLA B*0801	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.456896
	0.076178	-4.380717	28634.889801

HLA B*0803	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.472719
	0.091985	-4.380734	29697.459422

HLA A*0206	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.508711
	0.127871	-4.380840	32263.468778

HLA A*0203	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.444542
	0.063696	-4.380846	27831.840314

HLA B*1501	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.355682
	-0.025590	-4.381272	22682.036851

HLA B*4001	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.414948
	0.033425	-4.381523	25998.471210

HLA B*4402	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.424078
	0.042326	-4.381752	26550.818236

HLA A*0206	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.551418
	0.169649	-4.381769	35597.348243

HLA A*0219	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.424635
	0.042326	-4.382309	26584.882034

HLA A*0203	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.458754
	0.076178	-4.382576	28757.687412

HLA B*0802	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.481001
	0.098300	-4.382701	30269.220164

HLA B*5301	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.601262
	0.218305	-4.382957	39926.567150

HLA B*0702	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.446706
	0.063696	-4.383010	27970.858721

HLA A*2403	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.357736
	-0.025590	-4.383326	22789.536979

HLA B*4801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.416792
	0.033425	-4.383367	26109.115329

HLA A*2602	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.628629
	0.245175	-4.383454	42523.477467
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HLA A*3101	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.424099	0.040514	-4.383585	26552.111000
HLA B*4002	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.625687	0.241980	-4.383708	42236.431453
HLA B*0702	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.474620	0.090830	-4.383790	29827.718170
HLA B*0803	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.507073	0.123229	-4.383844	32142.042226
HLA A*2501	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.477670	0.093374	-4.384295	30037.906596
HLA B*0801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.449011	0.064686	-4.384324	28119.697502
HLA B*1509	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.506387	0.122021	-4.384367	32091.307922
HLA A*0216	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.349308	-0.035101	-4.384409	22351.563052
HLA B*1517	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.493031	0.108361	-4.384669	31119.355609
HLA A*2501	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.476742	0.091985	-4.384757	29973.786940
HLA B*4601	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.359845	-0.025590	-4.385436	22900.519746
HLA B*4403	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.628166	0.241980	-4.386186	42478.182290
HLA A*0203	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.351613	-0.035101	-4.386714	22470.500388
HLA B*3901	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.510039	0.123229	-4.386809	32362.235757
HLA A*0203	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.451508	0.064686	-4.386822	28281.871650
HLA B*5301	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.544975	0.157927	-4.387049	35073.197384

HLA A*0203	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.361502	-0.025590	-4.387092	22988.028456
HLA A*0216	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.429818	0.042326	-4.387492	26904.052480
HLA A*2603	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.629867	0.241980	-4.387887	42644.885379
HLA B*0802	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.451609	0.063696	-4.387913	28288.451492
HLA A*0212	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.430476	0.042326	-4.388149	26944.836785
HLA B*4801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.430595	0.042326	-4.388269	26952.272008
HLA B*5101	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.496980	0.108361	-4.388619	31403.646480
HLA B*5101	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.511977	0.123229	-4.388748	32506.996350
HLA B*0803	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.497269	0.108361	-4.388908	31424.549934
HLA B*3801	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.549630	0.160477	-4.389153	35451.097865
HLA A*2602	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.549632	0.160477	-4.389156	35451.289652
HLA A*2603	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.623657	0.234162	-4.389495	42039.472946
HLA B*7301	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.556044	0.166493	-4.389551	35978.560495
HLA A*3301	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.634824	0.245175	-4.389650	43134.459933
HLA B*5401	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.558407	0.168569	-4.389838	36174.902154
HLA A*0250	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.547999	0.157927	-4.390073	35318.247574

HLA B*5401	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.559951	0.169649	-4.390302	36303.707276
HLA B*0803	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.512383	0.122021	-4.390363	32537.434241
HLA A*1101	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.498787	0.108361	-4.390426	31534.564212
HLA B*5301	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.557047	0.166493	-4.390554	36061.767853
HLA A*0206	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.464964	0.073876	-4.391088	29171.828225
HLA A*3301	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.625269	0.234162	-4.391107	42195.779025
HLA B*1503	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.489410	0.098300	-4.391110	30861.003162
HLA A*6801	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.625358	0.234162	-4.391196	42204.454347
HLA A*2501	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.465175	0.073876	-4.391299	29186.035155
HLA B*2705	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.433779	0.042326	-4.391453	27150.568847
HLA B*2705	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.465762	0.073876	-4.391887	29225.535164
HLA B*2705	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.457809	0.065526	-4.392284	28695.213858
HLA A*0301	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.367061	-0.025590	-4.392651	23284.161750
HLA B*4001	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.435231	0.042326	-4.392905	27241.493566
HLA B*0702	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.426611	0.033425	-4.393186	26706.111288
HLA A*8001	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.458120	0.064686	-4.393433	28715.712582

HLA B*3801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.560057	0.166493	-4.393563	36312.546309
HLA A*3002	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.436462	0.042326	-4.394136	27318.826819
HLA B*4501	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.648181	0.253787	-4.394394	44481.680571
HLA A*2602	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.470821	0.076178	-4.394642	29567.929478
HLA B*4002	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.571694	0.176828	-4.394865	37298.700646
HLA A*2402	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.561391	0.166493	-4.394898	36424.299731
HLA B*5101	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.435980	0.040514	-4.395466	27288.546289
HLA B*3901	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.487587	0.092119	-4.395468	30731.717952
HLA A*3101	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.351305	-0.044895	-4.396200	22454.581287
HLA A*0101	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.390255	-0.005967	-4.396222	24561.490801
HLA B*7301	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.488616	0.092119	-4.396497	30804.624067
HLA B*3801	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.566407	0.169649	-4.396759	36847.443495
HLA A*0211	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.462574	0.065526	-4.397049	29011.769704
HLA B*5101	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.495728	0.098300	-4.397428	31313.225404
HLA A*0250	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.495815	0.098300	-4.397515	31319.493872
HLA B*1509	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.489824	0.091985	-4.397839	30890.401166

HLA B*0803	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.491217	0.093374	-4.397843	30989.658685
HLA A*0219	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.363179	-0.035101	-4.398280	23076.995126
HLA B*4001	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.363217	-0.035101	-4.398318	23078.992717
HLA A*0101	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.372777	-0.025590	-4.398367	23592.659759
HLA B*4002	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.632966	0.234162	-4.398804	42950.272361
HLA B*1509	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.432292	0.033425	-4.398867	27057.751830
HLA B*4501	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.617300	0.218305	-4.398994	41428.533108
HLA A*0301	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.354110	-0.044895	-4.399005	22600.094038
HLA B*3501	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.364279	-0.035101	-4.399380	23135.496138
HLA A*2603	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.463272	0.063696	-4.399576	29058.421458
HLA A*0201	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.393784	-0.005967	-4.399751	24761.882017
HLA B*3901	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.498084	0.098300	-4.399785	31483.596495
HLA B*2705	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.498503	0.098300	-4.400203	31513.928549
HLA B*1517	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.231439	-0.168791	-4.400230	17038.797256
HLA B*1503	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.463949	0.063696	-4.400253	29103.731164
HLA A*0211	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.522279	0.122021	-4.400259	33287.358570

HLA B*4403	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.634535	0.234162	-4.400374	43105.767105
HLA B*5801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.355694	-0.044895	-4.400588	22682.650396
HLA B*1502	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.492946	0.092119	-4.400827	31113.295518
HLA B*3801	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.569556	0.168569	-4.400987	37115.530419
HLA A*3101	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.395081	-0.005967	-4.401048	24835.937925
HLA B*3901	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.434606	0.033425	-4.401181	27202.320418
HLA B*3801	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.578049	0.176828	-4.401221	37848.533760
HLA A*0211	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.492274	0.090830	-4.401445	31065.193369
HLA A*6901	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.366393	-0.035101	-4.401494	23248.415233
HLA B*3901	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.498519	0.096880	-4.401639	31515.121980
HLA A*0201	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.366539	-0.035101	-4.401640	23256.214364
HLA A*0219	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.466848	0.064686	-4.402161	29298.671915
HLA B*5101	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.476091	0.073876	-4.402215	29928.903680
HLA A*2902	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.465972	0.063696	-4.402276	29239.610067
HLA A*3201	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.570930	0.168569	-4.402361	37233.179167
HLA B*1503	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.443088	0.040514	-4.402573	27738.795113

HLA B*5101	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.466402
0.063696	-4.402706	29268.571899

HLA B*4403	1:146-154	9	TLWQADTDP	0.196026	0.057761	-4.657107
0.253787	-4.403319	45405.334616

HLA B*4501	1:114-122	9	LKVYQNAGG	0.762278	-0.528116	-4.637580
0.234162	-4.403419	43409.052922

HLA A*3301	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.526064
0.122021	-4.404044	33578.736816

HLA B*3501	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.378585
-0.025590	-4.404175	23910.289336

HLA B*4002	1:75-83	9	DKFLSAATS	1.204544	-0.986239	-4.622670
0.218305	-4.404365	41944.061249

HLA A*6801	1:137-145	9	AYRKPITYD	0.853411	-0.611431	-4.646616
0.241980	-4.404637	44321.702064

HLA B*2705	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.496021
0.090830	-4.405192	31334.407700

HLA A*2402	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.565794
0.160477	-4.405318	36795.452316

HLA B*0803	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.503751
0.098300	-4.405452	31897.107018

HLA A*2301	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.479338
0.073876	-4.405462	30153.504700

HLA A*2501	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.471293
0.065526	-4.405768	29600.098769

HLA A*0212	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.370822	-
0.035101	-4.405923	23486.707169

HLA A*2402	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.479899
0.073876	-4.406024	30192.517296

HLA A*2402	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.504442
0.098300	-4.406142	31947.879970

HLA B*2705	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.503187
0.096880	-4.406308	31855.719537

HLA A*8001	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.439803	0.033425	-4.406378	27529.797236
HLA A*0201	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.380904	-0.025590	-4.406494	24038.301234
HLA B*4801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.361784	-0.044895	-4.406678	23002.956823
HLA B*3901	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.497607	0.090830	-4.406778	31449.039951
HLA A*6901	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.362005	-0.044895	-4.406899	23014.657482
HLA B*1517	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.447415	0.040514	-4.406901	28016.594484
HLA A*0211	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.530228	0.123229	-4.406998	33902.181296
HLA A*2601	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.401044	-0.005967	-4.407011	25179.294570
HLA B*1502	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.576675	0.169649	-4.407026	37728.940625
HLA B*3901	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.480961	0.073876	-4.407086	30266.436489
HLA B*0803	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.504071	0.096880	-4.407191	31920.583788
HLA A*2602	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.450329	0.042326	-4.408003	28205.168951
HLA A*3201	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.506413	0.098300	-4.408113	32093.217693
HLA B*4402	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.373054	-0.035101	-4.408155	23607.725340
HLA B*1509	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.499069	0.090830	-4.408239	31555.042678
HLA B*5101	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.484469	0.076178	-4.408291	30511.887336

HLA A*8001	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.450991	0.042326	-4.408665	28248.231279
HLA A*1101	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.473394	0.064686	-4.408707	29743.604646
HLA A*0202	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.578460	0.169649	-4.408812	37884.383092
HLA B*0702	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.451193	0.042326	-4.408867	28261.376839
HLA B*4601	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.373787	-0.035101	-4.408888	23647.606123
HLA A*0219	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.442538	0.033425	-4.409113	27703.702399
HLA B*1801	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.449767	0.040514	-4.409253	28168.724263
HLA B*4601	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.099485	-0.310145	-4.409630	12574.328708
HLA A*0206	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.099546	-0.310145	-4.409691	12576.097501
HLA A*0206	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.531978	0.122021	-4.409957	34039.095265
HLA B*1503	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.533679	0.123229	-4.410450	34172.679661
HLA B*0803	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.501618	0.090830	-4.410788	31740.806910
HLA B*4501	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.587957	0.176828	-4.411129	38721.915954
HLA A*2603	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.646863	0.235698	-4.411165	44346.885643
HLA A*0202	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.102440	-0.310145	-4.412585	12660.196931
HLA B*4402	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.453169	0.040514	-4.412655	28390.251047

HLA A*0250 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.506611 0.093374 -4.413236 32107.805151

HLA B*0802 1:213-221 9 PTQVLVPRS 1.263904 -1.221578 -4.455808 0.042326 -4.413482 28563.255491

HLA B*3901 1:86-94 9 PREAPYELN 0.811488 -0.746802 -4.478537 0.064686 -4.413850 30097.929630

HLA B*0802 1:217-225 9 LVPRSAIDS 0.966010 -0.900484 -4.479935 0.065526 -4.414409 30194.967468

HLA A*2301 1:157-165 9 VVFPIVQGE 0.697577 -0.605458 -4.506655 0.092119 -4.414537 32111.105614

HLA B*5101 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.508032 0.093374 -4.414658 32213.065613

HLA B*5101 1:171-179 9 GQQVSIAPN 0.716617 -0.624632 -4.507048 0.091985 -4.415063 32140.129549

HLA B*7301 1:194-202 9 NDGVIFFFN 0.826929 -0.753053 -4.489013 0.073876 -4.415137 30832.800728

HLA B*4002 1:156-164 9 PVVFPIVQG 0.934938 -0.699240 -4.651153 0.235698 -4.415455 44787.135385

HLA B*7301 1:175-183 9 SIAPNAGLD 0.851313 -0.682744 -4.584153 0.168569 -4.415584 38384.246689

HLA A*0216 1:201-209 9 FNPGELLPE 0.811387 -0.836977 -4.390074 -0.025590 -4.415664 24551.261561

HLA B*1517 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.479474 0.063696 -4.415778 30162.967557

HLA A*2403 1:38-46 9 GQACQIQMS 0.965607 -1.010502 -4.371012 -0.044895 -4.415907 23497.001323

HLA B*2705 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.492185 0.076178 -4.416006 31058.807773

HLA A*6802 1:201-209 9 FNPGELLPE 0.811387 -0.836977 -4.390466 -0.025590 -4.416056 24573.452458

HLA B*4001 1:201-209 9 FNPGELLPE 0.811387 -0.836977 -4.390640 -0.025590 -4.416230 24583.291962

HLA A*2301	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.544158	0.127871	-4.416286	35007.229247
HLA A*2603	1:187-195	9	YQNFAVTND	0.973541	-0.744146	-4.645961	0.229395	-4.416565	44254.855162
HLA B*4601	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.410827	-0.005967	-4.416794	25752.939892
HLA A*2301	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.540103	0.123229	-4.416873	34681.871713
HLA B*1801	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.510337	0.093374	-4.416963	32384.478063
HLA A*2602	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.583779	0.166493	-4.417286	38351.243816
HLA A*0211	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.493862	0.076178	-4.417684	31179.009414
HLA B*0702	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.411903	-0.005967	-4.417870	25816.827819
HLA A*2301	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.510234	0.091985	-4.418249	32376.770337
HLA B*5401	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.526757	0.108361	-4.418396	33632.368487
HLA B*0803	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.483553	0.064686	-4.418866	30447.579488
HLA A*2301	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.541031	0.122021	-4.419010	34756.062861
HLA B*5401	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.492904	0.073876	-4.419028	31110.265915
HLA B*4501	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.655892	0.235698	-4.420194	45278.517290
HLA A*2501	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.394975	-0.025590	-4.420565	24829.892476
HLA B*0802	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.497006	0.076178	-4.420828	31405.515328

HLA B*3901	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.497208	0.076178	-4.421030	31420.130158
HLA B*7301	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.519718	0.098300	-4.421419	33091.647965
HLA A*0206	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.485115	0.063696	-4.421419	30557.314249
HLA A*2402	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.591274	0.169649	-4.421626	39018.836118
HLA A*0201	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.297342	-0.124403	-4.421745	19830.880140
HLA B*5701	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.415906	-0.005967	-4.421874	26055.919317
HLA A*2402	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.518995	0.096880	-4.422115	33036.555056
HLA A*1101	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.464797	0.042326	-4.422471	29160.625415
HLA A*0206	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.397134	-0.025590	-4.422724	24953.646335
HLA B*3501	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.487476	0.064686	-4.422790	30723.904952
HLA A*2403	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.417102	-0.005967	-4.423070	26127.766647
HLA B*1801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.514011	0.090830	-4.423182	32659.647762
HLA B*3801	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.521509	0.098300	-4.423209	33228.344402
HLA A*2601	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.298890	-0.124403	-4.423293	19901.705722
HLA B*1517	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.497495	0.073876	-4.423619	31440.874492
HLA B*1801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.227607	-0.196092	-4.423699	16889.116260

HLA A*0101	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.388814	-0.035101	-4.423916	24480.173371
HLA A*2603	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.516786	0.092119	-4.424668	32868.980845
HLA A*2402	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.515708	0.090830	-4.424878	32787.463844
HLA A*0101	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.380413	-0.044895	-4.425307	24011.137284
HLA B*0802	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.490007	0.064686	-4.425320	30903.438781
HLA A*0250	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.594977	0.169649	-4.425328	39352.932367
HLA B*5401	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.516178	0.090830	-4.425348	32822.958351
HLA B*5401	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.549031	0.123229	-4.425801	35402.226022
HLA A*3002	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.502057	0.076178	-4.425879	31772.933722
HLA B*2705	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.489692	0.063696	-4.425996	30881.044219
HLA A*2501	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.468582	0.042326	-4.426256	29415.880631
HLA B*4801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.391270	-0.035101	-4.426371	24618.959905
HLA A*3002	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.596272	0.169649	-4.426623	39470.412521
HLA A*0206	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.549874	0.123229	-4.426645	35471.049274
HLA B*4501	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.585015	0.157927	-4.427089	38460.531601
HLA A*0212	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.401948	-0.025590	-4.427538	25231.792842

HLA A*0202	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.401965	-0.025590	-4.427555	25232.748369
HLA B*1801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.421905	-0.005967	-4.427872	26418.285909
HLA A*1101	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.461667	0.033425	-4.428243	28951.250038
HLA B*4801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.402709	-0.025590	-4.428300	25276.058015
HLA B*1502	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.594848	0.166493	-4.428355	39341.224884
HLA B*3801	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.550379	0.122021	-4.428359	35512.330582
HLA A*1101	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.492150	0.063696	-4.428454	31056.287505
HLA B*0801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.422567	-0.005967	-4.428535	26458.620107
HLA B*0803	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.494231	0.065526	-4.428706	31205.502636
HLA B*3901	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.494304	0.065526	-4.428778	31210.736442
HLA A*2601	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.383909	-0.044895	-4.428803	24205.204965
HLA B*0803	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.492608	0.063696	-4.428912	31089.066951
HLA A*2301	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.537617	0.108361	-4.429256	34483.931389
HLA B*5401	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.521544	0.092119	-4.429425	33231.040936
HLA A*2601	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.394597	-0.035101	-4.429698	24808.275250
HLA A*0250	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.557576	0.127871	-4.429704	36105.689867

HLA A*6801	1:29-37	9	CEELKGTDT	0.714161	-0.468986	-4.674892	0.245175	-4.429718	47303.413575
HLA A*6802	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.233859	-0.196092	-4.429951	17134.005614
HLA A*2602	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.598666	0.168569	-4.430097	39688.601007
HLA B*1502	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.606988	0.176828	-4.430159	40456.440234
HLA A*2602	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.522747	0.092119	-4.430628	33323.213970
HLA A*0211	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.473203	0.042326	-4.430877	29730.573823
HLA A*3301	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.597374	0.166493	-4.430880	39570.685506
HLA B*1509	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.529685	0.098300	-4.431385	33859.840731
HLA A*0202	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.554792	0.123229	-4.431562	35874.966789
HLA B*5301	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.601220	0.169649	-4.431571	39922.679370
HLA A*0219	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.425685	-0.005967	-4.431652	26649.247933
HLA A*3201	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.608482	0.176828	-4.431654	40595.878026
HLA A*2402	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.554883	0.123229	-4.431654	35882.536691
HLA B*1801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.396739	-0.035101	-4.431840	24930.977233
HLA B*5301	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.554155	0.122021	-4.432134	35822.409755
HLA A*2301	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.525745	0.093374	-4.432371	33554.040517

HLA B*3901	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.473241	0.040514	-4.432726	29733.147360
HLA A*2402	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.524915	0.092119	-4.432797	33490.023818
HLA B*3501	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.475264	0.042326	-4.432938	29871.964869
HLA B*1517	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.497767	0.064686	-4.433081	31460.611315
HLA B*5401	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.561224	0.127871	-4.433353	36410.311766
HLA A*0216	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.498345	0.064686	-4.433659	31502.507999
HLA A*0202	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.533266	0.098300	-4.434966	34140.157954
HLA B*5701	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.399935	-0.035101	-4.435036	25115.082073
HLA B*0802	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.475612	0.040514	-4.435097	29895.891841
HLA A*8001	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.409934	-0.025590	-4.435524	25700.052463
HLA B*2705	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.410164	-0.025590	-4.435755	25713.681450
HLA B*7301	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.612824	0.176828	-4.435995	41003.769854
HLA B*5301	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.605009	0.168569	-4.436440	40272.575107
HLA B*0802	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.469888	0.033425	-4.436463	29504.493813
HLA A*2402	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.530122	0.093374	-4.436748	33893.928984
HLA B*3801	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.529137	0.092119	-4.437019	33817.187149

HLA B*4403	1:156-164	9	PVVFPIVQG	0.934938	-0.699240	-4.673527	0.235698	-4.437829	47154.965478
HLA A*0203	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.431944	-0.005967	-4.437911	27036.096343
HLA A*3002	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.478468	0.040514	-4.437954	30093.208033
HLA B*1801	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.536376	0.098300	-4.438076	34385.571293
HLA A*0202	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.566353	0.127871	-4.438482	36842.858947
HLA B*5701	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.413268	-0.025590	-4.438858	25898.101528
HLA A*2603	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.599446	0.160477	-4.438969	39759.949090
HLA A*2602	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.566959	0.127871	-4.439088	36894.318323
HLA B*4001	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.394214	-0.044895	-4.439108	24786.408659
HLA B*2705	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.404081	-0.035101	-4.439183	25356.040848
HLA B*3801	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.532582	0.093374	-4.439208	34086.454147
HLA B*0801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.394378	-0.044895	-4.439273	24795.796857
HLA B*1509	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.563041	0.123229	-4.439811	36562.892834
HLA A*2402	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.568130	0.127871	-4.440258	36993.850236
HLA B*5101	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.505170	0.064686	-4.440484	32001.503614
HLA B*0803	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.514730	0.073876	-4.440855	32713.758170

HLA B*7301	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.562900	0.122021	-4.440879	36551.026688
HLA A*3001	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.272280	-0.168791	-4.441071	18718.887452
HLA B*5401	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.481661	0.040514	-4.441147	30315.269785
HLA A*2301	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.406147	-0.035101	-4.441248	25476.903381
HLA B*0702	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.406203	-0.035101	-4.441304	25480.211449
HLA B*4601	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.396525	-0.044895	-4.441420	24918.706736
HLA A*0250	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.532286	0.090830	-4.441456	34063.227168
HLA B*1503	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.515499	0.073876	-4.441623	32771.681131
HLA B*1517	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.475327	0.033425	-4.441902	29876.328496
HLA B*5401	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.507908	0.065526	-4.442382	32203.830674
HLA B*7301	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.612272	0.169649	-4.442623	40951.673902
HLA B*5301	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.603167	0.160477	-4.442691	40102.126618
HLA A*6802	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.437644	-0.005967	-4.443611	27393.267343
HLA B*1503	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.319657	-0.124403	-4.444060	20876.485980
HLA A*2301	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.534957	0.090830	-4.444128	34273.397295
HLA B*0803	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.477594	0.033425	-4.444170	30032.706990

HLA A*2301	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.542473	0.098300	-4.444173	34871.703053
HLA A*6901	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.248475	-0.196092	-4.444567	17720.462433
HLA B*1503	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.553062	0.108361	-4.444701	35732.408208
HLA B*2705	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.478377	0.033425	-4.444952	30086.859467
HLA A*3201	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.614889	0.169649	-4.445240	41199.219117
HLA A*2402	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.410148	-0.035101	-4.445249	25712.707711
HLA A*3201	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.612121	0.166493	-4.445628	40937.497539
HLA A*0202	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.554110	0.108361	-4.445749	35818.727834
HLA A*0216	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.479335	0.033425	-4.445911	30153.341573
HLA B*5101	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.479998	0.033425	-4.446573	30199.378279
HLA B*4403	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.623638	0.176828	-4.446810	42037.653555
HLA A*8001	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.442152	-0.005967	-4.448120	27679.133971
HLA A*2402	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.570261	0.122021	-4.448240	37175.816599
HLA B*3501	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.442322	-0.005967	-4.448289	27689.917426
HLA A*2602	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.513828	0.065526	-4.448303	32645.869233
HLA B*1502	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.541785	0.093374	-4.448411	34816.471788

HLA A*3002	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.522326	0.073876	-4.448451	33290.960383
HLA A*3301	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.617142	0.168569	-4.448573	41413.519537
HLA A*2501	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.482016	0.033425	-4.448591	30340.044243
HLA B*3801	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.571917	0.123229	-4.448688	37317.874847
HLA B*5101	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.491395	0.042326	-4.449069	31002.402752
HLA A*0206	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.482573	0.033425	-4.449148	30378.969489
HLA A*1101	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.490272	0.040514	-4.449758	30922.336369
HLA A*0211	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.414748	-0.035101	-4.449849	25986.518807
HLA A*0216	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.444274	-0.005967	-4.450241	27814.680948
HLA A*0250	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.572782	0.122021	-4.450761	37392.242738
HLA A*0206	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.559317	0.108361	-4.450955	36250.718247
HLA A*2603	1:10-18	9	TAVVLLCCS	1.085894	-0.909066	-4.628142	0.176828	-4.451314	42475.884330
HLA B*1509	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.560080	0.108361	-4.451719	36314.510830
HLA A*1101	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.528078	0.076178	-4.451899	33734.778520
HLA B*1509	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.526140	0.073876	-4.452264	33584.550351
HLA A*6802	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.236622	-0.215742	-4.452364	17243.360155

HLA A*2301	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.517082	0.064686	-4.452396	32891.393493
HLA A*1101	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.256491	-0.196092	-4.452584	18050.593828
HLA B*5401	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.256689	-0.196092	-4.452781	18058.798435
HLA A*3002	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.543648	0.090830	-4.452818	34966.156765
HLA B*1801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.518750	0.065526	-4.453225	33017.972977
HLA B*5401	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.547019	0.093374	-4.453645	35238.662103
HLA B*2705	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.143669	-0.310145	-4.453814	13920.961234
HLA A*3101	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.428861	-0.025590	-4.454452	26844.879636
HLA B*1503	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.530841	0.076178	-4.454662	33950.084346
HLA B*5401	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.546810	0.091985	-4.454825	35221.699471
HLA B*1502	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.488947	0.033425	-4.455522	30828.130625
HLA B*5701	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.410683	-0.044895	-4.455578	25744.442740
HLA B*4403	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.622539	0.166493	-4.456046	41931.356062
HLA A*2602	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.625741	0.169649	-4.456093	42241.687152
HLA A*3002	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.564812	0.108361	-4.456451	36712.339530
HLA A*0301	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.332072	-0.124403	-4.456475	21481.869646

HLA A*2501	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.521180	0.064686	-4.456493	33203.187298
HLA A*0219	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.412220	-0.044895	-4.457115	25835.689640
HLA A*6802	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.412432	-0.044895	-4.457326	25848.271842
HLA B*1509	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.533646	0.076178	-4.457468	34170.091573
HLA B*4002	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.615528	0.157927	-4.457601	41259.887975
HLA A*0211	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.532382	0.073876	-4.458506	34070.783415
HLA A*3201	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.522355	0.063696	-4.458659	33293.121658
HLA B*1502	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.414302	-0.044895	-4.459196	25959.821535
HLA B*0803	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.500002	0.040514	-4.459487	31622.887093
HLA B*3801	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.552073	0.091985	-4.460088	35651.117992
HLA A*0250	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.568684	0.108361	-4.460323	37041.111700
HLA A*0250	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.583641	0.123229	-4.460412	38339.004687
HLA B*3901	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.502804	0.042326	-4.460478	31827.641166
HLA B*3801	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.568985	0.108361	-4.460624	37066.770286
HLA A*0211	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.524396	0.063696	-4.460700	33450.007557
HLA A*6801	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.627510	0.166493	-4.461017	42414.115822

HLA A*0202	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.552261	0.090830	-4.461432	35666.550819
HLA A*3201	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.589493	0.127871	-4.461622	38859.159351
HLA B*4002	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.622184	0.160477	-4.461708	41897.116606
HLA A*2902	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.417135	-0.044895	-4.462030	26129.745598
HLA B*4002	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.555602	0.093374	-4.462228	35941.986772
HLA B*1503	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.504675	0.042326	-4.462349	31964.995167
HLA B*5401	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.560684	0.098300	-4.462384	36365.035517
HLA B*0803	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.538632	0.076178	-4.462453	34564.617071
HLA B*0702	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.437533	-0.025590	-4.463124	27386.303086
HLA B*0803	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.505734	0.042326	-4.463408	32043.080501
HLA B*5301	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.537379	0.073876	-4.463504	34465.094557
HLA A*6802	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.428720	-0.035101	-4.463822	26836.167381
HLA A*0219	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.438384	-0.025590	-4.463974	27439.988421
HLA B*3901	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.458507	-0.005967	-4.464475	28741.356581
HLA A*8001	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.429425	-0.035101	-4.464526	26879.756950
HLA A*2402	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.530860	0.065526	-4.465334	33951.553707

HLA B*5401	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.529067	0.063696	-4.465371	33811.699177
HLA B*7301	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.589089	0.123229	-4.465860	38823.017685
HLA B*4402	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.440296	-0.025590	-4.465887	27561.090971
HLA A*6801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.531621	0.065526	-4.466095	34011.116315
HLA A*1101	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.460589	-0.005967	-4.466556	28879.449239
HLA A*2603	1:43-51	9	IQMSDPAYN	0.678035	-0.520108	-4.624496	0.157927	-4.466569	42120.743514
HLA B*1501	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.270581	-0.196092	-4.466674	18645.814335
HLA B*3801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.557853	0.090830	-4.467023	36128.745903
HLA B*5301	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.557900	0.090830	-4.467070	36132.655165
HLA A*2902	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.461200	-0.005967	-4.467167	28920.098821
HLA A*2603	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.500706	0.033425	-4.467282	31674.251657
HLA B*1801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.532467	0.064686	-4.467780	34077.419551
HLA A*2402	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.576426	0.108361	-4.468064	37707.311233
HLA A*2402	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.560057	0.091985	-4.468072	36312.546309
HLA A*0202	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.534083	0.065526	-4.468558	34204.492169
HLA B*3501	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.423681	-0.044895	-4.468575	26526.554679

HLA B*5401	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.443482	-0.025590	-4.469073	27764.017293
HLA A*2301	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.545300	0.076178	-4.469121	35099.391572
HLA B*1502	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.532880	0.063696	-4.469184	34109.881494
HLA A*0206	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.545495	0.076178	-4.469316	35115.155468
HLA B*5401	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.545880	0.076178	-4.469701	35146.324225
HLA B*1517	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.463836	-0.005967	-4.469803	29096.174643
HLA A*6801	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.560954	0.090830	-4.470125	36387.666600
HLA B*5301	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.593405	0.123229	-4.470176	39210.763037
HLA B*1517	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.435581	-0.035101	-4.470682	27263.461064
HLA B*3801	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.567660	0.096880	-4.470780	36953.845356
HLA A*3301	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.640482	0.169649	-4.470833	43700.049076
HLA A*0101	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.346489	-0.124403	-4.470891	22206.929657
HLA A*2602	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.592980	0.122021	-4.470959	39172.387044
HLA A*2603	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.547729	0.076178	-4.471551	35296.281610
HLA B*4002	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.599775	0.127871	-4.471903	39790.074065
HLA B*1801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.514324	0.042326	-4.471998	32683.155333

HLA B*5801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.347720	-0.124403	-4.472123	22269.970771
HLA B*4501	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.633229	0.160477	-4.472753	42976.304142
HLA B*7301	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.466839	-0.005967	-4.472806	29298.037911
HLA A*2301	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.536665	0.063696	-4.472969	34408.459629
HLA A*2301	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.538655	0.065526	-4.473130	34566.487029
HLA B*3501	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.277172	-0.196092	-4.473264	18930.917413
HLA B*3801	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.539130	0.065526	-4.473604	34604.281850
HLA A*2603	1:144-152	9	YDTLWQADT	0.627145	-0.460652	-4.640247	0.166493	-4.473754	43676.414228
HLA B*1502	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.595809	0.122021	-4.473788	39428.369409
HLA A*0250	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.571012	0.096880	-4.474133	37240.229792
HLA B*1502	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.582631	0.108361	-4.474269	38249.922142
HLA B*5301	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.602399	0.127871	-4.474528	40031.247315
HLA B*3801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.539818	0.064686	-4.475132	34659.176507
HLA B*1502	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.572112	0.096880	-4.475232	37334.635112
HLA A*2603	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.573540	0.098300	-4.475241	37457.638846
HLA A*0206	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.469322	-0.005967	-4.475289	29466.051413

HLA B*4403	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.567629	0.091985	-4.475644	36951.246537
HLA B*4501	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.645660	0.169649	-4.476012	44224.220795
HLA A*2603	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.599885	0.123229	-4.476656	39800.192567
HLA A*2603	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.647197	0.169649	-4.477548	44380.966198
HLA A*3201	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.586401	0.108361	-4.478040	38583.487379
HLA B*1801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.511486	0.033425	-4.478061	32470.262539
HLA A*0250	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.570091	0.091985	-4.478106	37161.338991
HLA B*1503	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.472698	-0.005967	-4.478665	29696.013518
HLA A*1101	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.443628	-0.035101	-4.478729	27773.331271
HLA B*5301	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.587668	0.108361	-4.479307	38696.158328
HLA A*0211	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.512893	0.033425	-4.479468	32575.653860
HLA B*3501	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.355207	-0.124403	-4.479610	22657.263514
HLA B*2705	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.474545	-0.005967	-4.480512	29822.554948
HLA B*4002	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.650493	0.169649	-4.480844	44719.102653
HLA A*2602	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.574238	0.093374	-4.480864	37517.871799
HLA A*2402	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.557207	0.076178	-4.481028	36075.036425

HLA B*5401	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.514902	0.033425	-4.481477	32726.680101
HLA B*5301	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.574903	0.093374	-4.481529	37575.355602
HLA B*4501	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.650629	0.168569	-4.482060	44733.136528
HLA B*4002	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.651275	0.168569	-4.482706	44799.736416
HLA A*3301	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.591476	0.108361	-4.483115	39036.993874
HLA A*0211	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.547980	0.064686	-4.483294	35316.719065
HLA A*2402	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.526039	0.042326	-4.483712	33576.738646
HLA B*4403	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.581355	0.096880	-4.484475	38137.725200
HLA A*2301	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.527500	0.042326	-4.485174	33689.913034
HLA A*2603	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.607815	0.122021	-4.485794	40533.554063
HLA A*6801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.519267	0.033425	-4.485843	33057.293558
HLA A*3201	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.609429	0.123229	-4.486200	40684.481114
HLA B*4001	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.362216	-0.124403	-4.486619	23025.865817
HLA B*4403	1:197-205	9	VIFFFNPGE	0.720374	-0.559897	-4.647305	0.160477	-4.486828	44392.011993
HLA B*4501	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.609048	0.122021	-4.487028	40648.840772
HLA A*6801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.363153	-0.124403	-4.487556	23075.621883

HLA A*0203	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.177553	-0.310145	-4.487698	15050.589019
HLA B*4501	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.584898	0.096880	-4.488018	38450.129648
HLA A*1101	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.462680	-0.025590	-4.488270	29018.833334
HLA B*3901	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.453169	-0.035101	-4.488270	28390.251047
HLA B*1801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.462988	-0.025590	-4.488578	29039.406139
HLA A*3201	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.582024	0.093374	-4.488650	38196.572000
HLA A*2902	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.292688	-0.196092	-4.488780	19619.487557
HLA A*3002	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.364434	-0.124403	-4.488837	23143.758203
HLA B*4403	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.657776	0.168569	-4.489207	45475.395393
HLA A*2501	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.483529	-0.005967	-4.489497	30445.932353
HLA A*2603	1:175-183	9	SIAPNAGLD	0.851313	-0.682744	-4.658460	0.168569	-4.489891	45547.042677
HLA B*1517	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.445369	-0.044895	-4.490264	27884.890453
HLA B*5401	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.555017	0.064686	-4.490331	35893.603269
HLA B*5301	1:127-135	9	TTYKAFDWD	0.819008	-0.722128	-4.587611	0.096880	-4.490732	38691.134448
HLA B*0802	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.484887	-0.005967	-4.490855	30541.283223
HLA B*4403	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.612998	0.122021	-4.490977	41020.188253

HLA A*3201	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.556688	0.065526	-4.491162	36031.931408
HLA A*2301	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.524819	0.033425	-4.491394	33482.596372
HLA A*3002	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.556986	0.065526	-4.491460	36056.695866
HLA A*8001	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.446880	-0.044895	-4.491774	27982.058586
HLA A*3201	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.584148	0.091985	-4.492163	38383.831382
HLA A*2403	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.368562	-0.124403	-4.492965	23364.792501
HLA B*3901	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.448172	-0.044895	-4.493067	28065.441484
HLA A*1101	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.448520	-0.044895	-4.493414	28087.921460
HLA B*3901	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.467943	-0.025590	-4.493533	29372.627293
HLA B*3801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.558729	0.063696	-4.495033	36201.723295
HLA A*2501	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.370848	-0.124403	-4.495251	23488.104876
HLA A*2602	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.559138	0.063696	-4.495442	36235.816771
HLA A*0206	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.560482	0.064686	-4.495795	36348.120603
HLA B*4601	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.371691	-0.124403	-4.496094	23533.766630
HLA B*4501	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.451259	-0.044895	-4.496154	28265.658109
HLA A*2603	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.562051	0.065526	-4.496526	36479.713289

HLA B*7301	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.605028	0.108361	-4.496667	40274.318106
HLA A*3002	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.530557	0.033425	-4.497132	33927.868009
HLA B*3801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.539778	0.042326	-4.497452	34655.989114
HLA A*3201	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.588455	0.090830	-4.497625	38766.351460
HLA B*1502	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.563454	0.065526	-4.497928	36597.722423
HLA B*3801	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.572384	0.073876	-4.498509	37358.071708
HLA A*3201	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.541019	0.042326	-4.498693	34755.122742
HLA A*2402	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.539635	0.040514	-4.499120	34644.554412
HLA B*5301	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.591310	0.092119	-4.499191	39022.002561
HLA B*1517	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.473704	-0.025590	-4.499294	29764.852299
HLA B*4403	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.669155	0.169649	-4.499506	46682.600372
HLA A*2501	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.454866	-0.044895	-4.499760	28501.358512
HLA A*3301	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.591751	0.091985	-4.499766	39061.710435
HLA B*5701	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.375545	-0.124403	-4.499947	23743.492333
HLA B*5101	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.474409	-0.025590	-4.499999	29813.198886
HLA B*1509	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.566144	0.065526	-4.500619	36825.124112

HLA A*0212	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.305330	-0.196092	-4.501423	20199.017182
HLA B*5301	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.599824	0.098300	-4.501524	39794.594780
HLA A*6801	1:163-171	9	QGELSKQTG	0.927669	-0.758020	-4.671263	0.169649	-4.501614	46909.686193
HLA B*1502	1:125-133	9	PTTTYKAFD	1.155703	-1.032474	-4.625135	0.123229	-4.501906	42182.769385
HLA B*0803	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.457464	-0.044895	-4.502359	28672.402954
HLA A*3301	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.600769	0.098300	-4.502469	39881.233263
HLA B*0702	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.458127	-0.044895	-4.503021	28716.178632
HLA B*2705	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.378672	-0.124403	-4.503075	23915.075840
HLA B*0803	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.497525	-0.005967	-4.503492	31443.085762
HLA B*1502	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.468981	-0.035101	-4.504082	29442.946306
HLA A*2402	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.568947	0.064686	-4.504261	37063.561991
HLA B*5401	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.546669	0.042326	-4.504343	35210.268597
HLA A*0202	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.546709	0.042326	-4.504383	35213.506968
HLA A*2301	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.545403	0.040514	-4.504888	35107.747455
HLA A*0206	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.547365	0.042326	-4.505039	35266.696925
HLA B*4403	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.634986	0.127871	-4.507115	43150.564271

HLA B*1502	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.605632	0.098300	-4.507332	40330.352106
HLA A*2602	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.598269	0.090830	-4.507439	39652.331442
HLA B*1509	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.549785	0.042326	-4.507459	35463.758034
HLA B*4801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.383505	-0.124403	-4.507908	24182.692475
HLA B*3801	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.584618	0.076178	-4.508440	38425.384312
HLA B*0802	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.473417	-0.035101	-4.508518	29745.213785
HLA B*5301	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.585168	0.076178	-4.508990	38474.058348
HLA B*0803	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.473950	-0.035101	-4.509052	29781.764680
HLA B*5301	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.573024	0.063696	-4.509328	37413.084197
HLA B*5801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.340826	-0.168791	-4.509617	21919.278668
HLA A*0211	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.484107	-0.025590	-4.509698	30486.477770
HLA A*2602	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.618658	0.108361	-4.510296	41558.279395
HLA A*3301	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.638393	0.127871	-4.510522	43490.383021
HLA A*2602	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.386599	-0.124403	-4.511002	24355.605157
HLA A*0211	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.505041	-0.005967	-4.511008	31991.983179
HLA B*4002	1:39-47	9	QACQIQMSD	0.891798	-0.769777	-4.633177	0.122021	-4.511157	42971.189512

HLA A*0202	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.587830	0.076178	-4.511652	38710.605617
HLA B*5101	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.506792	-0.005967	-4.512759	32121.182811
HLA B*5301	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.604974	0.091985	-4.512989	40269.307187
HLA A*0216	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.388728	-0.124403	-4.513130	24475.273765
HLA B*1503	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.487646	-0.025590	-4.513236	30735.874613
HLA A*2501	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.478440	-0.035101	-4.513541	30091.254485
HLA A*3201	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.317562	-0.196092	-4.513654	20775.986649
HLA B*1502	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.604702	0.090830	-4.513872	40244.044226
HLA A*3201	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.554439	0.040514	-4.513925	35845.866658
HLA A*0250	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.590226	0.076178	-4.514048	38924.804544
HLA B*0801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.204305	-0.310145	-4.514450	16006.807903
HLA A*0250	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.557284	0.042326	-4.514958	36081.477344
HLA A*0202	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.579008	0.063696	-4.515312	37932.166624
HLA B*0702	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.391058	-0.124403	-4.515461	24606.976097
HLA A*2602	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.607852	0.091985	-4.515867	40537.062728
HLA A*2402	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.579936	0.063696	-4.516240	38013.310774

HLA B*7301	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.582374	0.065526	-4.516849	38227.373657
HLA A*3001	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.302997	-0.215742	-4.518739	20090.798596
HLA B*0802	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.493397	-0.025590	-4.518987	31145.629648
HLA B*5301	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.585560	0.065526	-4.520035	38508.833500
HLA B*5101	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.485639	-0.035101	-4.520740	30594.201000
HLA A*2603	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.561293	0.040514	-4.520778	36416.024511
HLA B*7301	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.611994	0.090830	-4.521165	40925.540051
HLA A*0250	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.595236	0.073876	-4.521360	39376.357787
HLA B*1509	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.516180	-0.005967	-4.522147	32823.135920
HLA B*3801	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.555745	0.033425	-4.522321	35953.849702
HLA A*3001	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.212335	-0.310145	-4.522480	16305.543251
HLA A*2603	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.650458	0.127871	-4.522586	44715.473920
HLA A*0211	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.398711	-0.124403	-4.523113	25044.393568
HLA A*0202	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.587865	0.064686	-4.523179	38713.747046
HLA B*3901	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.213092	-0.310145	-4.523237	16333.972005
HLA A*3301	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.616837	0.093374	-4.523462	41384.404245

HLA A*0101 1:57-65 9 PSYYPDQKS 0.896699 -1.065490 -4.356192 -0.168791 -4.524983 22708.679972

HLA A*2603 1:28-36 9 YCEELKGTD 0.955740 -0.847379 -4.634159 0.108361 -4.525798 43068.471661

HLA B*5401 1:204-212 9 GELLPEAAG 0.791497 -0.797464 -4.520045 -0.005967 -4.526012 33116.541402

HLA B*4403 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.649342 0.123229 -4.526113 44600.716195

HLA B*4002 1:127-135 9 TTYKAFDWD 0.819008 -0.722128 -4.623404 0.096880 -4.526524 42014.917801

HLA B*7301 1:213-221 9 PTQVLVPRS 1.263904 -1.221578 -4.569163 0.042326 -4.526837 37082.013481

HLA A*6801 1:71-79 9 AQTRDKFLS 0.986232 -0.892858 -4.620727 0.093374 -4.527353 41756.823590

HLA B*4002 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.650763 0.123229 -4.527534 44746.932729

HLA A*6901 1:50-58 9 YNINISLPS 0.643875 -0.954020 -4.217514 -0.310145 -4.527659 16501.124373

HLA A*3002 1:30-38 9 EELKGTDTG 0.811906 -0.748210 -4.591897 0.063696 -4.528201 39074.814443

HLA A*0301 1:57-65 9 PSYYPDQKS 0.896699 -1.065490 -4.359594 -0.168791 -4.528385 22887.267430

HLA B*4501 1:125-133 9 PTTTYKAFD 1.155703 -1.032474 -4.651978 0.123229 -4.528749 44872.261178

HLA B*1502 1:145-153 9 DTLWQADTD 1.026181 -0.950003 -4.604948 0.076178 -4.528770 40266.910881

HLA B*4403 1:157-165 9 VVFPIVQGE 0.697577 -0.605458 -4.621430 0.092119 -4.529311 41824.422283

HLA B*0802 1:38-46 9 GQACQIQMS 0.965607 -1.010502 -4.484603 -0.044895 -4.529498 30521.297545

HLA A*3301 1:23-31 9 AAPKTYCEE 0.685714 -0.594884 -4.620337 0.090830 -4.529508 41719.341058

HLA A*0250	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.595177	0.064686	-4.530490	39371.032603
HLA A*8001	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.406177	-0.124403	-4.530580	25478.695198
HLA B*5101	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.486182	-0.044895	-4.531076	30632.457995
HLA A*6901	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.315941	-0.215742	-4.531682	20698.578124
HLA B*4403	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.607972	0.076178	-4.531794	40548.248622
HLA A*2902	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.317228	-0.215742	-4.532970	20760.032576
HLA A*0250	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.596723	0.063696	-4.533027	39511.431688
HLA B*4002	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.624014	0.090830	-4.533185	42074.056354
HLA A*0301	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.337647	-0.196092	-4.533740	21759.424500
HLA A*6901	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.365148	-0.168791	-4.533939	23181.851890
HLA B*1509	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.489537	-0.044895	-4.534432	30870.020028
HLA B*1509	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.575147	0.040514	-4.534633	37596.502515
HLA B*4801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.338778	-0.196092	-4.534870	21816.119665
HLA A*0206	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.339001	-0.196092	-4.535093	21827.334711
HLA B*1509	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.509773	-0.025590	-4.535363	32342.458203
HLA B*4002	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.627703	0.092119	-4.535584	42432.935361

HLA B*3801	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.576339	0.040514	-4.535824	37699.764270
HLA A*2602	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.577429	0.040514	-4.536914	37794.516661
HLA B*0803	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.511657	-0.025590	-4.537248	32483.088289
HLA B*5301	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.602127	0.064686	-4.537440	40006.133701
HLA A*6801	1:167-175	9	SKQTGQQVS	1.053333	-0.925462	-4.666455	0.127871	-4.538584	46393.323073
HLA A*3201	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.612680	0.073876	-4.538805	40990.240710
HLA B*7301	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.579734	0.040514	-4.539219	37995.629177
HLA B*4501	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.630283	0.090830	-4.539453	42685.739562
HLA B*1501	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.370827	-0.168791	-4.539618	23486.961291
HLA A*3002	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.605585	0.064686	-4.540899	40325.988688
HLA B*4403	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.639552	0.098300	-4.541252	43606.529967
HLA B*1502	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.615147	0.073876	-4.541272	41223.743566
HLA B*4002	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.650399	0.108361	-4.542038	44709.426685
HLA A*3002	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.498622	-0.044895	-4.543517	31522.624578
HLA A*3301	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.586228	0.042326	-4.543902	38568.044274
HLA B*4002	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.643231	0.098300	-4.544931	43977.528846

HLA B*4002	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.234841	-0.310145	-4.544986	17172.795159
HLA B*1502	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.610841	0.064686	-4.546154	40816.975608
HLA B*4403	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.501289	-0.044895	-4.546184	31716.776017
HLA A*2402	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.579994	0.033425	-4.546570	38018.452317
HLA A*3301	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.612342	0.065526	-4.546817	40958.320762
HLA B*4501	1:84-92	9	STPREAPYE	0.746095	-0.647795	-4.645517	0.098300	-4.547217	44209.629067
HLA B*4002	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.502887	-0.044895	-4.547781	31833.668177
HLA A*6802	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.379539	-0.168791	-4.548329	23962.863971
HLA B*5301	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.593314	0.042326	-4.550988	39202.491000
HLA A*2603	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.625022	0.073876	-4.551147	42171.817010
HLA A*2402	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.355099	-0.196092	-4.551192	22651.625845
HLA B*4501	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.659574	0.108361	-4.551213	45663.988264
HLA B*1517	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.427311	-0.124403	-4.551714	26749.200187
HLA B*5301	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.592679	0.040514	-4.552165	39145.270895
HLA A*6801	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.644281	0.091985	-4.552296	44084.004895
HLA A*6801	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.661002	0.108361	-4.552641	45814.434118

HLA B*1801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.507947	-0.044895	-4.552842	32206.792535
HLA B*4501	1:157-165	9	VVFPIVQGE	0.697577	-0.605458	-4.645284	0.092119	-4.553166	44185.957657
HLA A*2301	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.547825	-0.005967	-4.553793	35304.111386
HLA B*0801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.338634	-0.215742	-4.554376	21808.921462
HLA A*2301	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.528799	-0.025590	-4.554389	33790.853006
HLA B*4601	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.358501	-0.196092	-4.554594	22829.764613
HLA A*2902	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.386261	-0.168791	-4.555051	24336.638944
HLA A*2603	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.648980	0.090830	-4.558150	44563.573790
HLA A*2402	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.532892	-0.025590	-4.558482	34110.804160
HLA B*5301	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.591998	0.033425	-4.558573	39083.905288
HLA A*0201	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.390008	-0.168791	-4.558799	24547.542894
HLA B*5701	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.390546	-0.168791	-4.559337	24577.972822
HLA A*3301	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.623046	0.063696	-4.559351	41980.383002
HLA A*3101	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.390906	-0.168791	-4.559696	24598.324752
HLA A*0201	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.364201	-0.196092	-4.560294	23131.366211
HLA B*4403	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.593734	0.033425	-4.560309	39240.471909

HLA A*0250	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.593842	0.033425	-4.560418	39250.238308
HLA A*2602	1:194-202	9	NDGVIFFFN	0.826929	-0.753053	-4.634298	0.073876	-4.560422	43082.220599
HLA A*8001	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.250622	-0.310145	-4.560767	17808.300702
HLA A*2602	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.625605	0.064686	-4.560919	42228.434906
HLA A*2603	1:171-179	9	GQQVSIAPN	0.716617	-0.624632	-4.653865	0.091985	-4.561880	45067.616625
HLA A*2603	1:71-79	9	AQTRDKFLS	0.986232	-0.892858	-4.655324	0.093374	-4.561949	45219.277751
HLA B*4403	1:28-36	9	YCEELKGTD	0.955740	-0.847379	-4.670701	0.108361	-4.562340	46849.072875
HLA A*3301	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.603764	0.040514	-4.563250	40157.269302
HLA A*0203	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.394676	-0.168791	-4.563467	24812.838810
HLA A*0101	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.347828	-0.215742	-4.563569	22275.513452
HLA B*5801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.348901	-0.215742	-4.564643	22330.653769
HLA B*7301	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.519817	-0.044895	-4.564712	33099.167750
HLA A*3201	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.629665	0.064686	-4.564978	42625.049441
HLA A*0219	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.440717	-0.124403	-4.565120	27587.793235
HLA B*4403	1:23-31	9	AAPKTYCEE	0.685714	-0.594884	-4.656383	0.090830	-4.565554	45329.741161
HLA A*2601	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.396838	-0.168791	-4.565629	24936.642577

HLA B*4002	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.642190	0.076178	-4.566012	43872.259335
HLA B*3501	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.397719	-0.168791	-4.566510	24987.283104
HLA B*4002	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.599967	0.033425	-4.566543	39807.729292
HLA B*3801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.532246	-0.035101	-4.567347	34060.094581
HLA A*8001	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.373329	-0.196092	-4.569421	23622.672746
HLA A*6801	1:30-38	9	EELKGTDTG	0.811906	-0.748210	-4.633236	0.063696	-4.569540	42977.001639
HLA B*1502	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.544099	-0.025590	-4.569689	35002.494936
HLA B*4501	1:145-153	9	DTLWQADTD	1.026181	-0.950003	-4.646029	0.076178	-4.569851	44261.798708
HLA A*6801	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.612048	0.040514	-4.571534	40930.632628
HLA B*4601	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.402874	-0.168791	-4.571665	25285.631674
HLA B*0801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.376207	-0.196092	-4.572299	23779.742782
HLA B*3901	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.448426	-0.124403	-4.572828	28081.844016
HLA A*3301	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.638208	0.064686	-4.573521	43471.800018
HLA A*3301	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.377918	-0.196092	-4.574010	23873.581570
HLA A*0101	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.378263	-0.196092	-4.574355	23892.574675
HLA B*4402	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.450117	-0.124403	-4.574520	28191.439478

HLA B*7301	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.548937	-0.025590	-4.574527	35394.565966
HLA A*2602	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.549087	-0.025590	-4.574677	35406.822852
HLA B*4801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.406433	-0.168791	-4.575224	25493.723853
HLA B*1509	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.540523	-0.035101	-4.575624	34715.472869
HLA A*0203	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.380138	-0.196092	-4.576230	23995.944074
HLA A*2301	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.531360	-0.044895	-4.576255	33990.698849
HLA A*6801	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.618714	0.042326	-4.576388	41563.675562
HLA A*2602	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.610333	0.033425	-4.576909	40769.307357
HLA B*1502	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.571560	-0.005967	-4.577527	37287.200855
HLA B*5401	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.542457	-0.035101	-4.577558	34870.382514
HLA B*1502	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.619924	0.042326	-4.577598	41679.637289
HLA A*0250	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.552073	-0.025590	-4.577663	35651.117992
HLA B*4002	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.644382	0.065526	-4.578857	44094.261140
HLA B*4501	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.614720	0.033425	-4.581295	41183.174651
HLA B*4001	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.412664	-0.168791	-4.581455	25862.119342
HLA B*4501	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.646795	0.064686	-4.582109	44339.928748

HLA A*0202	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.576393	-0.005967	-4.582360	37704.455447
HLA A*0250	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.547950	-0.035101	-4.583051	35314.235378
HLA B*1801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.459224	-0.124403	-4.583627	28788.819431
HLA A*0301	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.368026	-0.215742	-4.583768	23335.990854
HLA B*4002	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.648724	0.064686	-4.584037	44537.303381
HLA A*2403	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.388081	-0.196092	-4.584174	24438.888495
HLA A*3301	1:188-196	9	QNFAVTNDG	0.673013	-0.639588	-4.618195	0.033425	-4.584770	41514.012329
HLA A*2403	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.369354	-0.215742	-4.585095	23407.428471
HLA A*2603	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.628032	0.042326	-4.585706	42465.085581
HLA B*4002	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.550720	-0.035101	-4.585821	35540.198588
HLA B*4402	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.417380	-0.168791	-4.586170	26144.451074
HLA B*4002	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.627236	0.040514	-4.586721	42387.278004
HLA A*2601	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.392101	-0.196092	-4.588194	24666.152869
HLA B*3901	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.372683	-0.215742	-4.588425	23587.554964
HLA A*2601	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.373235	-0.215742	-4.588977	23617.561458
HLA B*1509	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.420187	-0.168791	-4.588978	26314.017697

HLA B*3801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.583495	-0.005967	-4.589462	38326.147438
HLA B*0702	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.393732	-0.196092	-4.589824	24758.935093
HLA B*1503	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.374123	-0.215742	-4.589865	23665.907324
HLA B*4501	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.632820	0.042326	-4.590494	42935.868691
HLA A*0212	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.421782	-0.168791	-4.590573	26410.855114
HLA B*4501	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.656179	0.065526	-4.590653	45308.411269
HLA B*4002	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.633495	0.042326	-4.591168	43002.584340
HLA A*0250	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.546594	-0.044895	-4.591489	35204.173648
HLA A*2603	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.565992	-0.025590	-4.591582	36812.177099
HLA B*4001	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.397106	-0.196092	-4.593198	24952.026430
HLA B*5101	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.469089	-0.124403	-4.593492	29450.274239
HLA B*3801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.568275	-0.025590	-4.593866	37006.260540
HLA A*2603	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.658890	0.064686	-4.594204	45592.157020
HLA B*0702	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.379522	-0.215742	-4.595264	23961.956533
HLA A*2402	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.550645	-0.044895	-4.595539	35534.046527
HLA B*5301	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.571644	-0.025590	-4.597235	37294.463468

HLA A*0216	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.401730	-0.196092	-4.597822	25219.101423
HLA B*4403	1:217-225	9	LVPRSAIDS	0.966010	-0.900484	-4.663382	0.065526	-4.597857	46066.196417
HLA A*3301	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.473544	-0.124403	-4.597947	29753.904644
HLA B*0702	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.429989	-0.168791	-4.598780	26914.679578
HLA B*4801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.289243	-0.310145	-4.599388	19464.502809
HLA A*0219	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.403912	-0.196092	-4.600005	25346.166289
HLA B*0802	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.475997	-0.124403	-4.600400	29922.427899
HLA B*5401	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.555567	-0.044895	-4.600461	35939.070258
HLA A*6901	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.234991	-0.365615	-4.600606	17178.741975
HLA A*0203	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.384997	-0.215742	-4.600738	24265.909640
HLA A*0250	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.594827	-0.005967	-4.600794	39339.309445
HLA B*3801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.556500	-0.044895	-4.601394	36016.340481
HLA A*0201	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.386479	-0.215742	-4.602221	24348.886267
HLA B*1501	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.386780	-0.215742	-4.602522	24365.752877
HLA A*6801	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.667830	0.064686	-4.603143	46540.380553
HLA A*2601	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.293919	-0.310145	-4.604064	19675.183431

HLA A*2301	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.408292	-0.196092	-4.604384	25603.050915
HLA A*3002	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.598485	-0.005967	-4.604452	39672.071708
HLA B*4403	1:86-94	9	PREAPYELN	0.811488	-0.746802	-4.669430	0.064686	-4.604743	46712.157806
HLA B*0801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.435957	-0.168791	-4.604748	27287.070049
HLA B*0803	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.480412	-0.124403	-4.604814	30228.146023
HLA A*3101	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.390118	-0.215742	-4.605860	24553.785263
HLA B*2705	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.410110	-0.196092	-4.606203	25710.482161
HLA A*2402	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.600327	-0.005967	-4.606294	39840.692309
HLA B*4402	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.410745	-0.196092	-4.606837	25748.064134
HLA B*7301	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.438602	-0.168791	-4.607393	27453.797493
HLA B*1801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.298056	-0.310145	-4.608201	19863.520963
HLA B*4501	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.573132	-0.035101	-4.608233	37422.395785
HLA A*8001	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.439895	-0.168791	-4.608685	27535.606242
HLA B*4001	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.393286	-0.215742	-4.609027	24733.498980
HLA A*6802	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.244909	-0.365615	-4.610523	17575.534149
HLA B*1801	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.246250	-0.365615	-4.611865	17629.909736

HLA B*4403	1:213-221	9	PTQVLVPRS	1.263904	-1.221578	-4.654743	0.042326	-4.612417	45158.894178
HLA A*0212	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.302358	-0.310145	-4.612503	20061.256930
HLA A*2602	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.606666	-0.005967	-4.612633	40426.466857
HLA B*4501	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.653273	0.040514	-4.612758	45006.218162
HLA A*3002	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.587402	-0.025590	-4.612993	38672.509919
HLA A*3201	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.607307	-0.005967	-4.613275	40486.216807
HLA A*0212	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.398231	-0.215742	-4.613973	25016.769386
HLA A*0219	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.446041	-0.168791	-4.614832	27928.068139
HLA B*5301	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.608952	-0.005967	-4.614919	40639.825637
HLA B*4601	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.400604	-0.215742	-4.616346	25153.834836
HLA A*3201	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.592146	-0.025590	-4.617736	39097.228253
HLA B*2705	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.402329	-0.215742	-4.618070	25253.915730
HLA A*0201	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.308775	-0.310145	-4.618920	20359.850450
HLA B*5101	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.422844	-0.196092	-4.618937	26475.515807
HLA B*7301	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.423051	-0.196092	-4.619144	26488.123013
HLA A*2403	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.450425	-0.168791	-4.619216	28211.425705

HLA A*2301	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.495129	-0.124403	-4.619532	31270.057911
HLA B*4403	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.585452	-0.035101	-4.620553	38499.251580
HLA A*3002	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.425542	-0.196092	-4.621634	26640.455046
HLA B*5701	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.406337	-0.215742	-4.622079	25488.069833
HLA A*0206	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.406997	-0.215742	-4.622739	25526.845723
HLA B*5301	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.588140	-0.035101	-4.623241	38738.258941
HLA B*0802	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.455169	-0.168791	-4.623959	28521.255859
HLA A*8001	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.408240	-0.215742	-4.623982	25600.003884
HLA A*2603	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.499952	-0.124403	-4.624355	31619.294695
HLA B*4403	1:206-214	9	LLPEAAGPT	0.415766	-0.375252	-4.668777	0.040514	-4.628262	46641.957896
HLA A*2501	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.432414	-0.196092	-4.628506	27065.364631
HLA B*7301	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.594808	-0.035101	-4.629909	39337.606912
HLA B*4002	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.604720	-0.025590	-4.630311	40245.785990
HLA A*0202	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.434972	-0.196092	-4.631065	27225.287308
HLA A*3201	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.586390	-0.044895	-4.631284	38582.443732
HLA A*3301	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.596594	-0.035101	-4.631695	39499.677051

HLA A*6801	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.607495	-0.025590	-4.633085	40503.742675
HLA A*3301	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.628030	-0.005967	-4.633997	42464.855850
HLA A*0211	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.438053	-0.196092	-4.634145	27419.065334
HLA A*0216	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.466876	-0.168791	-4.635667	29300.574007
HLA B*0802	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.441847	-0.196092	-4.637939	27659.674478
HLA B*0802	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.424202	-0.215742	-4.639944	26558.432088
HLA A*2602	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.605139	-0.035101	-4.640240	40284.559749
HLA B*4801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.425109	-0.215742	-4.640851	26613.949809
HLA B*5401	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.331825	-0.310145	-4.641970	21469.670585
HLA A*2602	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.597204	-0.044895	-4.642099	39555.275250
HLA B*4501	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.519004	-0.124403	-4.643407	33037.269960
HLA A*2402	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.519046	-0.124403	-4.643449	33040.487220
HLA B*5301	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.600249	-0.044895	-4.645144	39833.580331
HLA B*1509	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.430212	-0.215742	-4.645954	26928.515649
HLA A*2501	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.477999	-0.168791	-4.646789	30060.665457
HLA B*1517	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.431237	-0.215742	-4.646979	26992.107221

HLA B*0801	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.283285	-0.365615	-4.648900	19199.283470
HLA B*5101	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.480115	-0.168791	-4.648906	30207.548148
HLA B*2705	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.480865	-0.168791	-4.649656	30259.723973
HLA A*6801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.339894	-0.310145	-4.650039	21872.252581
HLA B*5801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.340540	-0.310145	-4.650685	21904.816575
HLA A*1101	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.482303	-0.168791	-4.651094	30360.075478
HLA A*0101	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.342029	-0.310145	-4.652174	21980.076233
HLA B*4402	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.436915	-0.215742	-4.652657	27347.365537
HLA A*2603	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.647676	-0.005967	-4.653643	44429.972841
HLA A*3301	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.628347	-0.025590	-4.653937	42495.880750
HLA A*2501	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.439190	-0.215742	-4.654932	27490.953114
HLA A*0219	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.441069	-0.215742	-4.656811	27610.189357
HLA A*0216	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.442409	-0.215742	-4.658150	27695.460558
HLA A*2603	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.623380	-0.035101	-4.658481	42012.644902
HLA B*3901	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.463533	-0.196092	-4.659625	29075.876213
HLA B*1801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.444422	-0.215742	-4.660164	27824.162447

HLA A*0211	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.351444	-0.310145	-4.661589	22461.749562
HLA B*1502	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.351747	-0.310145	-4.661892	22477.430542
HLA A*6801	1:76-84	9	KFLSAATSS	0.874409	-0.909510	-4.627057	-0.035101	-4.662158	42369.853990
HLA B*1502	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.447676	-0.215742	-4.663418	28033.423436
HLA B*4001	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.356300	-0.310145	-4.666445	22714.331842
HLA A*3201	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.356685	-0.310145	-4.666830	22734.493435
HLA A*0219	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.358743	-0.310145	-4.668888	22842.489327
HLA A*0301	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.359514	-0.310145	-4.669659	22883.058019
HLA A*0250	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.545457	-0.124403	-4.669860	35112.116094
HLA A*3101	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.361185	-0.310145	-4.671330	22971.245622
HLA A*3001	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.305922	-0.365615	-4.671537	20226.573121
HLA A*2501	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.362040	-0.310145	-4.672185	23016.525159
HLA A*3301	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.628305	-0.044895	-4.673199	42491.742787
HLA B*7301	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.549392	-0.124403	-4.673795	35431.732718
HLA B*1502	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.549416	-0.124403	-4.673819	35433.649588
HLA A*0206	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.505544	-0.168791	-4.674335	32029.042266

HLA A*3201	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.508883	-0.168791	-4.677673	32276.212845
HLA B*1509	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.554183	-0.124403	-4.678586	35824.735373
HLA B*4501	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.653359	-0.025590	-4.678950	45015.227774
HLA B*1502	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.510311	-0.168791	-4.679102	32382.550959
HLA B*5101	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.314298	-0.365615	-4.679913	20620.453998
HLA A*6801	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.635055	-0.044895	-4.679949	43157.334556
HLA B*0702	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.369864	-0.310145	-4.680009	23434.923662
HLA A*0216	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.373002	-0.310145	-4.683147	23604.915774
HLA A*3002	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.514747	-0.168791	-4.683538	32714.997038
HLA B*4403	1:201-209	9	FNPGELLPE	0.811387	-0.836977	-4.658209	-0.025590	-4.683799	45520.685030
HLA B*3901	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.516025	-0.168791	-4.684816	32811.418424
HLA A*0211	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.516540	-0.168791	-4.685330	32850.315305
HLA B*1801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.516711	-0.168791	-4.685502	32863.291176
HLA A*6801	1:204-212	9	GELLPEAAG	0.791497	-0.797464	-4.680508	-0.005967	-4.686475	47919.000531
HLA A*2603	1:38-46	9	GQACQIQMS	0.965607	-1.010502	-4.643837	-0.044895	-4.688732	44038.953400
HLA B*0803	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.492995	-0.196092	-4.689088	31116.830428

HLA B*0803	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.528884	-0.168791	-4.697675	33797.434619
HLA A*2301	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.530493	-0.168791	-4.699284	33922.912628
HLA A*1101	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.486431	-0.215742	-4.702173	30650.029162
HLA B*4402	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.392400	-0.310145	-4.702545	24683.105718
HLA A*2403	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.394087	-0.310145	-4.704232	24779.168764
HLA A*2602	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.536484	-0.168791	-4.705275	34394.129376
HLA A*1101	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.396568	-0.310145	-4.706713	24921.133388
HLA B*1517	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.398565	-0.310145	-4.708710	25035.994759
HLA B*5401	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.540965	-0.168791	-4.709756	34750.798520
HLA B*5301	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.586862	-0.124403	-4.711265	38624.420626
HLA B*0702	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.348293	-0.365615	-4.713908	22299.386831
HLA B*3801	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.590325	-0.124403	-4.714728	38933.649862
HLA B*4002	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.590532	-0.124403	-4.714935	38952.189427
HLA A*0202	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.501407	-0.215742	-4.717148	31725.356389
HLA A*6801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.522117	-0.196092	-4.718210	33274.935305
HLA B*5701	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.409882	-0.310145	-4.720027	25696.993888

HLA B*3801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.554629	-0.168791	-4.723420	35861.577796
HLA A*0211	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.509710	-0.215742	-4.725451	32337.734382
HLA B*0803	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.510990	-0.215742	-4.726732	32433.219315
HLA B*5801	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.361450	-0.365615	-4.727065	22985.292639
HLA A*2601	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.361692	-0.365615	-4.727307	22998.104040
HLA A*6801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.512874	-0.215742	-4.728616	32574.244045
HLA A*2301	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.514117	-0.215742	-4.729859	32667.599558
HLA A*0301	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.366903	-0.365615	-4.732518	23275.723642
HLA A*2402	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.565237	-0.168791	-4.734028	36748.305489
HLA A*0202	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.565750	-0.168791	-4.734540	36791.670384
HLA A*2501	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.370961	-0.365615	-4.736576	23494.204934
HLA B*1509	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.542436	-0.196092	-4.738528	34868.684751
HLA A*0101	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.375089	-0.365615	-4.740704	23718.586170
HLA A*6801	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.579367	-0.168791	-4.748158	37963.576570
HLA B*1509	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.441239	-0.310145	-4.751384	27620.945952
HLA B*5101	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.441422	-0.310145	-4.751567	27632.603659

HLA A*6801	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.389846	-0.365615	-4.755461	24538.381440
HLA A*0201	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.391686	-0.365615	-4.757300	24642.545089
HLA B*3901	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.393943	-0.365615	-4.759558	24770.992907
HLA B*1509	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.395651	-0.365615	-4.761266	24868.608795
HLA B*0802	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.451280	-0.310145	-4.761425	28267.034369
HLA B*5301	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.593337	-0.168791	-4.762128	39204.611869
HLA A*0250	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.594888	-0.168791	-4.763679	39344.843189
HLA B*3801	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.568132	-0.196092	-4.764224	36994.050369
HLA B*4403	1:196-204	9	GVIFFFNPG	0.529052	-0.653455	-4.639963	-0.124403	-4.764366	43647.833152
HLA A*3101	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.399751	-0.365615	-4.765366	25104.486463
HLA A*3301	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.598309	-0.168791	-4.767099	39655.978360
HLA B*1502	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.571052	-0.196092	-4.767145	37243.654863
HLA B*4001	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.401781	-0.365615	-4.767396	25222.103118
HLA B*7301	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.457450	-0.310145	-4.767595	28671.472282
HLA B*5301	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.574410	-0.196092	-4.770502	37532.691355
HLA B*4002	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.575265	-0.196092	-4.771357	37606.673536

HLA B*4601	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.406156	-0.365615	-4.771771	25477.454696
HLA A*0250	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.577309	-0.196092	-4.773401	37784.090428
HLA A*0203	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.409967	-0.365615	-4.775582	25701.999019
HLA B*3801	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.562204	-0.215742	-4.777946	36492.543373
HLA A*2301	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.470337	-0.310145	-4.780482	29534.996233
HLA B*1503	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.415070	-0.365615	-4.780685	26005.785979
HLA A*2402	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.567185	-0.215742	-4.782927	36913.484340
HLA B*1501	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.417502	-0.365615	-4.783117	26151.806914
HLA A*2402	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.474831	-0.310145	-4.784976	29842.244524
HLA A*0212	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.419846	-0.365615	-4.785461	26293.384183
HLA B*5701	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.421221	-0.365615	-4.786836	26376.728909
HLA B*0803	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.479157	-0.310145	-4.789302	30140.946527
HLA A*2602	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.579513	-0.215742	-4.795255	37976.312188
HLA A*3002	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.487444	-0.310145	-4.797589	30721.578059
HLA B*4501	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.601506	-0.196092	-4.797599	39949.037294
HLA B*7301	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.582154	-0.215742	-4.797895	38207.938848

HLA A*3002	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.582640	-0.215742	-4.798382	38250.749863
HLA A*0250	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.583077	-0.215742	-4.798819	38289.258645
HLA A*2603	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.630128	-0.168791	-4.798919	42670.501225
HLA A*2602	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.603621	-0.196092	-4.799713	40144.019460
HLA B*5301	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.435038	-0.365615	-4.800653	27229.411622
HLA B*4403	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.604612	-0.196092	-4.800705	40235.771875
HLA B*4801	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.438607	-0.365615	-4.804222	27454.094539
HLA A*2403	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.441828	-0.365615	-4.807443	27658.477418
HLA A*3301	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.594733	-0.215742	-4.810475	39330.797514
HLA B*4402	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.446008	-0.365615	-4.811623	27925.952990
HLA B*4002	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.643388	-0.168791	-4.812179	43993.471944
HLA B*4501	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.645092	-0.168791	-4.813882	44166.360631
HLA A*2902	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.449643	-0.365615	-4.815257	28160.648768
HLA B*0802	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.451844	-0.365615	-4.817459	28303.759371
HLA A*2603	1:54-62	9	ISLPSYYPD	0.496117	-0.692209	-4.625060	-0.196092	-4.821152	42175.467486
HLA B*4403	1:57-65	9	PSYYPDQKS	0.896699	-1.065490	-4.652756	-0.168791	-4.821546	44952.684723

HLA A*8001	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.456087	-0.365615	-4.821702	28581.649773
HLA A*0219	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.458350	-0.365615	-4.823965	28730.940803
HLA A*2602	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.472395	-0.365615	-4.838010	29675.296621
HLA B*4002	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.625074	-0.215742	-4.840816	42176.836495
HLA A*0250	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.532161	-0.310145	-4.842306	34053.461819
HLA A*3201	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.627026	-0.215742	-4.842768	42366.874284
HLA B*3801	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.534158	-0.310145	-4.844303	34210.414042
HLA A*2603	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.634324	-0.215742	-4.850066	43084.784446
HLA A*2602	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.542915	-0.310145	-4.853060	34907.187680
HLA B*1517	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.488397	-0.365615	-4.854012	30789.129552
HLA B*2705	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.490921	-0.365615	-4.856536	30968.541905
HLA A*1101	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.494057	-0.365615	-4.859672	31193.012581
HLA A*0216	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.494506	-0.365615	-4.860121	31225.260630
HLA B*5301	1:50-58	9	YNINISLPS	0.643875	-0.954020	-4.552052	-0.310145	-4.862197	35649.382217
HLA B*4403	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.651069	-0.215742	-4.866810	44778.413671
HLA B*4501	1:159-167	9	FPIVQGELS	0.883442	-1.099184	-4.651825	-0.215742	-4.867567	44856.484944

HLA B*4403	1:50-58 9	YNINISLPS	0.643875	-0.954020	-4.559627	-
0.310145	-4.869772	36276.614325				
HLA A*0206	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.514669	-
0.365615	-4.880284	32709.157071				
HLA A*3301	1:50-58 9	YNINISLPS	0.643875	-0.954020	-4.578721	-
0.310145	-4.888866	37907.139408				
HLA A*3002	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.523727	-
0.365615	-4.889341	33398.473458				
HLA B*4501	1:50-58 9	YNINISLPS	0.643875	-0.954020	-4.585196	-
0.310145	-4.895341	38476.556114				
HLA B*0803	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.534389	-
0.365615	-4.900003	34228.556157				
HLA A*2603	1:50-58 9	YNINISLPS	0.643875	-0.954020	-4.591380	-
0.310145	-4.901525	39028.336216				
HLA A*2301	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.539092	-
0.365615	-4.904707	34601.286695				
HLA B*3801	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.548246	-
0.365615	-4.913861	35338.315392				
HLA A*0211	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.553777	-
0.365615	-4.919391	35791.222301				
HLA A*0202	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.554914	-
0.365615	-4.920529	35885.060347				
HLA B*1502	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.566654	-
0.365615	-4.932269	36868.380202				
HLA A*2402	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.573956	-
0.365615	-4.939571	37493.523600				
HLA A*3301	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.576555	-
0.365615	-4.942170	37718.532482				
HLA B*7301	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.593231	-
0.365615	-4.958846	39195.068863				
HLA A*0250	1:47-55 9	DPAYNINIS	0.849651	-1.215266	-4.599239	-
0.365615	-4.964854	39741.025067				

HLA A*3201	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.613623	-0.365615	-4.979237	41079.260049
HLA A*2603	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.623984	-0.365615	-4.989599	42071.097451
HLA B*4002	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.645491	-0.365615	-5.011106	44206.998284
HLA B*4501	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.647681	-0.365615	-5.013296	44430.453566
HLA B*4403	1:47-55	9	DPAYNINIS	0.849651	-1.215266	-4.658427	-0.365615	-5.024042	45543.593145