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	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-1.116997	2.784052	1.667055	13.091725
HLA B*5801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-1.283712	2.784052	1.500341	19.218152
HLA A*0202	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-0.635329	2.016506	1.381177	4.318460
HLA A*3001	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-1.360183	2.719390	1.359207	22.918313
HLA B*1801	1:36-44	9	VEFAGRACY	1.217312	1.307358	-1.181218	2.524670	1.343452	15.178110
HLA B*1517	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-1.461460	2.719390	1.257931	28.937403
HLA B*1517	1:135-143	9	AADAARATY	1.474911	1.206254	-1.443448	2.681165	1.237717	27.761850
HLA B*3501	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-1.566298	2.784052	1.217754	36.838189
HLA B*1503	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-1.604050	2.784052	1.180002	40.183689
HLA A*2902	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-1.549847	2.719390	1.169543	35.468856
HLA A*6802	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-0.757418	1.919326	1.161908	5.720284
HLA B*1501	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-1.671781	2.719390	1.047609	46.965695
HLA B*1503	1:73-81	9	LEHASVSFY	1.292112	1.245827	-1.503722	2.537939	1.034217	31.894962
HLA B*1503	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-1.153264	2.158014	1.004750	14.231921
HLA B*1517	1:53-61	9	KTATNAGYL	1.501925	0.397625	-0.921445	1.899550	0.978105	8.345349
HLA B*1503	1:72-80	9	VLEHASVSF	1.635346	1.096028	-1.819986	2.731374	0.911388	66.067256
HLA A*6801	1:54-62	9	TATNAGYLR	1.132899	0.685523	-0.933615	1.818422	0.884807	8.582521
HLA A*2403	1:142-150	9	TYSELLAKL	1.344148	0.587133	-1.122128	1.931281	0.809153	13.247323
HLA B*1517	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-0.897287	1.691549	0.794262	7.893818
HLA A*3101	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-1.041677	1.834955	0.793278	11.007205
HLA B*1801	1:73-81	9	LEHASVSFY	1.292112	1.245827	-1.753839	2.537939	0.784100	56.733407
HLA B*1501	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-2.000497	2.784052	0.783555	100.114550
HLA A*2902	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-1.899075	2.660014	0.760939	79.263753
HLA B*1501	1:72-80	9	VLEHASVSF	1.635346	1.096028	-1.984897	2.731374	0.746478	96.582094
HLA A*8001	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-1.916395	2.660014	0.743619	82.488809
HLA A*6801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-0.889614	1.621061	0.731447	7.755570
HLA A*0250	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.562053	1.273350	0.711297	3.647986
HLA A*0211	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.568289	1.273350	0.705061	3.700741
HLA A*3101	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-1.365098	2.044564	0.679466	23.179164
HLA A*3001	1:138-146	9	AARATYSEL	1.196073	0.462758	-1.025099	1.658831	0.633732	10.594955
HLA B*4403	1:73-81	9	LEHASVSFY	1.292112	1.245827	-1.923274	2.537939	0.614664	83.805848
HLA B*1503	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.118949	2.719390	0.600441	131.506989
HLA A*3101	1:79-87	9	SFYITGISR	1.120990	0.841293	-1.370257	1.962283	0.592026	23.456178
HLA A*6901	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-1.342270	1.919326	0.577056	21.992276
HLA A*3002	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.144901	2.719390	0.574489	139.605088
HLA B*3901	1:167-175	9	ARQAARAVL	1.496924	0.533348	-1.462592	2.030272	0.567680	29.012958
HLA A*3101	1:160-168	9	AILRRKQAR	1.023219	0.831799	-1.289599	1.855018	0.565418	19.480470
HLA B*1501	1:73-81	9	LEHASVSFY	1.292112	1.245827	-1.989173	2.537939	0.548766	97.537738
HLA B*1503	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-2.112601	2.642684	0.530083	129.598665
HLA B*3501	1:135-143	9	AADAARATY	1.474911	1.206254	-2.152894	2.681165	0.528271	142.198231
HLA B*1801	1:91-99	9	HELIRHRHF	1.404658	1.013097	-1.970898	2.417755	0.446857	93.518684
HLA A*0219	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.829678	1.273350	0.443672	6.755824
HLA A*3002	1:135-143	9	AADAARATY	1.474911	1.206254	-2.241169	2.681165	0.439996	174.248499
HLA B*1517	1:138-146	9	AARATYSEL	1.196073	0.462758	-1.223856	1.658831	0.434975	16.743881
HLA B*1503	1:36-44	9	VEFAGRACY	1.217312	1.307358	-2.092968	2.524670	0.431702	123.870597
HLA A*3101	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-1.076257	1.502929	0.426672	11.919466
HLA A*0212	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-1.592739	2.016506	0.423767	39.150686
HLA A*0216	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.852388	1.273350	0.420962	7.118500
HLA A*0202	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.861251	1.273350	0.412099	7.265253
HLA B*5701	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-2.377519	2.784052	0.406533	238.516846
HLA B*1503	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-1.055887	1.451496	0.395610	11.373307
HLA A*3002	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-2.269593	2.660014	0.390421	186.034338
HLA B*1517	1:211-219	9	LAIECLRQL	1.635667	0.528719	-1.785458	2.164386	0.378928	61.018037
HLA A*0203	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.897856	1.273350	0.375494	7.904159
HLA A*0250	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-0.692031	1.056254	0.364222	4.920751
HLA A*0203	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-1.664413	2.016506	0.352093	46.175623
HLA B*1517	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-1.241820	1.561696	0.319876	17.450999
HLA A*0206	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-0.960441	1.273350	0.312909	9.129380
HLA A*0206	1:227-235	9	FADFEVTTL	1.891662	0.342213	-1.960683	2.233875	0.273192	91.344589
HLA A*2301	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-1.393052	1.665496	0.272444	24.720198
HLA A*6801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-1.498295	1.758557	0.260262	31.498856
HLA A*0250	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-0.774776	1.014245	0.239470	5.953544
HLA B*1501	1:36-44	9	VEFAGRACY	1.217312	1.307358	-2.291913	2.524670	0.232757	195.845331
HLA B*2705	1:209-217	9	RRLAIECLR	0.972846	0.851605	-1.597852	1.824451	0.226599	39.614288
HLA A*8001	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.493264	2.719390	0.226126	311.360909
HLA A*3001	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-1.445182	1.665496	0.220314	27.872911
HLA A*2403	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-2.424528	2.642684	0.218156	265.783217
HLA A*0250	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-1.804672	2.016506	0.211834	63.778210
HLA B*3901	1:139-147	9	ARATYSELL	1.529098	0.642980	-1.966073	2.172078	0.206005	92.485265
HLA A*3201	1:72-80	9	VLEHASVSF	1.635346	1.096028	-2.531852	2.731374	0.199522	340.292226
HLA A*0301	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.520457	2.719390	0.198933	331.479768
HLA A*0203	1:77-85	9	SVSFYITGI	0.979963	0.379282	-1.160796	1.359245	0.198449	14.480913
HLA B*4402	1:73-81	9	LEHASVSFY	1.292112	1.245827	-2.347540	2.537939	0.190399	222.607416
HLA A*0250	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-0.785043	0.962074	0.177031	6.095970
HLA A*6901	1:233-241	9	TTLADGTEV	1.178752	0.144786	-1.155693	1.323538	0.167845	14.311754
HLA A*6802	1:77-85	9	SVSFYITGI	0.979963	0.379282	-1.193529	1.359245	0.165716	15.614532
HLA B*1517	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-1.762461	1.919326	0.156864	57.871065
HLA A*1101	1:141-149	9	ATYSELLAK	0.738811	0.394589	-0.983950	1.133400	0.149450	9.637186
HLA A*6901	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-1.125643	1.273350	0.147707	13.354971
HLA B*1503	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-1.789979	1.928720	0.138741	61.656468
HLA B*1503	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-2.427953	2.554540	0.126587	267.887903
HLA B*1502	1:72-80	9	VLEHASVSF	1.635346	1.096028	-2.618811	2.731374	0.112563	415.729810
HLA B*0801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.614779	2.719390	0.104611	411.888295
HLA B*4403	1:36-44	9	VEFAGRACY	1.217312	1.307358	-2.423959	2.524670	0.100711	265.435483
HLA A*0202	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.143087	2.233875	0.090787	139.023252
HLA A*3101	1:54-62	9	TATNAGYLR	1.132899	0.685523	-1.736147	1.818422	0.082275	54.468729
HLA A*3101	1:87-95	9	RSCTHELIR	1.036000	0.794609	-1.751367	1.830609	0.079242	56.411443
HLA A*3002	1:36-44	9	VEFAGRACY	1.217312	1.307358	-2.454653	2.524670	0.070017	284.873893
HLA A*0101	1:135-143	9	AADAARATY	1.474911	1.206254	-2.640281	2.681165	0.040884	436.798120
HLA B*2705	1:167-175	9	ARQAARAVL	1.496924	0.533348	-2.000934	2.030272	0.029338	100.215340
HLA A*3001	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-0.884675	0.910145	0.025470	7.667876
HLA A*2403	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-1.642083	1.665496	0.023413	43.861478
HLA A*8001	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-2.598888	2.615600	0.016712	397.088705
HLA B*3501	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-1.434849	1.451496	0.016647	27.217566
HLA B*2705	1:139-147	9	ARATYSELL	1.529098	0.642980	-2.196270	2.172078	-0.024193	157.134080
HLA A*3001	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-1.159706	1.130392	-0.029314	14.444609
HLA A*0211	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-2.048196	2.016506	-0.031690	111.736855
HLA B*4402	1:91-99	9	HELIRHRHF	1.404658	1.013097	-2.451213	2.417755	-0.033458	282.626580
HLA A*0211	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-0.997403	0.962074	-0.035330	9.940389
HLA B*4402	1:36-44	9	VEFAGRACY	1.217312	1.307358	-2.561089	2.524670	-0.036419	363.989637
HLA A*0203	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.055135	1.014245	-0.040890	11.353635
HLA B*1502	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-2.765062	2.719390	-0.045672	582.186203
HLA B*1503	1:138-146	9	AARATYSEL	1.196073	0.462758	-1.712587	1.658831	-0.053755	51.592504
HLA A*2403	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-2.715793	2.660014	-0.055780	519.748457
HLA B*1517	1:72-80	9	VLEHASVSF	1.635346	1.096028	-2.789327	2.731374	-0.057953	615.640795
HLA A*0206	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-2.074694	2.016506	-0.058188	118.766494
HLA A*3002	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-2.680363	2.615600	-0.064763	479.030289
HLA A*0202	1:77-85	9	SVSFYITGI	0.979963	0.379282	-1.428971	1.359245	-0.069725	26.851644
HLA A*6801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-1.775511	1.693800		
HLA A*3001	1:41-49	9	RACYQSWSK	0.781972	0.322141	-1.187890	1.104113	-0.0837	
HLA A*3001	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-2.130344	2.044564		

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HLA A*0201	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-1.362330	1.273350	-0.088980	23.031917
HLA A*3101	1:89-97 9	CTHELIRHR	1.005015	0.652731	-1.747246	1.657746	-0.089500	55.878689	
HLA A*0201	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-2.111553	2.016506	-0.095047	129.286344	
HLA B*1501	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-2.650665	2.554540	-0.096126	447.368586
HLA B*3901	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-2.046369	1.928720	-0.117648	111.267555
HLA A*0206	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-0.751422	0.625007	-0.126415	5.641852
HLA B*3501	1:72-80 9	VLEHASVSF	1.635346	1.096028	-2.869595	2.731374	-0.138221	740.619591	
HLA B*1502	1:36-44 9	VEFAGRACY	1.217312	1.307358	-2.673089	2.524670	-0.148419	471.073821	
HLA A*0212	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-1.423205	1.273350	-0.149855	26.497521
HLA A*3101	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-1.799456	1.621061	-0.178395	63.016817
HLA B*0702	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-1.632577	1.451496	-0.181081	42.911851
HLA B*5301	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.431346	2.233875	-0.197471	269.988806
HLA B*1503	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-2.516303	2.313503	-0.202800	328.324383
HLA A*0219	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.252971	1.014245	-0.238726	17.904861
HLA B*1503	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-1.932221	1.691549	-0.240672	85.550227	
HLA B*0702	1:138-146	9	AARATYSEL	1.196073	0.462758	-1.908783	1.658831	-0.249951	81.055540
HLA A*6901	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-1.421927	1.167504	-0.254423	26.419654
HLA B*1517	1:238-246	9	GTEVATSPL	1.240590	0.206169	-1.704518	1.446759	-0.257759	50.642889
HLA B*5801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.159261	1.899550	-0.259712	144.298328	
HLA B*1517	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-1.714090	1.451496	-0.262594	51.771444
HLA B*4403	1:91-99 9	HELIRHRHF	1.404658	1.013097	-2.691368	2.417755	-0.273613	491.323982	
HLA A*0202	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-2.829198	2.554540	-0.274659	674.835858
HLA A*0206	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-1.242821	0.962074	-0.280747	17.491263	
HLA B*1502	1:73-81 9	LEHASVSFY	1.292112	1.245827	-2.827192	2.537939	-0.289253	671.725276	
HLA A*0219	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-1.252900	0.962074	-0.290827	17.901955	
HLA A*1101	1:41-49 9	RACYQSWSK	0.781972	0.322141	-1.395571	1.104113	-0.291458	24.863977	
HLA B*2705	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-2.908197	2.615600	-0.292598	809.463433
HLA A*0202	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.314570	1.014245	-0.300325	20.633350
HLA A*3001	1:141-149	9	ATYSELLAK	0.738811	0.394589	-1.437617	1.133400	-0.304217	27.391573
HLA A*6801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-1.813520	1.502929	-0.310592	65.090931
HLA A*0211	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-1.369313	1.056254	-0.313059	23.405221
HLA B*3501	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.547819	2.233875	-0.313944	353.036109
HLA A*0216	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-1.287085	0.962074	-0.325012	19.368031	
HLA A*0250	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-1.115620	0.784286	-0.331334	13.050287	
HLA A*3101	1:164-172	9	RKQARQAAR	1.130763	0.814899	-2.284517	1.945662	-0.338855	192.538260
HLA B*1517	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.574796	2.233875	-0.340921	375.660831
HLA B*5301	1:175-183	9	LPNATETRI	1.064730	0.080627	-1.486651	1.145357	-0.341294	30.665548
HLA B*1503	1:91-99 9	HELIRHRHF	1.404658	1.013097	-2.762214	2.417755	-0.344459	578.381420	
HLA A*0211	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.579612	2.233875	-0.345738	379.850200
HLA A*6802	1:233-241	9	TTLADGTEV	1.178752	0.144786	-1.703832	1.323538	-0.380295	50.562953
HLA B*5301	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.168736	2.784052	-0.384684	1474.81085
HLA B*1503	1:139-147	9	ARATYSELL	1.529098	0.642980	-2.562494	2.172078	-0.390416	365.169092
HLA A*6801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-2.231466	1.834955	-0.396511	170.398462
HLA A*6802	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-2.416553	2.016506	-0.400047	260.947657	
HLA A*3101	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-2.243937	1.843851	-0.400085	175.362504
HLA B*4002	1:91-99 9	HELIRHRHF	1.404658	1.013097	-2.818950	2.417755	-0.401195	659.097550	
HLA B*4601	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.191940	2.784052	-0.407888	1555.75010
HLA B*1501	1:135-143	9	AADAARATY	1.474911	1.206254	-3.091372	2.681165	-0.410208	1234.16289
HLA B*1502	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-1.977327	1.561696	-0.415630	94.913192	
HLA A*0216	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-2.448788	2.016506	-0.432282	281.053071	
HLA A*6802	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-1.498469	1.056254	-0.442215	31.511468
HLA B*1503	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.060237	2.615600	-0.444638	1148.78064
HLA A*3002	1:73-81 9	LEHASVSFY	1.292112	1.245827	-2.988014	2.537939	-0.450075	972.778446	
HLA B*1517	1:39-47 9	AGRACYQSW	1.340001	0.305812	-2.097216	1.645813	-0.451403	125.088130	
HLA A*0211	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-1.238056	0.784286	-0.453770	17.300411	
HLA B*1503	1:208-216	9	IRRLAIECL	1.768404	0.464239	-2.693511	2.232643	-0.460868	493.754075
HLA A*0301	1:141-149	9	ATYSELLAK	0.738811	0.394589	-1.594628	1.133400	-0.461228	39.321345
HLA A*2301	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.193777	2.731374	-0.462403	1562.345701	
HLA B*1503	1:52-60 9	PKTATNAGY	1.018085	1.128286	-2.610344	2.146371	-0.463973	407.702733	
HLA A*0206	1:211-219	9	LAIECLRQL	1.635667	0.528719	-2.628491	2.164386	-0.464105	425.099941
HLA B*3901	1:154-162	9	FADQPNAIL	1.350025	0.365694	-2.192257	1.715719	-0.476538	155.688834
HLA B*5701	1:39-47 9	AGRACYQSW	1.340001	0.305812	-2.127990	1.645813	-0.482177	134.273297	
HLA A*3301	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-2.005671	1.502929	-0.502742	101.314304
HLA A*6801	1:89-97 9	CTHELIRHR	1.005015	0.652731	-2.163204	1.657746	-0.505458	145.614202	
HLA A*0202	1:142-150	9	TYSELLAKL	1.344148	0.587133	-2.440565	1.931281	-0.509284	275.781505
HLA B*1503	1:164-172	9	RKQARQAAR	1.130763	0.814899	-2.467537	1.945662	-0.521875	293.452103
HLA A*3301	1:89-97 9	CTHELIRHR	1.005015	0.652731	-2.188038	1.657746	-0.530292	154.183461	
HLA B*1501	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-2.845005	2.313503	-0.531503	699.850837
HLA A*0203	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-1.318559	0.784286	-0.534273	20.823761	
HLA A*0206	1:77-85 9	SVSFYITGI	0.979963	0.379282	-1.900061	1.359245	-0.540816	79.444057	
HLA A*2603	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.166626	2.615600	-0.551027	1467.66348
HLA B*2705	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-2.487217	1.928720	-0.558496	307.055239
HLA A*3101	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.280666	2.719390	-0.561276	1908.38410
HLA A*3301	1:54-62 9	TATNAGYLR	1.132899	0.685523	-2.384784	1.818422	-0.566362	242.540163	
HLA B*2705	1:208-216	9	IRRLAIECL	1.768404	0.464239	-2.809143	2.232643	-0.576500	644.381327
HLA A*2902	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.198678	2.615600	-0.583079	1580.07667
HLA A*0203	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-1.647238	1.056254	-0.590984	44.385185
HLA A*8001	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.136553	2.537939	-0.598614	1369.471757	
HLA A*0201	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.832873	2.233875	-0.598998	680.569913
HLA A*0219	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-2.626616	2.016506	-0.610110	423.268702	
HLA A*0250	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.483991	0.873495	-0.610497	30.478326
HLA A*1101	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-1.554678	0.937566	-0.617112	35.865569
HLA A*3001	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-2.316432	1.691549	-0.624883	207.220371	
HLA A*3301	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-2.674409	2.044564	-0.629845	472.508233
HLA A*2902	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.160137	2.524670	-0.635467	1445.896513	
HLA A*2403	1:222-230	9	VAPAVFADF	0.948144	1.210036	-2.801803	2.158180	-0.643623	633.582475
HLA B*0801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.098607	1.451496	-0.647111	125.489386
HLA A*0206	1:70-78 9	FSVLEHASV	1.102668	0.135344	-1.893426	1.238012	-0.655414	78.239572	
HLA A*6802	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.560671	1.899550	-0.661121	363.639298	
HLA B*5801	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.225832	1.561696	-0.664135	168.202175	
HLA B*4002	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.204759	2.537939	-0.666820	1602.354593	
HLA B*1503	1:167-175	9	ARQAARAVL	1.496924	0.533348	-2.698280	2.030272	-0.668008	499.206404
HLA B*4501	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-1.603129	0.923260	-0.679869	40.098562
HLA A*2603	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.406063	2.719390	-0.686672	2547.19682
HLA A*0202	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.586783	1.899550	-0.687233	386.173962	
HLA A*2402	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-2.362863	1.665496	-0.697367	230.601947
HLA A*3301	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.421973	2.719390	-0.702583	2642.24580
HLA A*0216	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.720326	1.014245	-0.706081	52.520132
HLA A*0203	1:227-235	9	FADFEVTTL	1.891662	0.342213	-2.948923	2.233875	-0.715049	889.043902
HLA A*3101	1:132-140	9	LTEAADAAR	1.180631	0.577926	-2.473909	1.758557	-0.715352	297.789259
HLA A*2602	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-2.732023	2.016506	-0.715517	539.539756	
HLA A*2402	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.500700	2.784052	-0.716648	3167.37701
HLA A*6801	1:79-87 9	SFYITGISR	1.120990	0.841293	-2.700277	1.962283	-0.737994	501.507243	
HLA B*1501	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-2.897343	2.158014	-0.739329	789.482693	
HLA A*2301	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.382793	2.642684	-0.740109	2414.310955	
HLA A*0206	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.622254	0.873495	-0.748759	41.903819
HLA B*0801	1:91-99 9	HELIRHRHF	1.404658	1.013097	-3.167928	2.417755	-0.750173	1472.068782	
HLA B*3501	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.310998	2.554540	-0.756458	2046.43352
HLA B*4002	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.281352	2.524670	-0.756682	1911.401140	
HLA B*0702	1:166-174	9	QARQAARAV	0.923681	0.228464	-1.910310	1.152145	-0.758165	81.341067
HLA A*3301	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-2.428761	1.665496	-0.763265	268.386907
HLA A*3001	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-1.703099	0.937566	-0.765533	50.477680
HLA A*3001	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.665604	1.899550	-0.766054	463.024008	
HLA A*6801	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-2.685894	1.919326	-0.766568	485.169692	
HLA B*4501	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-1.502947	0.735649	-0.767298	31.838072
HLA A*2301	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.562618	2.784052		
HLA B*5801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.334182	2.554540		

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HLA A*3301	1:79-87 9	SFYITGISR	1.120990	0.841293	-2.754522	1.962283	-0.792239	568.227332		
HLA B*0702	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-2.484970	1.691549	-0.793421	305.471294		
HLA B*1502	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.460571	2.660014	-0.800557	2887.8229	
HLA A*2402	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.461534	2.660014	-0.801520	2894.23536	
HLA A*2602	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-2.727588	1.919326	-0.808262	534.057014		
HLA A*0216	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-1.864551	1.056254	-0.808298	73.206779	
HLA B*1503	1:222-230	9	VAPAVFADF	0.948144	1.210036	-2.967902	2.158180	-0.809722	928.75752	
HLA A*0203	1:211-219	9	LAIECLRQL	1.635667	0.528719	-2.975698	2.164386	-0.811311	945.579262	
HLA A*0211	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.835173	1.014245	-0.820928	68.418467	
HLA A*0202	1:211-219	9	LAIECLRQL	1.635667	0.528719	-2.988709	2.164386	-0.824323	974.33743	
HLA A*6802	1:74-82 9	EHASVSFYI	0.978340	0.173645	-1.981466	1.151985	-0.829481	95.822251		
HLA A*2301	1:222-230	9	VAPAVFADF	0.948144	1.210036	-2.989527	2.158180	-0.831347	976.17348	
HLA B*3501	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.552764	2.719390	-0.833374	3570.79031	
HLA A*0206	1:233-241	9	TTLADGTEV	1.178752	0.144786	-2.157194	1.323538	-0.833656	143.61299	
HLA A*6901	1:28-36 9	DADGGPALV	0.931987	-0.051421	-1.727205	0.880566	-0.846639	53.358683		
HLA B*1517	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-2.876686	2.027215	-0.849471	752.81097	
HLA A*6802	1:177-185	9	NATETRIVV	1.258391	0.095723	-2.204808	1.354114	-0.850694	160.25382	
HLA B*3901	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.090076	2.233875	-0.856201	1230.48285	
HLA A*2602	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.758808	1.899550	-0.859258	573.862149		
HLA A*2402	1:142-150	9	TYSELLAKL	1.344148	0.587133	-2.790559	1.931281	-0.859277	617.38847	
HLA B*1502	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.417566	2.554540	-0.863026	2615.56539	
HLA A*3001	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.315262	1.451496	-0.863766	206.66284	
HLA B*5701	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-2.556691	1.691549	-0.865142	360.322003		
HLA A*6901	1:154-162	9	FADQPNAIL	1.350025	0.365694	-2.582573	1.715719	-0.866853	382.44827	
HLA A*2602	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.487176	2.615600	-0.871577	3070.26685	
HLA B*4501	1:133-141	9	TEAADAARA	1.018713	-0.271480	-1.619458	0.747233	-0.872224	41.634919	
HLA B*1501	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.538292	2.660014	-0.878278	3453.75495	
HLA B*5801	1:135-143	9	AADAARATY	1.474911	1.206254	-3.560785	2.681165	-0.879621	3637.35332	
HLA A*0211	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.766700	0.873495	-0.893205	58.438619	
HLA A*6802	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-2.168283	1.273350	-0.894933	147.32733	
HLA B*2705	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-2.246672	1.349023	-0.897648	176.47026	
HLA A*2603	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.438354	2.537939	-0.900415	2743.808685		
HLA A*1101	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-2.737695	1.834955	-0.902740	546.63207	
HLA B*5801	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-2.931908	2.027215	-0.904693	854.88606	
HLA B*3901	1:27-35 9	TDADGGPAL	1.505710	0.284927	-2.696668	1.790637	-0.906031	497.357190		
HLA B*3501	1:30-38 9	DGGPALVEF	1.593417	0.842818	-3.343327	2.436235	-0.907091	2204.583517		
HLA B*1517	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.463775	2.554540	-0.909236	2909.21122	
HLA B*1503	1:135-143	9	AADAARATY	1.474911	1.206254	-3.591033	2.681165	-0.909868	3899.71402	
HLA A*3301	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-2.534587	1.621061	-0.913526	342.44184	
HLA A*6901	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.157337	2.233875	-0.923462	1436.60252	
HLA A*2402	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.568280	2.642684	-0.925596	3700.669894		
HLA A*2902	1:135-143	9	AADAARATY	1.474911	1.206254	-3.608052	2.681165	-0.926887	4055.57492	
HLA A*0211	1:233-241	9	TTLADGTEV	1.178752	0.144786	-2.255614	1.323538	-0.932076	180.14146	
HLA A*1101	1:87-95 9	RSCTHELIR	1.036000	0.794609	-2.762891	1.830609	-0.932282	579.283269		
HLA A*0202	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.807374	0.873495	-0.933880	64.176234	
HLA A*0202	1:139-147	9	ARATYSELL	1.529098	0.642980	-3.109924	2.172078	-0.937846	1288.02418	
HLA B*2705	1:164-172	9	RKQARQAAR	1.130763	0.814899	-2.885060	1.945662	-0.939397	767.46663	
HLA B*1503	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-1.571702	0.625007	-0.946695	37.299421	
HLA B*4501	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.495141	2.537939	-0.957202	3127.093587		
HLA A*2403	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.512104	2.554540	-0.957565	3251.65275	
HLA A*2402	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.118979	2.158180	-0.960798	1315.16103	
HLA B*1517	1:70-78 9	FSVLEHASV	1.102668	0.135344	-2.201228	1.238012	-0.963215	158.938020		
HLA A*2902	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.502020	2.537939	-0.964082	3177.021625		
HLA A*8001	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.489028	2.524670	-0.964358	3083.383322		
HLA B*0803	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.684429	2.719390	-0.965039	4835.36750	
HLA B*1501	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.422103	1.451496	-0.970607	264.30348	
HLA B*1501	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.532594	1.561696	-0.970898	340.874462		
HLA A*3001	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-1.596456	0.625007	-0.971449	39.487193	
HLA A*0206	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.986020	1.014245	-0.971774	96.832172	
HLA B*5101	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.757024	2.784052	-0.972972	5715.10054	
HLA A*0250	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.211779	2.233875	-0.977904	1628.46673	
HLA B*5701	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-3.007519	2.027215	-0.980304	1017.46473	
HLA A*0201	1:77-85 9	SVSFYITGI	0.979963	0.379282	-2.340289	1.359245	-0.981044	218.921854		
HLA A*6802	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-1.998909	1.014245	-0.984664	99.749091	
HLA A*0216	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.874560	0.873495	-1.001066	74.913503	
HLA A*0202	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.733040	2.731374	-1.001666	5408.045444		
HLA A*0206	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-2.059812	1.056254	-1.003559	114.76575	
HLA A*0203	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.878258	0.873495	-1.004764	75.554127	
HLA A*0203	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-1.633691	0.625007	-1.008684	43.022030	
HLA A*2403	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-2.204860	1.194587	-1.010273	160.272903		
HLA A*2602	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.549029	2.537939	-1.011090	3540.207085		
HLA A*3002	1:53-61 9	KTATNAGYL	1.501925	0.397625	-2.912403	1.899550	-1.012853	817.340112		
HLA B*1517	1:203-211	9	HADVEIRRL	1.774485	0.250562	-3.043349	2.025047	-1.018302	1104.96624	
HLA B*0702	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.807613	2.784052	-1.023561	6421.15252	
HLA B*1503	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-2.648405	1.621061	-1.027344	445.04638	
HLA B*3501	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.704090	2.660014	-1.044076	5059.29470	
HLA A*3001	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-2.887127	1.834955	-1.052172	771.12903	
HLA B*5701	1:135-143	9	AADAARATY	1.474911	1.206254	-3.735907	2.681165	-1.054742	5443.85694	
HLA A*1101	1:54-62 9	TATNAGYLR	1.132899	0.685523	-2.873796	1.818422	-1.055374	747.818277		
HLA A*6901	1:177-185	9	NATETRIVV	1.258391	0.095723	-2.413866	1.354114	-1.059752	259.33766	
HLA A*6801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-2.193225	1.133400	-1.059825	156.03623	
HLA A*2403	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-2.905961	1.843851	-1.062109	805.30524	
HLA A*0206	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.793718	2.731374	-1.062344	6218.965277		
HLA A*6901	1:77-85 9	SVSFYITGI	0.979963	0.379282	-2.425195	1.359245	-1.065949	266.191882		
HLA B*4001	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.591977	2.524670	-1.067307	3908.204251		
HLA B*1502	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.855293	2.784052	-1.071241	7166.27442	
HLA B*5701	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.791660	2.719390	-1.072270	6189.56293	
HLA A*6802	1:70-78 9	FSVLEHASV	1.102668	0.135344	-2.310690	1.238012	-1.072678	204.498584		
HLA B*1501	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.716904	2.642684	-1.074220	5210.795979		
HLA A*2403	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-3.858367	2.784052	-1.074314	7217.16378	
HLA B*4002	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.014272	1.939903	-1.074369	1033.407915		
HLA A*3101	1:41-49 9	RACYQSWSK	0.781972	0.322141	-2.188663	1.104113	-1.084550	154.405496		
HLA B*3501	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.246072	2.158180	-1.087892	1762.26807	
HLA B*3501	1:154-162	9	FADQPNAIL	1.350025	0.365694	-2.811690	1.715719	-1.095970	648.171287	
HLA A*0202	1:70-78 9	FSVLEHASV	1.102668	0.135344	-2.341032	1.238012	-1.103019	219.296427		
HLA A*3001	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-2.257808	1.154646	-1.103163	181.05398	
HLA A*2602	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.746724	2.642684	-1.104040	5581.150490		
HLA A*0212	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-1.988689	0.873495	-1.115194	97.429099	
HLA A*0206	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.567757	1.451496	-1.116260	369.62118	
HLA B*1502	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-3.432814	2.313503	-1.119311	2709.02954	
HLA A*0250	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.674552	2.554540	-1.120013	4726.63702	
HLA A*0211	1:77-85 9	SVSFYITGI	0.979963	0.379282	-2.481066	1.359245	-1.121820	302.737040		
HLA B*1517	1:154-162	9	FADQPNAIL	1.350025	0.365694	-2.839498	1.715719	-1.123779	691.03221	
HLA A*0216	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.366070	2.233875	-1.132195	2323.10891	
HLA A*0219	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.366925	2.233875	-1.133050	2327.68808	
HLA B*4501	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.659210	2.524670	-1.134540	4562.576041		
HLA B*3501	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.698642	1.561696	-1.136946	499.622477		
HLA B*5301	1:135-143	9	AADAARATY	1.474911	1.206254	-3.818303	2.681165	-1.137138	6581.17051	
HLA A*2402	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.871101	2.731374	-1.139727	7431.915617		
HLA A*2301	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-3.299048	2.158014	-1.141035	1990.894110		
HLA B*5801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.592972	1.451496	-1.141475	391.71619	
HLA A*2301	1:142-150	9	TYSELLAKL	1.344148	0.587133	-3.074287	1.931281	-1.143006	1186.55269	
HLA B*1501	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.301647	2.158180	-1.143466	2002.84200	
HLA B*1502	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.759369	2.615600	-1.143769	5746.04021	
HLA B*1503	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.805940	2.660014	-1.145927	6396.46684	
HLA A*3002	1:52-60 9	PKTATNAGY	1.018085	1.128286	-3.293771	2.146371	-1.1474			
HLA A*0202	1:153-161	9	KFADQPNAI	0.977018	0.424809	-2.549647	1.401827			

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HLA A*2301	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-3.461971	2.313503	-1.148468	2897.14912
HLA B*1501	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-1.782451	0.625007	-1.157444	60.596968
HLA B*5301	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.322444	2.164386	-1.158058	2101.08844
HLA A*0216	1:233-241	9	TTLADGTEV	1.178752	0.144786	-2.491967	1.323538	-1.168429	310.432492
HLA A*0206	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-2.299671	1.126312	-1.173359	199.375239
HLA B*1517	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.833631	2.660014	-1.173618	6817.59476
HLA A*0250	1:233-241	9	TTLADGTEV	1.178752	0.144786	-2.497540	1.323538	-1.174002	314.441710
HLA A*1101	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.896964	2.719390	-1.177574	7887.94549
HLA B*1517	1:200-208	9	ASEHADVEI	1.329405	0.306162	-2.814082	1.635567	-1.178514	651.750787
HLA B*5701	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.344107	2.164386	-1.179720	2208.54669
HLA B*1502	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-3.338148	2.158014	-1.180135	2178.453484	
HLA A*1101	1:135-143	9	AADAARATY	1.474911	1.206254	-3.862849	2.681165	-1.181684	7292.04564
HLA A*2603	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.198951	2.016506	-1.182445	1581.068560	
HLA A*3301	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.041056	1.855018	-1.186038	1099.14733
HLA B*0702	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-2.178029	0.990022	-1.188007	150.670762
HLA A*2902	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.925285	2.731374	-1.193910	8419.466885	
HLA A*0206	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.749294	2.554540	-1.194754	5614.28001
HLA A*0250	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.926586	2.731374	-1.195212	8444.738540	
HLA B*0802	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.926271	2.719390	-1.206881	8438.61895
HLA A*6802	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-2.246004	1.032480	-1.213524	176.199343
HLA A*2602	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.933837	2.719390	-1.214447	8586.90619
HLA A*2902	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.775787	2.554540	-1.221247	5967.42353
HLA B*1503	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-2.068162	0.846009	-1.222153	116.993671
HLA A*2403	1:72-80 9	VLEHASVSF	1.635346	1.096028	-3.954959	2.731374	-1.223584	9014.851742	
HLA B*1503	1:86-94 9	SRSCTHELI	1.200502	0.345702	-2.773360	1.546204	-1.227156	593.417419	
HLA A*0201	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-2.194151	0.962074	-1.232077	156.369177	
HLA B*1502	1:135-143	9	AADAARATY	1.474911	1.206254	-3.916474	2.681165	-1.235309	8250.38137
HLA B*4001	1:91-99 9	HELIRHRHF	1.404658	1.013097	-3.654502	2.417755	-1.236747	4513.378416	
HLA A*2301	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.791820	2.554540	-1.237280	6191.84032
HLA A*2501	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-3.897354	2.660014	-1.237340	7895.03237
HLA A*0201	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.405743	2.164386	-1.241356	2545.32342
HLA A*6901	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-2.207492	0.962074	-1.245418	161.246957	
HLA A*3201	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.700639	1.451496	-1.249143	501.925239
HLA B*1509	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.179102	1.928720	-1.250382	1510.43574
HLA A*1101	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-2.043361	0.789295	-1.254067	110.499727	
HLA A*0212	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.488600	2.233875	-1.254725	3080.34891
HLA A*0212	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-2.311329	1.056254	-1.255076	204.799723
HLA A*3201	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.812787	2.554540	-1.258247	6498.10242
HLA B*1501	1:91-99 9	HELIRHRHF	1.404658	1.013097	-3.677780	2.417755	-1.260025	4761.901909	
HLA A*0206	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-2.169538	0.905427	-1.264111	147.753557
HLA A*6801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-3.990417	2.719390	-1.271027	9781.76030
HLA A*3301	1:132-140	9	LTEAADAAR	1.180631	0.577926	-3.031235	1.758557	-1.272678	1074.57087
HLA B*5801	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.919453	2.642684	-1.276769	8307.171402	
HLA A*2602	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.064379	2.784052	-1.280327	11597.8851
HLA A*0211	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.180122	1.899550	-1.280572	1513.986246	
HLA A*3002	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.069919	2.784052	-1.285867	11746.7814
HLA B*4002	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-2.211321	0.923260	-1.288062	162.675139
HLA A*6901	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.188641	1.899550	-1.289092	1543.978194	
HLA A*0203	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.191277	1.899550	-1.291728	1553.378481	
HLA A*3002	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-3.934880	2.642684	-1.292196	8607.556654	
HLA B*1801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-2.939464	1.646900	-1.292565	869.889685
HLA A*3201	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.012211	2.719390	-1.292821	10285.1549
HLA A*3201	1:153-161	9	KFADQPNAI	0.977018	0.424809	-2.696231	1.401827	-1.294404	496.856982
HLA A*0212	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-2.261135	0.962074	-1.299061	182.446261	
HLA A*0201	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-1.924623	0.625007	-1.299616	84.066493
HLA B*1801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.087192	2.784052	-1.303140	12223.4078
HLA A*2501	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.022769	2.719390	-1.303379	10538.2725
HLA A*0201	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-2.320553	1.014245	-1.306308	209.196033
HLA A*0212	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.039991	2.731374	-1.308617	10964.558522	
HLA A*0206	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.093686	2.784052	-1.309634	12407.5570
HLA A*3002	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.001237	1.691549	-1.309688	1002.851990	
HLA A*3002	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.865288	2.554540	-1.310749	7333.10906
HLA A*2902	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.096191	2.784052	-1.312139	12479.3174
HLA A*2601	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-3.929260	2.615600	-1.313660	8496.88854
HLA B*0702	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.035109	2.719390	-1.315719	10841.9879
HLA A*6801	1:174-182	9	VLPNATETR	1.038504	0.740297	-3.096913	1.778801	-1.318111	1250.00735
HLA B*0801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.102530	2.784052	-1.318478	12662.7998
HLA A*0203	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.873384	2.554540	-1.318845	7471.09862
HLA B*1503	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.484225	2.164386	-1.319839	3049.47566
HLA A*0250	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-2.406192	1.080003	-1.326189	254.795746
HLA A*3001	1:135-143	9	AADAARATY	1.474911	1.206254	-4.008146	2.681165	-1.326981	10189.3441
HLA A*0212	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-2.342789	1.014245	-1.328544	220.185629
HLA B*3501	1:36-44 9	VEFAGRACY	1.217312	1.307358	-3.853522	2.524670	-1.328852	7137.102324	
HLA B*1517	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.868465	2.537939	-1.330526	7386.941298	
HLA A*0202	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.115428	2.784052	-1.331376	13044.5293
HLA A*0206	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.238577	1.899550	-1.339028	1732.116571	
HLA B*0801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.893599	2.554540	-1.339060	7827.07397
HLA A*0211	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.894022	2.554540	-1.339483	7834.69953
HLA A*8001	1:135-143	9	AADAARATY	1.474911	1.206254	-4.021045	2.681165	-1.339880	10496.5094
HLA A*2402	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.895277	2.554540	-1.340737	7857.36577
HLA B*0801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-2.493330	1.147510	-1.345820	311.408076
HLA A*0202	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.907610	1.561696	-1.345914	808.369396	
HLA B*1503	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.908841	1.561696	-1.347145	810.664198	
HLA B*1503	1:198-206	9	MRASEHADV	0.792968	0.319530	-2.463360	1.112498	-1.350862	290.642982
HLA A*3002	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.083880	2.731374	-1.352505	12130.523115	
HLA A*2602	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.013917	2.660014	-1.353903	10325.6301
HLA A*2602	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.521892	2.164386	-1.357506	3325.76926
HLA B*5701	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.257340	1.899550	-1.357790	1808.589911	
HLA A*6801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.143688	2.784052	-1.359636	13921.5637
HLA B*3901	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.148317	2.784052	-1.364264	14070.7259
HLA A*3001	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.027854	2.660014	-1.367840	10662.3690
HLA A*0211	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.534490	2.164386	-1.370104	3423.65546
HLA B*0801	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.386722	2.016506	-1.370216	2436.248272	
HLA B*2705	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.013080	2.642684	-1.370396	10305.762949	
HLA B*0803	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.106096	2.731374	-1.374722	12767.217586	
HLA B*2705	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-2.533370	1.154646	-1.378724	341.483556
HLA A*3001	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.167300	2.784052	-1.383248	14699.4249
HLA A*0250	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.550631	2.164386	-1.386245	3553.29296
HLA B*3901	1:74-82 9	EHASVSFYI	0.978340	0.173645	-2.538238	1.151985	-1.386253	345.332878	
HLA A*0211	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.117797	2.731374	-1.386423	13115.857672	
HLA B*7301	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-2.452876	1.066259	-1.386617	283.711173
HLA B*3501	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.927531	2.537939	-1.389592	8463.123935	
HLA B*1503	1:30-38 9	DGGPALVEF	1.593417	0.842818	-3.827349	2.436235	-1.391114	6719.681059	
HLA A*1101	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-3.013050	1.621061	-1.391989	1030.50487
HLA B*4001	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.930162	2.537939	-1.392223	8514.558310	
HLA A*2601	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.119822	2.719390	-1.400432	13177.1640
HLA B*0801	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.133618	2.731374	-1.402244	13602.480977	
HLA B*0801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-2.743879	1.334180	-1.409699	554.471148
HLA A*0206	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.126948	1.715719	-1.411229	1339.51748
HLA B*0802	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.196147	2.784052	-1.412095	15708.9559
HLA A*3001	1:166-174	9	QARQAARAV	0.923681	0.228464	-2.568791	1.152145	-1.416646	370.50206
HLA B*5301	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-3.446286	2.027215	-1.419071	2794.38143
HLA A*6801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.034719	2.615600	-1.419119	10832.2557
HLA A*2501	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.338712	1.919326	-1.419386	2181.283768	
HLA B*7301	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.038572	2.615600	-1.422973	10928.7894
HLA A*1101	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-2.930527	1.502929		
HLA B*4501	1:201-209	9	SEHADVEIR	1.214047	0.687630	-3.331636	1.901677		

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HLA A*3101	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.215376	2.784052	-1.431323	16420.0889
HLA A*0250	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-2.993700	1.561696	-1.432004	985.597726	
HLA B*1517	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.076493	2.642684	-1.433809	11925.943538	
HLA B*5701	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-3.992828	2.554540	-1.438288	9836.20537
HLA A*6802	1:224-232	9	PAVFADFEV	1.069788	0.050175	-2.560657	1.119963	-1.440694	363.627495
HLA B*5701	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.003178	1.561696	-1.441481	1007.343330	
HLA A*6802	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.227565	2.784052	-1.443512	16887.4717
HLA A*0202	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-2.230963	0.784286	-1.446676	170.201303	
HLA B*1801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.166408	2.719390	-1.447017	14669.2374
HLA B*1801	1:30-38 9	DGGPALVEF	1.593417	0.842818	-3.883929	2.436235	-1.447694	7654.713809	
HLA A*3001	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.379866	1.928720	-1.451146	2398.09148
HLA B*3501	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.617728	2.164386	-1.453341	4146.93863
HLA B*4501	1:91-99 9	HELIRHRHF	1.404658	1.013097	-3.872947	2.417755	-1.455192	7463.584691	
HLA B*5401	1:175-183	9	LPNATETRI	1.064730	0.080627	-2.602445	1.145357	-1.457088	400.354445
HLA B*0702	1:167-175	9	ARQAARAVL	1.496924	0.533348	-3.489037	2.030272	-1.458765	3083.45004
HLA B*5801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.178225	2.719390	-1.458835	15073.8937
HLA A*6801	1:73-81 9	LEHASVSFY	1.292112	1.245827	-3.998222	2.537939	-1.460283	9959.143854	
HLA A*0202	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-2.081052	0.619672	-1.461379	120.517924	
HLA A*0301	1:135-143	9	AADAARATY	1.474911	1.206254	-4.143378	2.681165	-1.462213	13911.6258
HLA A*6802	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-2.588851	1.126312	-1.462538	388.016804
HLA B*0702	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.194188	2.731374	-1.462814	15638.239158	
HLA B*1801	1:135-143	9	AADAARATY	1.474911	1.206254	-4.148815	2.681165	-1.467650	14086.8729
HLA A*0101	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.130315	2.660014	-1.470301	13499.4088
HLA A*3101	1:209-217	9	RRLAIECLR	0.972846	0.851605	-3.295270	1.824451	-1.470819	1973.65023
HLA A*0211	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.190088	1.715719	-1.474369	1549.13207
HLA A*3201	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.395076	1.919326	-1.475751	2483.569471	
HLA A*2301	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.169244	1.691549	-1.477695	1476.535232	
HLA A*0206	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-2.097437	0.619672	-1.477765	125.151757	
HLA A*6901	1:70-78 9	FSVLEHASV	1.102668	0.135344	-2.719153	1.238012	-1.481141	523.784898	
HLA A*3201	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.500108	2.016506	-1.483602	3163.061894	
HLA B*0702	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.648910	2.164386	-1.484523	4455.63876
HLA A*0206	1:165-173	9	KQARQAARA	1.079552	-0.087775	-2.478702	0.991777	-1.486925	301.093915
HLA B*1502	1:91-99 9	HELIRHRHF	1.404658	1.013097	-3.906691	2.417755	-1.488936	8066.604584	
HLA A*2301	1:30-38 9	DGGPALVEF	1.593417	0.842818	-3.928470	2.436235	-1.492235	8481.457589	
HLA B*0702	1:135-143	9	AADAARATY	1.474911	1.206254	-4.173409	2.681165	-1.492244	14907.6437
HLA A*0101	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.212627	2.719390	-1.493236	16316.4851
HLA A*0203	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.225774	2.731374	-1.494400	16817.999180	
HLA B*1517	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-3.115770	1.621061	-1.494708	1305.47793
HLA A*0301	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-3.116113	1.621061	-1.495051	1306.50946
HLA B*1509	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.279251	2.784052	-1.495199	19021.7712
HLA A*1101	1:79-87 9	SFYITGISR	1.120990	0.841293	-3.462483	1.962283	-1.500200	2900.567907	
HLA A*3001	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.038784	2.537939	-1.500845	10934.111911	
HLA B*4801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.952635	1.451496	-1.501139	896.675687
HLA B*0802	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.233499	2.731374	-1.502125	17119.829441	
HLA B*1509	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.146949	2.642684	-1.504265	14026.493188	
HLA B*1503	1:39-47 9	AGRACYQSW	1.340001	0.305812	-3.150932	1.645813	-1.505119	1415.571884	
HLA A*3001	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.238269	2.731374	-1.506895	17308.876858	
HLA B*7301	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.437419	1.928720	-1.508699	2737.90724
HLA B*3901	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.240517	2.731374	-1.509143	17398.721856	
HLA A*6901	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.295007	2.784052	-1.510954	19724.5271
HLA A*0101	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.295063	2.784052	-1.511011	19727.0883
HLA A*3101	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-2.963086	1.451496	-1.511590	918.514260
HLA A*2603	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.037482	2.524670	-1.512812	10901.390577	
HLA A*0250	1:77-85 9	SVSFYITGI	0.979963	0.379282	-2.873303	1.359245	-1.514057	746.969180	
HLA A*6801	1:135-143	9	AADAARATY	1.474911	1.206254	-4.196833	2.681165	-1.515668	15733.7907
HLA B*3801	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.159312	2.642684	-1.516628	14431.520653	
HLA A*2602	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-2.685663	1.167504	-1.518159	484.912538
HLA B*4402	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.181886	2.660014	-1.521872	15201.4826
HLA A*2601	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.308244	2.784052	-1.524191	20334.9729
HLA B*1517	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.682451	2.158180	-1.524271	4813.39188
HLA A*2501	1:142-150	9	TYSELLAKL	1.344148	0.587133	-3.455848	1.931281	-1.524567	2856.59118
HLA A*0216	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.080059	2.554540	-1.525520	12024.2851
HLA B*3801	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.257685	2.731374	-1.526311	18100.269125	
HLA B*4801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.455618	1.928720	-1.526898	2855.07711
HLA A*2902	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.170190	2.642684	-1.527506	14797.563448	
HLA A*0203	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-2.699521	1.168653	-1.530868	500.634386
HLA B*4402	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.316629	2.784052	-1.532577	20731.4134
HLA B*1509	1:74-82 9	EHASVSFYI	0.978340	0.173645	-2.686317	1.151985	-1.534331	485.642370	
HLA B*1501	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.150093	2.615600	-1.534493	14128.3913
HLA B*5801	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.268678	2.731374	-1.537304	18564.286944	
HLA A*3001	1:87-95 9	RSCTHELIR	1.036000	0.794609	-3.368988	1.830609	-1.538378	2338.770629	
HLA A*6801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-3.213973	1.675398	-1.538575	1636.71593
HLA B*1503	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-2.411563	0.872645	-1.538918	257.966371
HLA A*0203	1:70-78 9	FSVLEHASV	1.102668	0.135344	-2.778139	1.238012	-1.540127	599.983273	
HLA B*4801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.324951	2.784052	-1.540899	21132.4956
HLA B*4601	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.275273	2.731374	-1.543899	18848.347364	
HLA A*0203	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.328823	2.784052	-1.544771	21321.7447
HLA B*5101	1:175-183	9	LPNATETRI	1.064730	0.080627	-2.691100	1.145357	-1.545743	491.021062
HLA B*4601	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.265314	2.719390	-1.545924	18421.0257
HLA B*4501	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-2.477353	0.927121	-1.550232	300.160385
HLA A*0216	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.283405	2.731374	-1.552031	19204.581366	
HLA A*0301	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.336155	2.784052	-1.552103	21684.8030
HLA A*6802	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.786392	2.233875	-1.552518	6114.94334
HLA A*0206	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.710960	2.158180	-1.552779	5139.96157
HLA A*3201	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.215507	2.660014	-1.555493	16425.0642
HLA A*0301	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.288400	2.731374	-1.557026	19426.736507	
HLA B*3501	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.177676	2.615600	-1.562076	15054.8235
HLA A*0201	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.293705	2.731374	-1.562331	19665.499724	
HLA B*5701	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-3.876885	2.313503	-1.563382	7531.56454
HLA A*2501	1:135-143	9	AADAARATY	1.474911	1.206254	-4.245938	2.681165	-1.564773	17617.2293
HLA A*0219	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.350431	2.784052	-1.566379	22409.4373
HLA A*2501	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.350595	2.784052	-1.566543	22417.9252
HLA A*3101	1:135-143	9	AADAARATY	1.474911	1.206254	-4.249018	2.681165	-1.567853	17742.6212
HLA B*1502	1:52-60 9	PKTATNAGY	1.018085	1.128286	-3.716321	2.146371	-1.569951	5203.809589	
HLA A*3001	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-2.443920	0.872645	-1.571275	277.920257
HLA A*8001	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.303185	2.731374	-1.571811	20099.495597	
HLA A*3201	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.357216	2.784052	-1.573164	22762.3064
HLA A*8001	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.358321	2.784052	-1.574268	22820.2565
HLA B*1801	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-3.732707	2.158014	-1.574693	5403.892555	
HLA A*0301	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-3.410221	1.834955	-1.575266	2571.70466
HLA A*3001	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.431211	1.855018	-1.576194	2699.05287
HLA A*0202	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.269576	1.691549	-1.578027	1860.271026	
HLA A*6801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.238438	2.660014	-1.578424	17315.6201
HLA A*6802	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-2.554459	0.973692	-1.580767	358.474917
HLA A*3201	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.480630	1.899550	-1.581081	3024.338928	
HLA A*0219	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.313027	2.731374	-1.581653	20560.191314	
HLA A*3001	1:79-87 9	SFYITGISR	1.120990	0.841293	-3.545063	1.962283	-1.582780	3508.025457	
HLA A*0101	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.314768	2.731374	-1.583394	20642.776947	
HLA B*2705	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-2.625587	1.041264	-1.584323	422.266941
HLA B*4402	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.227800	2.642684	-1.585116	16896.610118	
HLA B*1509	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.245874	2.660014	-1.585861	17614.6562
HLA A*0201	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.370028	2.784052	-1.585976	23443.7999
HLA B*2705	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.370524	2.784052	-1.586472	23470.5760
HLA B*1503	1:209-217	9	RRLAIECLR	0.972846	0.851605	-3.411086	1.824451	-1.586635	2576.82961
HLA B*4501	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-2.622147	1.034236	-1.587911	418.935763	
HLA A*1101	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.250747	2.660014		
HLA B*5401	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.374990	2.784052		

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HLA B*4402	1:135-143	9	AADAARATY	1.474911	1.206254	-4.272268	2.681165	-1.591103	18718.3811
HLA B*4001	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.322573	2.731374	-1.591199	21017.115410	
HLA A*0301	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.129535	2.537939	-1.591596	13475.184566	
HLA B*4001	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.235081	2.642684	-1.592397	17182.273871	
HLA A*3001	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-2.381772	0.789295	-1.592477	240.863851	
HLA A*6901	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.757287	2.164386	-1.592901	5718.56441
HLA B*1501	1:138-146	9	AARATYSEL	1.196073	0.462758	-3.251894	1.658831	-1.593063	1786.05158
HLA B*1503	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-2.751285	1.154646	-1.596639	564.007046
HLA B*4001	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.382339	2.784052	-1.598287	24117.8899
HLA A*6802	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.329676	2.731374	-1.598301	21363.657275	
HLA A*8001	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.241727	2.642684	-1.599043	17447.263902	
HLA B*1801	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.331421	2.731374	-1.600047	21449.702328	
HLA B*4001	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.319780	2.719390	-1.600389	20882.3596
HLA B*0803	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.385314	2.784052	-1.601262	24283.6383
HLA A*0301	1:87-95 9	RSCTHELIR	1.036000	0.794609	-3.432339	1.830609	-1.601730	2706.070736	
HLA A*0206	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.321948	2.719390	-1.602558	20986.8928
HLA A*3101	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.334022	2.731374	-1.602648	21578.544591	
HLA B*0802	1:135-143	9	AADAARATY	1.474911	1.206254	-4.285355	2.681165	-1.604190	19291.0078
HLA A*0212	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.388551	2.784052	-1.604499	24465.3451
HLA A*6802	1:57-65 9	NAGYLRHII	1.129740	0.203828	-2.939455	1.333568	-1.605887	869.870861	
HLA B*2705	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-3.920055	2.313503	-1.606552	8318.68423
HLA A*0206	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-3.765172	2.158014	-1.607158	5823.336537	
HLA B*3801	1:135-143	9	AADAARATY	1.474911	1.206254	-4.289182	2.681165	-1.608017	19461.7651
HLA B*0803	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.268798	2.660014	-1.608784	18569.4096
HLA A*0250	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.328877	2.719390	-1.609487	21324.3978
HLA A*0202	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.325536	1.715719	-1.609817	2116.10033
HLA A*0203	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.329208	2.719390	-1.609818	21340.6702
HLA B*1801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.269898	2.660014	-1.609884	18616.4837
HLA B*4402	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.227273	2.615600	-1.611674	16876.1469
HLA A*2501	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.343258	2.731374	-1.611884	22042.354108	
HLA A*2601	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.345318	2.731374	-1.613944	22147.181937	
HLA B*1503	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.554470	1.939903	-1.614568	3584.842455	
HLA A*0250	1:81-89 9	YITGISRSC	1.133968	-0.008438	-2.740679	1.125530	-1.615149	550.400670	
HLA A*6801	1:87-95 9	RSCTHELIR	1.036000	0.794609	-3.445910	1.830609	-1.615301	2791.963718	
HLA B*5701	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.774824	2.158180	-1.616643	5954.20212
HLA B*2705	1:86-94 9	SRSCTHELI	1.200502	0.345702	-3.164009	1.546204	-1.617805	1458.845035	
HLA A*0206	1:135-143	9	AADAARATY	1.474911	1.206254	-4.299344	2.681165	-1.618179	19922.4961
HLA B*3801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.278563	2.660014	-1.618549	18991.6437
HLA A*2402	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.338178	2.719390	-1.618788	21786.0446
HLA A*2501	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.174344	2.554540	-1.619804	14939.7764
HLA B*2705	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.352961	2.731374	-1.621587	22540.385952	
HLA A*0201	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.177389	2.554540	-1.622849	15044.8905
HLA A*0301	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.283395	2.660014	-1.623382	19204.1657
HLA B*5701	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.354954	2.731374	-1.623580	22644.029466	
HLA A*0212	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.180180	2.554540	-1.625641	15141.8946
HLA A*3001	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.270278	2.642684	-1.627594	18632.806414	
HLA A*2601	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.288024	2.660014	-1.628010	19409.9283
HLA A*3101	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.289622	2.660014	-1.629608	19481.4636
HLA A*0203	1:233-241	9	TTLADGTEV	1.178752	0.144786	-2.953298	1.323538	-1.629760	898.044689
HLA B*3901	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.272741	2.642684	-1.630057	18738.746332	
HLA A*6802	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.794954	2.164386	-1.630567	6236.68717
HLA B*2705	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.350130	2.719390	-1.630740	22393.9249
HLA B*4801	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.364135	2.731374	-1.632761	23127.862609	
HLA A*2403	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.051038	2.417755	-1.633283	11247.044886	
HLA A*2603	1:135-143	9	AADAARATY	1.474911	1.206254	-4.315743	2.681165	-1.634578	20689.1741
HLA B*1509	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.355116	2.719390	-1.635726	22652.4836
HLA A*1101	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.419790	2.784052	-1.635738	26289.9705
HLA B*4601	1:135-143	9	AADAARATY	1.474911	1.206254	-4.317672	2.681165	-1.636507	20781.2699
HLA A*0216	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.422278	2.784052	-1.638226	26441.0199
HLA B*4002	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.430450	1.790637	-1.639813	2694.326105	
HLA A*6901	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.656363	2.016506	-1.639857	4532.758070	
HLA A*6901	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.371499	2.731374	-1.640125	23523.329110	
HLA A*3001	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.257366	2.615600	-1.641766	18086.9568
HLA A*6802	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.362871	2.719390	-1.643481	23060.6463
HLA A*2601	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.181703	2.537939	-1.643764	15195.069376	
HLA B*4801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.363363	2.719390	-1.643972	23086.7350
HLA A*2301	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.304306	2.660014	-1.644292	20151.4296
HLA B*5801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.305208	2.660014	-1.645194	20193.3357
HLA A*6801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-3.367334	1.721985	-1.645349	2329.88021
HLA A*6901	1:135-143	9	AADAARATY	1.474911	1.206254	-4.326859	2.681165	-1.645694	21225.5312
HLA B*4402	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.378366	2.731374	-1.646992	23898.262624	
HLA A*3201	1:135-143	9	AADAARATY	1.474911	1.206254	-4.328870	2.681165	-1.647705	21324.0518
HLA A*3002	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-3.314010	1.665496	-1.648513	2060.67585
HLA A*3201	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.008224	1.359245	-1.648979	1019.117382	
HLA B*5801	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.815756	2.164386	-1.651370	6542.68936
HLA A*6901	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.370928	2.719390	-1.651538	23492.4255
HLA A*0202	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.571034	1.919326	-1.651708	3724.208127	
HLA A*3101	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.206518	2.554540	-1.651978	16088.5886
HLA B*2705	1:135-143	9	AADAARATY	1.474911	1.206254	-4.335676	2.681165	-1.654511	21660.8845
HLA A*0211	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.438741	2.784052	-1.654689	27462.5616
HLA B*2705	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.314954	2.660014	-1.654940	20651.6011
HLA A*2602	1:135-143	9	AADAARATY	1.474911	1.206254	-4.336261	2.681165	-1.655096	21690.0827
HLA B*3801	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.440503	2.784052	-1.656451	27574.2151
HLA A*1101	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-2.493405	0.836190	-1.657215	311.461991	
HLA B*4402	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.377316	2.719390	-1.657926	23840.5411
HLA A*0212	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.378387	2.719390	-1.658997	23899.4262
HLA B*3801	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.378524	2.719390	-1.659134	23906.9264
HLA B*5801	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.899708	2.233875	-1.665833	7937.94525
HLA B*1503	1:227-235	9	FADFEVTTL	1.891662	0.342213	-3.899840	2.233875	-1.665965	7940.35044
HLA A*0201	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.385741	2.719390	-1.666351	24307.5597
HLA B*4601	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.326635	2.660014	-1.666622	21214.6254
HLA B*0801	1:135-143	9	AADAARATY	1.474911	1.206254	-4.348666	2.681165	-1.667502	22318.5764
HLA B*3901	1:135-143	9	AADAARATY	1.474911	1.206254	-4.348782	2.681165	-1.667617	22324.4936
HLA A*2601	1:135-143	9	AADAARATY	1.474911	1.206254	-4.350755	2.681165	-1.669590	22426.1737
HLA A*1101	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.401948	2.731374	-1.670574	25231.792842	
HLA B*0802	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.226188	2.554540	-1.671648	16834.0199
HLA A*2603	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.332655	2.660014	-1.672641	21510.7101
HLA A*3001	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.078385	1.401827	-1.676558	1197.80061
HLA B*4801	1:135-143	9	AADAARATY	1.474911	1.206254	-4.359563	2.681165	-1.678398	22885.6578
HLA A*2601	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.234315	2.554540	-1.679775	17151.9975
HLA A*2403	1:135-143	9	AADAARATY	1.474911	1.206254	-4.361236	2.681165	-1.680071	22973.9797
HLA A*2301	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.098531	2.417755	-1.680776	12546.740572	
HLA A*0219	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-2.554402	0.873495	-1.680908	358.428376
HLA B*4601	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.296741	2.615600	-1.681141	19803.4347
HLA A*2902	1:52-60 9	PKTATNAGY	1.018085	1.128286	-3.831272	2.146371	-1.684902	6780.665183	
HLA B*0801	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.625749	1.939903	-1.685846	4224.241610	
HLA A*8001	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.240919	2.554540	-1.686379	17414.8247
HLA B*5101	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.407129	2.719390	-1.687739	25534.5803
HLA B*0803	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.230450	2.537939	-1.692511	17000.034475	
HLA B*4403	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.354505	2.660014	-1.694491	22620.6437
HLA A*2601	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.616092	1.919326	-1.696767	4131.353593	
HLA B*4001	1:135-143	9	AADAARATY	1.474911	1.206254	-4.378806	2.681165	-1.697641	23922.4515
HLA A*0301	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.222654	2.524670	-1.697984	16697.606067	
HLA A*2403	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.418068	2.719390	-1.698678	26185.9254
HLA B*1503	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-3.049086	1.349023	-1.700063	1119.66074
HLA A*6901	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.360971	2.660014		
HLA A*0203	1:138-146	9	AARATYSEL	1.196073	0.462758	-3.359966	1.658831		

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HLA B*5301	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.317491	2.615600	-1.701892	20772.615(
HLA B*3501	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.344644	2.642684	-1.701960	22112.822058	
HLA A*2601	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.345262	2.642684	-1.702578	22144.306592	
HLA A*2602	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.257300	2.554540	-1.702760	18084.2172
HLA B*5301	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.422344	2.719390	-1.702954	26445.0254
HLA B*5701	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.346040	2.642684	-1.703356	22183.995335	
HLA B*0802	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.363698	2.660014	-1.703685	23104.6021
HLA B*4601	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.260150	2.554540	-1.705610	18203.2796
HLA A*0211	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.425018	2.719390	-1.705628	26608.3352
HLA A*0216	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.425452	2.719390	-1.706062	26634.9789
HLA A*2501	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.322587	2.615600	-1.706988	21017.7976
HLA B*4403	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.020566	2.313503	-1.707063	10484.9317
HLA B*3901	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-3.056539	1.349023	-1.707516	1139.04011
HLA B*1501	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.143914	2.436235	-1.707679	13928.795767	
HLA B*1517	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.144163	2.436235	-1.707928	13936.785501	
HLA B*5101	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.439935	2.731374	-1.708560	27538.138756	
HLA B*0801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.563652	1.855018	-1.708634	3661.43949
HLA B*1501	1:211-219	9	LAIECLRQL	1.635667	0.528719	-3.873507	2.164386	-1.709120	7473.20064
HLA A*0201	1:135-143	9	AADAARATY	1.474911	1.206254	-4.390941	2.681165	-1.709776	24600.3209
HLA A*3001	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.235419	2.524670	-1.710749	17195.664491	
HLA B*4001	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.371952	2.660014	-1.711939	23547.9028
HLA B*0803	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.266526	2.554540	-1.711987	18472.5199
HLA B*5701	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.372786	2.660014	-1.712773	23593.1702
HLA B*1509	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.444253	2.731374	-1.712879	27813.326712	
HLA B*1517	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-2.549586	0.836190	-1.713396	354.475269	
HLA A*3001	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.268119	2.554540	-1.713579	18540.3998
HLA A*0219	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.268850	2.554540	-1.714310	18571.6198
HLA A*3101	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.358212	2.642684	-1.715529	22814.578367	
HLA B*0803	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.358407	2.642684	-1.715724	22824.824887	
HLA B*1517	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.133562	2.417755	-1.715807	13600.714982	
HLA B*4601	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.358645	2.642684	-1.715961	22837.299752	
HLA A*3201	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.358913	2.642684	-1.716229	22851.388484	
HLA A*0219	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.436547	2.719390	-1.717157	27324.1478
HLA B*5801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.334299	2.615600	-1.718700	21592.3240
HLA B*5801	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.256682	2.537939	-1.718743	18058.505350	
HLA A*0101	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.257154	2.537939	-1.719215	18078.152627	
HLA A*0101	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.335054	2.615600	-1.719454	21629.8532
HLA A*0203	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.363473	2.642684	-1.720789	23092.605902	
HLA B*4801	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.363687	2.642684	-1.721003	23103.977189	
HLA B*5301	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.452495	2.731374	-1.721121	28346.205462	
HLA A*0301	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.363894	2.642684	-1.721210	23114.978924	
HLA A*2301	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.441582	2.719390	-1.722191	27642.7708
HLA A*0301	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.337826	2.615600	-1.722226	21768.3727
HLA A*0206	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-2.608600	0.885414	-1.723186	406.069439
HLA B*1801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.338982	2.615600	-1.723382	21826.3900
HLA B*0801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.383871	2.660014	-1.723858	24203.1098
HLA A*0212	1:135-143	9	AADAARATY	1.474911	1.206254	-4.405543	2.681165	-1.724378	25441.5063
HLA A*6801	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.249462	2.524670	-1.724792	17760.771820	
HLA A*0202	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.445985	2.719390	-1.726594	27924.4422
HLA A*0301	1:41-49 9	RACYQSWSK	0.781972	0.322141	-2.830791	1.104113	-1.726678	677.315636	
HLA B*2705	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.281511	2.554540	-1.726972	19121.0245
HLA A*1101	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.582965	1.855018	-1.727947	3827.93564
HLA A*2403	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.164707	2.436235	-1.728471	14611.893992	
HLA A*3201	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-3.756239	2.027215	-1.729024	5704.78323
HLA A*0219	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-2.785606	1.056254	-1.729352	610.387746
HLA B*1509	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.345114	2.615600	-1.729515	22136.7605
HLA A*0250	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.445360	1.715719	-1.729641	2788.43156
HLA B*0803	1:135-143	9	AADAARATY	1.474911	1.206254	-4.411165	2.681165	-1.730000	25773.0098
HLA A*0203	1:135-143	9	AADAARATY	1.474911	1.206254	-4.411409	2.681165	-1.730245	25787.5145
HLA A*3101	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-2.521110	0.789295	-1.731816	331.978671	
HLA B*2705	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.183392	1.451496	-1.731896	1525.43045
HLA B*4801	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.392259	2.660014	-1.732245	24675.0950
HLA B*0802	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.376647	2.642684	-1.733963	23803.811714	
HLA B*3901	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.453735	2.719390	-1.734345	28427.2899
HLA A*0206	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.296168	1.561696	-1.734472	1977.733150	
HLA B*3901	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.259250	2.524670	-1.734580	18165.601770	
HLA B*1517	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.259886	2.524670	-1.735217	18192.253527	
HLA A*0201	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.396939	2.660014	-1.736925	24942.4441
HLA B*4601	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.173461	2.436235	-1.737226	14909.418107	
HLA A*0219	1:135-143	9	AADAARATY	1.474911	1.206254	-4.418834	2.681165	-1.737669	26232.1483
HLA A*0101	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.380690	2.642684	-1.738006	24026.470093	
HLA A*0202	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-2.700193	0.962074	-1.738119	501.409581	
HLA B*0802	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.355475	2.615600	-1.739876	22671.2411
HLA A*6901	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.382696	2.642684	-1.740013	24137.730289	
HLA B*1509	1:135-143	9	AADAARATY	1.474911	1.206254	-4.421190	2.681165	-1.740025	26374.8739
HLA A*6901	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.356133	2.615600	-1.740534	22705.6088
HLA B*0801	1:208-216	9	IRRLAIECL	1.768404	0.464239	-3.974972	2.232643	-1.742329	9439.98929
HLA A*0201	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.385492	2.642684	-1.742808	24293.624666	
HLA B*4403	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.385617	2.642684	-1.742933	24300.591233	
HLA A*6802	1:135-143	9	AADAARATY	1.474911	1.206254	-4.424823	2.681165	-1.743658	26596.3902
HLA B*1509	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.162221	2.417755	-1.744466	14528.499328	
HLA B*0801	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.387386	2.642684	-1.744702	24399.785156	
HLA A*0301	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.300042	2.554540	-1.745502	19954.5320
HLA A*0216	1:135-143	9	AADAARATY	1.474911	1.206254	-4.426761	2.681165	-1.745596	26715.3594
HLA B*5301	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.288191	2.537939	-1.750252	19417.385171	
HLA B*4001	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.366581	2.615600	-1.750982	23258.4791
HLA B*4403	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.367173	2.615600	-1.751574	23290.2088
HLA A*3301	1:33-41 9	PALVEFAGR	1.046707	0.453047	-3.252486	1.499754	-1.752732	1788.488154	
HLA A*0250	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-2.947335	1.194587	-1.752748	885.798531	
HLA A*6801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.309280	2.554540	-1.754740	20383.5453
HLA A*0202	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-2.728462	0.973692	-1.754770	535.132875
HLA B*5301	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.397679	2.642684	-1.754995	24984.985176	
HLA A*0250	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.539962	2.784052	-1.755909	34670.6160
HLA A*6802	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.311051	2.554540	-1.756512	20466.8607
HLA A*3001	1:89-97 9	CTHELIRHR	1.005015	0.652731	-3.414507	1.657746	-1.756761	2597.206934	
HLA B*3901	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.697652	1.939903	-1.757750	4984.853384	
HLA B*1517	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.071277	2.313503	-1.757774	11783.5701
HLA A*0216	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.418094	2.660014	-1.758080	26187.4837
HLA A*0201	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-2.814890	1.056254	-1.758636	652.964826
HLA B*3901	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.418916	2.660014	-1.758902	26237.1157
HLA A*2603	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.543542	2.784052	-1.759490	34957.6454
HLA A*1101	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.297570	2.537939	-1.759631	19841.289308	
HLA A*3301	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.543838	2.784052	-1.759786	34981.4823
HLA A*2402	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.073875	2.313503	-1.760373	11854.2865
HLA A*0212	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.404986	2.642684	-1.762302	25408.907632	
HLA B*1517	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-2.763229	1.000751	-1.762478	579.734720
HLA A*0101	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.317348	2.554540	-1.762808	20765.7611
HLA B*4403	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.546996	2.784052	-1.762944	35236.7557
HLA A*1101	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.378799	2.615600	-1.763199	23922.0632
HLA A*0202	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-2.819589	1.056254	-1.763335	660.068119
HLA A*1101	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.288527	2.524670	-1.763857	19432.412546	
HLA B*7301	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.289168	2.524670	-1.764498	19461.133475	
HLA A*3101	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.380105	2.615600	-1.764505	23994.1267
HLA A*6802	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.380948	2.615600	-1.765349	24040.7722
HLA A*0206	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.409039	2.642684	-1.7663[illegible]	[illegible]	
HLA A*2501	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.409182	2.642684	-1.7664[illegible]		
HLA B*3901	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.382645	2.615600		

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HLA B*1509	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.001333	2.233875	-1.767458	10030.7342
HLA A*3101	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.293174	2.524670	-1.768504	19641.470689
HLA B*0702	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.384200	2.615600	-1.768601	24221.4479
HLA B*4601	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.306918	2.537939	-1.768980	20273.021945
HLA B*2705	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.294389	2.524670	-1.769719	19696.483064
HLA B*4601	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.294927	2.524670	-1.770257	19720.899461
HLA B*0801	1:138-146	9	AARATYSEL	1.196073	0.462758	-3.429867	1.658831	-1.771036	2690.71367
HLA B*0702	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.413891	2.642684	-1.771207	25935.256207
HLA B*1502	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.414123	2.642684	-1.771439	25949.150307
HLA B*5101	1:135-143	9	AADAARATY	1.474911	1.206254	-4.453510	2.681165	-1.772345	28412.5300
HLA A*2403	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.388121	2.615600	-1.772522	24441.1361
HLA A*2501	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.297199	2.524670	-1.772529	19824.336965
HLA A*6802	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.432985	2.660014	-1.772971	27100.9682
HLA B*3801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.388939	2.615600	-1.773339	24487.1934
HLA A*0206	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-2.806610	1.032480	-1.774130	640.634322
HLA A*0203	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.435351	2.660014	-1.775337	27249.0106
HLA B*4801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.391754	2.615600	-1.776154	24646.4114
HLA A*0212	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.437033	2.660014	-1.777019	27354.7638
HLA A*0201	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.393314	2.615600	-1.777714	24735.1046
HLA A*1101	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.421536	2.642684	-1.778852	26395.856996
HLA A*3101	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.317146	2.537939	-1.779207	20756.102117
HLA A*0203	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.395313	2.615600	-1.779714	24849.2430
HLA B*1801	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.422419	2.642684	-1.779735	26449.603937
HLA B*5701	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.395377	2.615600	-1.779777	24852.8730
HLA B*4801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.334689	2.554540	-1.780150	21611.7235
HLA B*1503	1:70-78	9	FSVLEHASV	1.102668	0.135344	-3.019060	1.238012	-1.781048	1044.864644
HLA B*0702	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.446048	2.660014	-1.786034	27928.5214
HLA A*2403	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.188524	1.401827	-1.786697	1543.56061
HLA A*6802	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.429775	2.642684	-1.787092	26901.432745
HLA B*4001	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-3.727026	1.939903	-1.787123	5333.663967
HLA A*2603	1:52-60	9	PKTATNAGY	1.018085	1.128286	-3.936459	2.146371	-1.790088	8638.905907
HLA A*2603	1:72-80	9	VLEHASVSF	1.635346	1.096028	-4.521910	2.731374	-1.790536	33259.097869
HLA A*0211	1:135-143	9	AADAARATY	1.474911	1.206254	-4.473387	2.681165	-1.792222	29743.1219
HLA B*0702	1:53-61	9	KTATNAGYL	1.501925	0.397625	-3.692432	1.899550	-1.792882	4925.290304
HLA B*1517	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.409513	2.615600	-1.793914	25675.1773
HLA A*3001	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.212030	2.417755	-1.794275	16294.079829
HLA A*0219	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.454678	2.660014	-1.794664	28489.0260
HLA A*0250	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.149024	1.354114	-1.794910	1409.36715
HLA B*1801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.350760	2.554540	-1.796220	22426.4163
HLA B*1509	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.351671	2.554540	-1.797132	22473.5396
HLA B*5101	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.458207	2.660014	-1.798193	28721.4610
HLA B*1517	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-3.957238	2.158014	-1.799224	9062.282349
HLA B*2705	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-2.424805	0.625007	-1.799798	265.952938
HLA A*0301	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.656048	1.855018	-1.801030	4529.47335
HLA A*6901	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.253515	1.451496	-1.802019	1792.73105
HLA A*0212	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.417852	2.615600	-1.802252	26172.8956
HLA A*0219	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.446184	2.642684	-1.803500	27937.286013
HLA A*2902	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.118732	2.313503	-1.805229	13144.1283
HLA B*0802	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.343310	2.537939	-1.805371	22044.977692
HLA B*5701	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.343928	2.537939	-1.805989	22076.365629
HLA B*0801	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.421738	2.615600	-1.806138	26408.1405
HLA B*5401	1:93-101	9	LIRHRHFSY	1.443589	1.275801	-4.525547	2.719390	-1.806157	33538.7959
HLA B*5801	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.330904	2.524670	-1.806234	21424.188601
HLA B*0802	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.224600	2.417755	-1.806844	16772.568895
HLA B*1503	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-3.641941	1.834955	-1.806986	4384.71531
HLA A*6802	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-3.115694	1.308218	-1.807477	1305.251954
HLA B*5301	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.467557	2.660014	-1.807544	29346.5788
HLA A*6901	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.362601	2.554540	-1.808062	23046.3039
HLA A*6801	1:72-80	9	VLEHASVSF	1.635346	1.096028	-4.540300	2.731374	-1.808926	34697.635801
HLA A*0203	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.347219	2.537939	-1.809281	22244.323721
HLA B*4402	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.126048	2.313503	-1.812545	13367.4351
HLA B*4403	1:135-143	9	AADAARATY	1.474911	1.206254	-4.494067	2.681165	-1.812902	31193.6875
HLA B*0801	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.339102	2.524670	-1.814432	21832.412891
HLA A*2402	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.232318	2.417755	-1.814563	17073.306730
HLA B*0801	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.354738	2.537939	-1.816799	22632.762115
HLA A*0216	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.460728	2.642684	-1.818044	28888.668553
HLA B*0702	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.372772	2.554540	-1.818233	23592.4044
HLA A*0212	1:53-61	9	KTATNAGYL	1.501925	0.397625	-3.717830	1.899550	-1.818280	5221.914617
HLA B*0801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.748608	1.928720	-1.819888	5605.41820
HLA B*5801	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-3.512405	1.691549	-1.820856	3253.905191
HLA B*0802	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.346728	2.524670	-1.822058	22219.187015
HLA B*2705	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.240024	2.417755	-1.822269	17378.966797
HLA A*2602	1:72-80	9	VLEHASVSF	1.635346	1.096028	-4.553990	2.731374	-1.822616	35808.846654
HLA B*0801	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.057866	2.233875	-1.823991	11425.2584
HLA A*0202	1:233-241	9	TTLADGTEV	1.178752	0.144786	-3.148479	1.323538	-1.824941	1407.59937
HLA A*0250	1:135-143	9	AADAARATY	1.474911	1.206254	-4.506225	2.681165	-1.825060	32079.3310
HLA A*3001	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.140206	2.313503	-1.826703	13810.3944
HLA B*0803	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.442709	2.615600	-1.827110	27714.6453
HLA B*1509	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.352303	2.524670	-1.827634	22506.268322
HLA B*7301	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.611853	2.784052	-1.827801	40912.2580
HLA A*6801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-3.872421	2.044564	-1.827857	7454.54568
HLA B*5101	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.443557	2.615600	-1.827958	27768.8241
HLA A*0211	1:100-108	9	SYSQLSQRY	1.299924	1.360090	-4.488261	2.660014	-1.828248	30779.4702
HLA B*5801	1:222-230	9	VAPAVFADF	0.948144	1.210036	-3.987405	2.158180	-1.829225	9714.15383
HLA A*0101	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.354834	2.524670	-1.830164	22637.782742
HLA B*5101	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.472872	2.642684	-1.830188	29707.904156
HLA B*5801	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.267170	2.436235	-1.830935	18499.922251
HLA B*5301	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.385506	2.554540	-1.830967	24294.4132
HLA A*2301	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.446767	2.615600	-1.831167	27974.7932
HLA B*3801	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.386442	2.554540	-1.831902	24346.7787
HLA B*4002	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.616083	2.784052	-1.832030	41312.5995
HLA B*5401	1:72-80	9	VLEHASVSF	1.635346	1.096028	-4.563877	2.731374	-1.832503	36633.377912
HLA A*2602	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-3.860378	2.027215	-1.833163	7250.66300
HLA B*2705	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.372502	2.537939	-1.834563	23577.731344
HLA A*2403	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.372746	2.537939	-1.834808	23591.000579
HLA A*0219	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.450813	2.615600	-1.835213	28236.6193
HLA A*2402	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.237125	1.401827	-1.835298	1726.33523
HLA A*3001	1:140-148	9	RATYSELLA	1.126115	-0.051132	-2.910655	1.074983	-1.835671	814.056964
HLA A*2601	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.360367	2.524670	-1.835697	22928.039687
HLA A*6901	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.374368	2.537939	-1.836429	23679.226184
HLA A*0206	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.374941	2.537939	-1.837002	23710.503708
HLA B*4002	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-2.410506	0.573275	-1.837231	257.339129
HLA B*0803	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.362362	2.524670	-1.837692	23033.590290
HLA B*4402	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.392442	2.554540	-1.837902	24685.5094
HLA B*1509	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.376348	2.537939	-1.838409	23787.462781
HLA B*3901	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-3.758612	1.919326	-1.839286	5736.039417
HLA A*3301	1:72-80	9	VLEHASVSF	1.635346	1.096028	-4.571384	2.731374	-1.840009	37272.074952
HLA B*0803	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.257962	2.417755	-1.840207	18111.827427
HLA A*0216	1:36-44	9	VEFAGRACY	1.217312	1.307358	-4.365580	2.524670	-1.840910	23204.939049
HLA A*0202	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.484791	2.642684	-1.842107	30534.509751
HLA B*4001	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.396878	2.554540	-1.842338	24938.9360
HLA A*2603	1:62-70	9	RHIIDVGHF	1.382898	1.259786	-4.485564	2.642684	-1.842880	30588.905099
HLA B*4801	1:73-81	9	LEHASVSFY	1.292112	1.245827	-4.382086	2.537939	-1.844147	24103.802720
HLA B*4403	1:201-209	9	SEHADVEIR	1.214047	0.687630	-3.747222	1.901677	-1.845545	5587.55516
HLA A*0212	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.010082	2.164386	-1.845696	10234.8670
HLA B*4501	1:219-227	9	LAAVAPAVF	1.673668	1.110384	-4.632313	2.784052		
HLA A*2301	1:135-143	9	AADAARATY	1.474911	1.206254	-4.530792	2.681165		

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HLA B*4403	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.581181	2.731374	-1.849807	38122.460511
HLA A*2402	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.286751	2.436235	-1.850515	19353.098687
HLA A*2501	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.389038	2.537939	-1.851099	24492.757932
HLA A*2603	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.770858	1.919326	-1.851532	5900.076503
HLA A*6802	1:142-150	9 TYSELLAKL	1.344148	0.587133	-3.783225	1.931281	-1.851944	6070.51214
HLA A*3001	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.288581	2.436235	-1.852346	19434.830622
HLA B*4601	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.017201	2.164386	-1.852815	10404.0192
HLA A*0201	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.390783	2.537939	-1.852845	24591.405866
HLA A*0206	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-2.637292	0.784286	-1.853006	433.802665
HLA A*2602	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.378021	2.524670	-1.853351	23879.264997
HLA A*3301	1:100-108	9 SYSQLSQRY	1.299924	1.360090	-4.513708	2.660014	-1.853695	32636.8633
HLA A*0211	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.496576	2.642684	-1.853892	31374.438948
HLA A*0212	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.392271	2.537939	-1.854332	24675.762503
HLA B*4002	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.585849	2.731374	-1.854475	38534.466435
HLA A*0201	1:233-241	9 TTLADGTEV	1.178752	0.144786	-3.178256	1.323538	-1.854719	1507.49693
HLA A*0211	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-2.480008	0.625007	-1.855001	302.000938
HLA A*0202	1:135-143	9 AADAARATY	1.474911	1.206254	-4.536296	2.681165	-1.855131	34379.2471
HLA A*2403	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.015232	2.158014	-1.857219	10356.959475
HLA B*0702	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.383314	2.524670	-1.858644	24172.097916
HLA A*6901	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.385584	2.524670	-1.860914	24298.750814
HLA B*1501	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.877552	2.016506	-1.861046	7543.144995
HLA B*7301	1:93-101	9 LIRHRHFSY	1.443589	1.275801	-4.580537	2.719390	-1.861147	38065.9930
HLA A*3301	1:135-143	9 AADAARATY	1.474911	1.206254	-4.542429	2.681165	-1.861264	34868.1188
HLA A*0216	1:181-189	9 TRIVVTGNY	1.308245	1.307355	-4.477463	2.615600	-1.861863	30023.6098
HLA B*5401	1:135-143	9 AADAARATY	1.474911	1.206254	-4.543519	2.681165	-1.862354	34955.7543
HLA B*3901	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.400827	2.537939	-1.862889	25166.765707
HLA B*1503	1:87-95 9	RSCTHELIR	1.036000	0.794609	-3.693771	1.830609	-1.863162	4940.501551
HLA B*5701	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.387922	2.524670	-1.863252	24429.899755
HLA A*0250	1:100-108	9 SYSQLSQRY	1.299924	1.360090	-4.523280	2.660014	-1.863267	33364.1615
HLA A*2402	1:135-143	9 AADAARATY	1.474911	1.206254	-4.544992	2.681165	-1.863827	35074.5256
HLA A*0301	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-2.994531	1.130392	-1.864140	987.487054
HLA B*1503	1:191-199	9 AWRHFIAMR	1.152543	0.892021	-3.909012	2.044564	-1.864448	8109.83577
HLA A*0202	1:100-108	9 SYSQLSQRY	1.299924	1.360090	-4.524892	2.660014	-1.864878	33488.2120
HLA B*5101	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.403076	2.537939	-1.865137	25297.398563
HLA B*5701	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.283576	2.417755	-1.865821	19212.167174
HLA B*4801	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.391340	2.524670	-1.866670	24622.955804
HLA A*0202	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.404796	2.537939	-1.866857	25397.775862
HLA B*7301	1:189-197	9 YRAWRHFIA	1.123021	-0.081757	-2.908409	1.041264	-1.867145	809.857649
HLA A*3201	1:200-208	9 ASEHADVEI	1.329405	0.306162	-3.503787	1.635567	-1.868220	3189.97282
HLA A*3101	1:174-182	9 VLPNATETR	1.038504	0.740297	-3.647514	1.778801	-1.868713	4441.34366
HLA A*0201	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.393880	2.524670	-1.869210	24767.374947
HLA A*3001	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.102455	2.232643	-1.869812	12660.6078
HLA B*1509	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.044808	2.172078	-1.872730	11086.8352
HLA A*0219	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.397630	2.524670	-1.872960	24982.146852
HLA A*0212	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.398165	2.524670	-1.873495	25012.980211
HLA B*4002	1:201-209	9 SEHADVEIR	1.214047	0.687630	-3.775317	1.901677	-1.873640	5960.9704
HLA A*6802	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.413012	2.537939	-1.875073	25882.834492
HLA B*1517	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-3.062051	1.185494	-1.876556	1153.588480
HLA A*0206	1:100-108	9 SYSQLSQRY	1.299924	1.360090	-4.537910	2.660014	-1.877897	34507.2585
HLA A*0219	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.416080	2.537939	-1.878142	26066.352419
HLA A*1101	1:146-154	9 LLAKLEAKF	1.509592	1.044948	-4.432917	2.554540	-1.878377	27096.7167
HLA A*6802	1:214-222	9 ECLRQLAAV	1.100507	0.066997	-3.046742	1.167504	-1.879237	1113.6319
HLA A*2402	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.038746	2.158014	-1.880732	10933.165515
HLA B*4002	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.523658	2.642684	-1.880975	33393.234090
HLA B*0702	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.419682	2.537939	-1.881743	26283.428967
HLA A*8001	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.299569	2.417755	-1.881814	19932.845539
HLA A*6901	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.318415	2.436235	-1.882179	20816.826406
HLA A*0206	1:173-181	9 AVLPNATET	1.134394	-0.118673	-2.898231	1.015721	-1.882510	791.098788
HLA B*3501	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.300974	2.417755	-1.883219	19997.434982
HLA A*2902	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.300995	2.417755	-1.883240	19998.408660
HLA A*0206	1:181-189	9 TRIVVTGNY	1.308245	1.307355	-4.499191	2.615600	-1.883591	31563.9208
HLA A*0206	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.408325	2.524670	-1.883655	25604.990124
HLA A*0101	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.118990	2.233875	-1.885116	13151.9525
HLA B*5101	1:146-154	9 LLAKLEAKF	1.509592	1.044948	-4.440879	2.554540	-1.886339	27598.0931
HLA A*2403	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.411562	2.524670	-1.886892	25796.584165
HLA A*2902	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.324262	2.436235	-1.888027	21099.025099
HLA A*3101	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.306467	2.417755	-1.888712	20251.975315
HLA A*3002	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.047439	2.158180	-1.889259	11154.2151
HLA A*3201	1:174-182	9 VLPNATETR	1.038504	0.740297	-3.668129	1.778801	-1.889328	4657.24152
HLA A*3201	1:181-189	9 TRIVVTGNY	1.308245	1.307355	-4.505849	2.615600	-1.890250	32051.5757
HLA B*4002	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.204089	2.313503	-1.890586	15998.8431
HLA B*7301	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.624520	2.731374	-1.893145	42123.022262
HLA B*4002	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-2.628815	0.735649	-1.893167	425.417425
HLA A*3001	1:161-169	9 ILRRKQARQ	1.020477	0.059526	-2.973461	1.080003	-1.893458	940.721845
HLA A*3001	1:39-47 9	AGRACYQSW	1.340001	0.305812	-3.539499	1.645813	-1.893686	3463.372114
HLA B*3501	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.684514	1.790637	-1.893877	4836.309314
HLA A*2402	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-3.202146	1.308218	-1.893928	1592.744090
HLA A*0203	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.418740	2.524670	-1.894070	26226.472404
HLA B*3801	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.433333	2.537939	-1.895394	27122.675687
HLA B*5701	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.332131	2.436235	-1.895896	21484.775206
HLA B*2705	1:192-200	9 WRHFIAMRA	1.140260	-0.074001	-2.963673	1.066259	-1.897414	919.757366
HLA B*3901	1:146-154	9 LLAKLEAKF	1.509592	1.044948	-4.452065	2.554540	-1.897525	28318.1563
HLA B*5301	1:154-162	9 FADQPNAIL	1.350025	0.365694	-3.613499	1.715719	-1.897779	4106.75254
HLA B*3501	1:184-192	9 VVTGNYRAW	1.568491	0.458724	-3.925454	2.027215	-1.898239	8422.74700
HLA B*4002	1:93-101	9 LIRHRHFSY	1.443589	1.275801	-4.617779	2.719390	-1.898389	41474.2795
HLA A*0211	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.438532	2.537939	-1.900593	27449.342195
HLA A*0216	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.439032	2.537939	-1.901094	27480.990478
HLA B*0803	1:188-196	9 NYRAWRHFI	1.295038	0.370458	-3.568755	1.665496	-1.903259	3704.71618
HLA B*4403	1:93-101	9 LIRHRHFSY	1.443589	1.275801	-4.623084	2.719390	-1.903694	41984.0169
HLA A*3201	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.062194	2.158180	-1.904013	11539.6804
HLA B*0702	1:175-183	9 LPNATETRI	1.064730	0.080627	-3.049773	1.145357	-1.904416	1121.43085
HLA B*4501	1:135-143	9 AADAARATY	1.474911	1.206254	-4.585772	2.681165	-1.904607	38527.5876
HLA B*5401	1:100-108	9 SYSQLSQRY	1.299924	1.360090	-4.565033	2.660014	-1.905019	36731.0135
HLA B*5101	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.139619	2.233875	-1.905744	13791.7285
HLA A*6801	1:201-209	9 SEHADVEIR	1.214047	0.687630	-3.809126	1.901677	-1.907449	6443.56263
HLA A*3301	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.433170	2.524670	-1.908500	27112.553160
HLA A*6802	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.433170	2.524670	-1.908500	27112.553160
HLA B*3801	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.433208	2.524670	-1.908538	27114.900076
HLA B*4501	1:93-101	9 LIRHRHFSY	1.443589	1.275801	-4.630847	2.719390	-1.911457	42741.1975
HLA A*3101	1:188-196	9 NYRAWRHFI	1.295038	0.370458	-3.577119	1.665496	-1.911623	3776.75758
HLA B*4501	1:72-80 9	VLEHASVSF	1.635346	1.096028	-4.643123	2.731374	-1.911749	43966.586184
HLA A*2603	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.330420	2.417755	-1.912665	21400.325989
HLA A*0301	1:79-87 9	SFYITGISR	1.120990	0.841293	-3.876382	1.962283	-1.914099	7522.850171
HLA B*5801	1:39-47 9	AGRACYQSW	1.340001	0.305812	-3.560175	1.645813	-1.914362	3632.240728
HLA A*0216	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.814389	1.899550	-1.914839	6522.121741
HLA A*0206	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.705861	1.790637	-1.915224	5079.974003
HLA B*3901	1:218-226	9 QLAAVAPAV	1.059036	0.214314	-3.189539	1.273350	-1.916189	1547.17224
HLA A*0203	1:165-173	9 KQARQAARA	1.079552	-0.087775	-2.908352	0.991777	-1.916576	809.752506
HLA A*2402	1:181-189	9 TRIVVTGNY	1.308245	1.307355	-4.532777	2.615600	-1.917177	34101.7631
HLA A*3301	1:182-190	9 RIVVTGNYR	0.991278	0.843677	-3.752494	1.834955	-1.917539	5655.80032
HLA B*5401	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.560555	2.642684	-1.917871	36354.216932
HLA A*0216	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.277137	1.359245	-1.917891	1892.940070
HLA B*0801	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.083057	2.164386	-1.918671	12107.5761
HLA B*5801	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.336743	2.417755	-1.918988	21714.150976
HLA B*4801	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.084044	2.164386	-1.919658	12135.117
HLA B*3501	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.078090	2.158014	-1.9200	
HLA A*3101	1:141-149	9 ATYSELLAK	0.738811	0.394589	-3.053771	1.133400		

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HLA B*1501	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.615185	1.691549	-1.923636	4122.735431
HLA B*5101	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.448571	2.524670	-1.923901	28091.264615
HLA A*0211	1:181-189 9	TRIVVTGNY	1.308245	1.307355	-4.541214	2.615600	-1.925614	34770.7320
HLA B*7301	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.568743	2.642684	-1.926059	37046.121746
HLA B*4601	1:222-230 9	VAPAVFADF	0.948144	1.210036	-4.084941	2.158180	-1.926761	12160.2218
HLA A*3201	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.344907	2.417755	-1.927152	22126.224444
HLA A*0250	1:142-150 9	TYSELLAKL	1.344148	0.587133	-3.859109	1.931281	-1.927828	7229.51226
HLA B*4501	1:100-108 9	SYSQLSQRY	1.299924	1.360090	-4.588453	2.660014	-1.928439	38766.1417
HLA A*2601	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.365197	2.436235	-1.928962	23184.485676
HLA A*2501	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.365294	2.436235	-1.929059	23189.628692
HLA A*0203	1:242-250 9	ATSPLATEA	1.133303	-0.159611	-2.902963	0.973692	-1.929271	799.765346
HLA A*0301	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.365703	2.436235	-1.929468	23211.467847
HLA A*3101	1:104-112 9	LSQRYVPEK	0.751083	0.186483	-2.867227	0.937566	-1.929661	736.591860
HLA B*4601	1:227-235 9	FADFEVTTL	1.891662	0.342213	-4.163696	2.233875	-1.929822	14577.9425
HLA B*1502	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.366739	2.436235	-1.930504	23266.910975
HLA B*5301	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.455284	2.524670	-1.930614	28528.817406
HLA B*0702	1:154-162 9	FADQPNAIL	1.350025	0.365694	-3.647082	1.715719	-1.931363	4436.92486
HLA B*2705	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-2.774154	0.842742	-1.931413	594.503501
HLA B*4402	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.367944	2.436235	-1.931709	23331.572693
HLA B*3501	1:175-183 9	LPNATETRI	1.064730	0.080627	-3.077111	1.145357	-1.931754	1194.29361
HLA B*4403	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.090425	2.158014	-1.932412	12314.738523
HLA B*2705	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.090881	2.158014	-1.932867	12327.669853
HLA A*0202	1:181-189 9	TRIVVTGNY	1.308245	1.307355	-4.550318	2.615600	-1.934719	35507.3358
HLA B*5101	1:211-219 9	LAIECLRQL	1.635667	0.528719	-4.099226	2.164386	-1.934840	12566.8481
HLA A*0101	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.371233	2.436235	-1.934998	23508.953282
HLA A*3101	1:33-41 9	PALVEFAGR	1.046707	0.453047	-3.435995	1.499754	-1.936241	2728.946009
HLA B*4801	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.354498	2.417755	-1.936743	22620.276605
HLA B*0802	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.375289	2.436235	-1.939053	23729.495447
HLA A*3201	1:227-235 9	FADFEVTTL	1.891662	0.342213	-4.173931	2.233875	-1.940056	14925.5584
HLA B*5401	1:181-189 9	TRIVVTGNY	1.308245	1.307355	-4.555872	2.615600	-1.940273	35964.3545
HLA B*7301	1:135-143 9	AADAARATY	1.474911	1.206254	-4.621994	2.681165	-1.940829	41878.7612
HLA A*0211	1:81-89 9	YITGISRSC	1.133968	-0.008438	-3.068056	1.125530	-1.942527	1169.650725
HLA A*2603	1:146-154 9	LLAKLEAKF	1.509592	1.044948	-4.497309	2.554540	-1.942769	31427.4401
HLA B*5301	1:222-230 9	VAPAVFADF	0.948144	1.210036	-4.101021	2.158180	-1.942841	12618.8963
HLA B*7301	1:100-108 9	SYSQLSQRY	1.299924	1.360090	-4.604643	2.660014	-1.944629	40238.6016
HLA B*0801	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.381331	2.436235	-1.945096	24061.980997
HLA A*0301	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.364067	2.417755	-1.946312	23124.234437
HLA A*0250	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.590128	2.642684	-1.947444	38915.961236
HLA A*3301	1:181-189 9	TRIVVTGNY	1.308245	1.307355	-4.563572	2.615600	-1.947972	36607.6232
HLA A*6901	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.366673	2.417755	-1.948918	23263.386842
HLA B*4002	1:135-143 9	AADAARATY	1.474911	1.206254	-4.630208	2.681165	-1.949043	42678.3505
HLA A*2301	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.473734	2.524670	-1.949064	29766.945692
HLA B*4801	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.385725	2.436235	-1.949490	24306.639307
HLA A*2403	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.263347	2.313503	-1.949845	18337.8025
HLA B*3901	1:142-150 9	TYSELLAKL	1.344148	0.587133	-3.881688	1.931281	-1.950406	7615.30934
HLA A*0216	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.512236	1.561696	-1.950540	3252.638002
HLA A*8001	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.387113	2.436235	-1.950878	24384.477944
HLA A*6802	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.388265	2.436235	-1.952030	24449.203182
HLA B*4601	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.369795	2.417755	-1.952040	23431.247321
HLA A*3101	1:211-219 9	LAIECLRQL	1.635667	0.528719	-4.117285	2.164386	-1.952898	13100.3985
HLA B*1503	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-3.138837	1.185494	-1.953342	1376.691970
HLA A*2403	1:184-192 9	VVTGNYRAW	1.568491	0.458724	-3.981874	2.027215	-1.954659	9591.22963
HLA B*1503	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.854278	1.899550	-1.954729	7149.545879
HLA A*3101	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.268251	2.313503	-1.954748	18546.0175
HLA A*3201	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.480057	2.524670	-1.955387	30203.462937
HLA A*0201	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.392578	2.436235	-1.956343	24693.256303
HLA A*0206	1:142-150 9	TYSELLAKL	1.344148	0.587133	-3.889276	1.931281	-1.957995	7749.54823
HLA B*0801	1:167-175 9	ARQAARAVL	1.496924	0.533348	-3.989233	2.030272	-1.958961	9755.12583
HLA A*3201	1:218-226 9	QLAAVAPAV	1.059036	0.214314	-3.233465	1.273350	-1.960115	1711.84578
HLA A*0211	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.522193	1.561696	-1.960497	3328.073042
HLA B*4001	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.397054	2.436235	-1.960819	24949.056878
HLA B*1502	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.977960	2.016506	-1.961454	9505.173463
HLA A*3101	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.397933	2.436235	-1.961698	24999.587370
HLA A*2603	1:222-230 9	VAPAVFADF	0.948144	1.210036	-4.119916	2.158180	-1.961735	13180.0157
HLA A*2601	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.379626	2.417755	-1.961871	23967.660999
HLA B*5401	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-2.942768	0.980281	-1.962486	876.531558
HLA A*2501	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.380565	2.417755	-1.962810	24019.582112
HLA B*4402	1:201-209 9	SEHADVEIR	1.214047	0.687630	-3.865199	1.901677	-1.963522	7331.60170
HLA B*4002	1:100-108 9	SYSQLSQRY	1.299924	1.360090	-4.624308	2.660014	-1.964294	42102.5179
HLA B*5801	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.278027	2.313503	-1.964524	18968.2328
HLA B*1503	1:79-87 9	SFYITGISR	1.120990	0.841293	-3.927587	1.962283	-1.965304	8464.222836
HLA B*5401	1:211-219 9	LAIECLRQL	1.635667	0.528719	-4.131297	2.164386	-1.966910	13529.9700
HLA A*0211	1:190-198 9	RAWRHFIAM	1.138328	0.313168	-3.419248	1.451496	-1.967751	2625.71638
HLA B*0702	1:184-192 9	VVTGNYRAW	1.568491	0.458724	-3.996530	2.027215	-1.969315	9920.42724
HLA A*0201	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.389009	2.417755	-1.971254	24491.167946
HLA A*0212	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.393025	2.417755	-1.975270	24718.651030
HLA B*4501	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.618592	2.642684	-1.975908	41551.984753
HLA A*2402	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.514552	2.537939	-1.976613	32700.310622
HLA A*0206	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.916883	1.939903	-1.976980	8258.151287
HLA B*3801	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.395083	2.417755	-1.977328	24836.072285
HLA A*0101	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.395351	2.417755	-1.977596	24851.394095
HLA A*0250	1:181-189 9	TRIVVTGNY	1.308245	1.307355	-4.593295	2.615600	-1.977695	39200.7943
HLA A*6801	1:41-49 9	RACYQSWSK	0.781972	0.322141	-3.082689	1.104113	-1.978576	1209.730936
HLA A*3001	1:167-175 9	ARQAARAVL	1.496924	0.533348	-4.008893	2.030272	-1.978621	10206.8884
HLA B*1509	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.293397	2.313503	-1.979894	19651.5678
HLA A*3301	1:146-154 9	LLAKLEAKF	1.509592	1.044948	-4.534772	2.554540	-1.980232	34258.7526
HLA A*0206	1:139-147 9	ARATYSELL	1.529098	0.642980	-4.152452	2.172078	-1.980374	14205.3388
HLA B*1503	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-3.996963	2.016506	-1.980457	9930.307148
HLA B*1501	1:227-235 9	FADFEVTTL	1.891662	0.342213	-4.214826	2.233875	-1.980951	16399.3157
HLA A*2301	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.518955	2.537939	-1.981016	33033.516886
HLA A*0212	1:217-225 9	RQLAAVAPA	0.688822	-0.063815	-2.606523	0.625007	-1.981516	404.132112
HLA A*0219	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.418756	2.436235	-1.982521	26227.465599
HLA B*0702	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.401145	2.417755	-1.983389	25185.152591
HLA A*0201	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.883069	1.899550	-1.983519	7639.572322
HLA A*0211	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.509778	2.524670	-1.985108	32342.808143
HLA A*3301	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.629221	2.642684	-1.986537	42581.488921
HLA A*3301	1:202-210 9	EHADVEIRR	1.104999	0.588801	-3.680858	1.693800	-1.987059	4795.76915
HLA A*3201	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.145558	2.158014	-1.987545	13981.643036
HLA A*6801	1:145-153 9	ELLAKLEAK	0.882949	0.153748	-3.025333	1.036697	-1.988637	1060.06661
HLA B*4801	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.146756	2.158014	-1.988743	14020.272263
HLA B*4402	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-3.023233	1.034236	-1.988996	1054.952047
HLA A*0212	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.426406	2.436235	-1.990171	26693.544737
HLA A*6901	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.781397	1.790637	-1.990760	6045.015693
HLA A*8001	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.138162	2.146371	-1.991791	13745.547129
HLA B*1503	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.911272	1.919326	-1.991947	8152.151923
HLA B*5401	1:146-154 9	LLAKLEAKF	1.509592	1.044948	-4.546615	2.554540	-1.992076	35205.8877
HLA B*0801	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.305802	2.313503	-1.992300	20220.9932
HLA B*1502	1:222-230 9	VAPAVFADF	0.948144	1.210036	-4.151225	2.158180	-1.993045	14165.2801
HLA A*0206	1:242-250 9	ATSPLATEA	1.133303	-0.159611	-2.966775	0.973692	-1.993083	926.34891
HLA A*2602	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.429439	2.436235	-1.993204	26880.629464
HLA A*0216	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.429696	2.436235	-1.993460	26896.485052
HLA A*6901	1:203-211 9	HADVEIRRL	1.774485	0.250562	-4.019142	2.025047	-1.994094	10450.6143
HLA A*2403	1:227-235 9	FADFEVTTL	1.891662	0.342213	-4.228589	2.233875	-1.994714	16927.3514
HLA B*3901	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.413087	2.417755	-1.995332	25887.315624
HLA A*6802	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-3.510272	1.513828	-1.996443	3237.960618
HLA A*0206	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.416705	2.417755	-1.9989	
HLA B*4601	1:187-195 9	GNYRAWRHF	1.272469	1.041034	-4.312515	2.313503		

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HLA B*3901	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.232052	2.232643	-1.999409	17062.8727	
HLA A*6801	1:62-70 9	RHIIDVGHF	1.382898	1.259786	-4.642122	2.642684	-1.999438	43865.376897		
HLA A*6801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-3.855157	1.855018	-2.000140	7164.02618	
HLA B*2705	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.436636	2.436235	-2.000401	27329.765603		
HLA B*4002	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.616233	2.615600	-2.000633	41326.9057	
HLA B*5401	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.539022	2.537939	-2.001083	34595.671477		
HLA B*1509	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.031392	2.030272	-2.001120	10749.5933	
HLA B*4402	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.160073	2.158014	-2.002060	14456.838463		
HLA A*2902	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.160679	2.158180	-2.002499	14477.0307	
HLA A*0216	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-2.786804	0.784286	-2.002518	612.074158		
HLA A*6801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-3.846403	1.843851	-2.002552	7021.06483	
HLA B*4801	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.035255	2.030272	-2.004982	10845.6251	
HLA B*4801	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.319662	2.313503	-2.006159	20876.7118	
HLA B*0702	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.442890	2.436235	-2.006655	27726.192617		
HLA B*1509	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.443233	2.436235	-2.006998	27748.100630		
HLA A*3301	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.545335	2.537939	-2.007396	35102.239945		
HLA B*7301	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.240463	2.232643	-2.007821	17396.5571	
HLA A*0250	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.176927	1.168653	-2.008274	1502.88804	
HLA B*0802	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.242512	2.233875	-2.008637	17478.8179	
HLA B*4001	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.322312	2.313503	-2.008810	21004.4984	
HLA A*2603	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.036547	2.027215	-2.009332	10877.9436	
HLA A*3301	1:164-172	9	RKQARQAAR	1.130763	0.814899	-3.955335	1.945662	-2.009672	9022.65821	
HLA A*0203	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.446384	2.436235	-2.010149	27950.135664		
HLA B*4501	1:181-189	9	TRIVVTGNY	1.308245	1.307355	-4.625868	2.615600	-2.010269	42254.0291	
HLA A*2603	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.446656	2.436235	-2.010421	27967.681197		
HLA A*0250	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.548535	2.537939	-2.010596	35361.837911		
HLA B*5401	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.535873	2.524670	-2.011204	34345.785592		
HLA A*0206	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.447554	2.436235	-2.011319	28025.538344		
HLA A*0250	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-2.827398	0.814245	-2.013153	672.045141	
HLA B*3501	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.327441	2.313503	-2.013938	21254.0276	
HLA A*0203	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-2.828451	0.814245	-2.014206	673.675905	
HLA B*3501	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.161370	2.146371	-2.015000	14500.074850		
HLA B*4402	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-2.751519	0.735649	-2.015871	564.312250	
HLA A*0219	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.180509	2.164386	-2.016123	15153.3672	
HLA A*0203	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.434016	2.417755	-2.016261	27165.407939		
HLA B*4801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-2.641517	0.625007	-2.016510	438.042844	
HLA A*0250	1:174-182	9	VLPNATETR	1.038504	0.740297	-3.795339	1.778801	-2.016538	6242.22295	
HLA B*5101	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.454422	2.436235	-2.018186	28472.231648		
HLA A*2402	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.544083	2.524670	-2.019413	35001.169444		
HLA A*2501	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.046682	2.027215	-2.019467	11134.8016	
HLA A*6802	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.439495	2.417755	-2.021740	27510.293905		
HLA A*3001	1:164-172	9	RKQARQAAR	1.130763	0.814899	-3.967829	1.945662	-2.022167	9286.00830	
HLA B*1509	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.737955	1.715719	-2.022236	5469.59859	
HLA A*6802	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-2.907694	0.885414	-2.022280	808.526846	
HLA A*2301	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.187915	2.164386	-2.023528	15413.9776	
HLA B*4001	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.257405	2.233875	-2.023531	18088.6203	
HLA A*2602	1:142-150	9	TYSELLAKL	1.344148	0.587133	-3.955743	1.931281	-2.024462	9031.15542	
HLA A*3101	1:53-61 9	KTATNAGYL	1.501925	0.397625	-3.924697	1.899550	-2.025148	8408.087486		
HLA B*3801	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.463481	2.436235	-2.027246	29072.415879		
HLA B*0801	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.200184	2.172078	-2.028106	15855.6385	
HLA B*7301	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.059736	2.030272	-2.029464	11474.5647	
HLA A*3201	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.567615	2.537939	-2.029676	36950.047143		
HLA A*3002	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.467529	2.436235	-2.031294	29344.673735		
HLA B*0802	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.048069	2.016506	-2.031563	11170.398825		
HLA A*2301	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.434012	1.401827	-2.032185	2716.51419	
HLA A*1101	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.468427	2.436235	-2.032192	29405.379487		
HLA A*0212	1:233-241	9	TTLADGTEV	1.178752	0.144786	-3.355784	1.323538	-2.032246	2268.73371	
HLA B*1517	1:233-241	9	TTLADGTEV	1.178752	0.144786	-3.355863	1.323538	-2.032326	2269.15105	
HLA A*0219	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.451797	2.417755	-2.034042	28300.697132		
HLA A*2601	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.348218	2.313503	-2.034715	22295.5267	
HLA A*0216	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.452770	2.417755	-2.035015	28364.153071		
HLA B*3501	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.060338	2.025047	-2.035290	11490.4672	
HLA B*1801	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.975352	1.939903	-2.035450	9448.266150		
HLA A*0250	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-3.065782	1.027504	-2.038278	1163.54154	
HLA A*0301	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.353565	2.313503	-2.040062	22571.7465	
HLA B*3901	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.476448	2.436235	-2.040213	29953.524433		
HLA A*0202	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.565977	2.524670	-2.041307	36810.982220		
HLA B*0802	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.355245	2.313503	-2.041742	22659.2247	
HLA A*1101	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.460030	2.417755	-2.042275	28842.289328		
HLA B*7301	1:73-81 9	LEHASVSFY	1.292112	1.245827	-4.580246	2.537939	-2.042307	38040.465978		
HLA A*0250	1:36-44 9	VEFAGRACY	1.217312	1.307358	-4.567876	2.524670	-2.043206	36972.242225		
HLA B*2705	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.088494	2.044564	-2.043930	12260.0973	
HLA A*0250	1:138-146	9	AARATYSEL	1.196073	0.462758	-3.704339	1.658831	-2.045508	5062.19678	
HLA A*3301	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-3.890089	1.843851	-2.046238	7764.06759	
HLA B*7301	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.602394	2.554540	-2.047855	40030.8141	
HLA B*5101	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.465960	2.417755	-2.048205	29238.819163		
HLA B*1801	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.212857	2.164386	-2.048470	16325.1378	
HLA A*3001	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.213162	2.164386	-2.048776	16336.6231	
HLA B*5101	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.208125	2.158180	-2.049945	16148.2325	
HLA B*1501	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.989905	1.939903	-2.050002	9770.230925		
HLA B*0803	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.282900	2.232643	-2.050257	19182.2570	
HLA B*0702	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.364490	2.313503	-2.050988	23146.7633	
HLA A*0201	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.767263	1.715719	-2.051543	5851.44235	
HLA A*2402	1:74-82 9	EHASVSFYI	0.978340	0.173645	-3.203725	1.151985	-2.051740	1598.544962		
HLA A*0211	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-3.246406	1.194587	-2.051818	1763.622378		
HLA A*6901	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.365371	2.313503	-2.051869	23193.7690	
HLA A*0250	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-3.971255	1.919326	-2.051929	9359.542414		
HLA A*8001	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.365740	2.313503	-2.052237	23213.4770	
HLA A*6802	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-2.278310	0.225691	-2.052619	189.805898		
HLA B*1501	1:39-47 9	AGRACYQSW	1.340001	0.305812	-3.698743	1.645813	-2.052930	4997.382024		
HLA B*4403	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.607641	2.554540	-2.053101	40517.3304	
HLA A*3001	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.288050	2.233875	-2.054175	19411.0834	
HLA B*5301	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.079340	2.025047	-2.054293	12004.3963	
HLA A*0202	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-3.994280	1.939903	-2.054377	9869.145907		
HLA B*0803	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.491048	2.436235	-2.054813	30977.590191		
HLA B*4002	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-3.984590	1.928720	-2.055870	9651.39951	
HLA B*3501	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.747429	1.691549	-2.055879	5590.215866		
HLA A*6802	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.214116	2.158180	-2.055936	16372.5446	
HLA B*0803	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.072762	2.016506	-2.056256	11823.927734		
HLA A*3101	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.748942	1.691549	-2.057392	5609.725969		
HLA B*3901	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.074533	2.016506	-2.058027	11872.256703		
HLA B*1801	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.373731	2.313503	-2.060228	23644.5359	
HLA B*7301	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-3.113011	1.052696	-2.060316	1297.21284	
HLA B*0801	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.218557	2.158180	-2.060376	16540.8075	
HLA B*0802	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.294748	2.232643	-2.062105	19712.7928	
HLA A*2403	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.227132	2.164386	-2.062746	16870.6699	
HLA A*0101	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.376503	2.313503	-2.063000	23795.9576	
HLA B*1503	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.092516	2.027215	-2.065301	12374.1745	
HLA B*1509	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.298164	2.232643	-2.065522	19868.4647	
HLA B*4002	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.620180	2.554540	-2.065640	41704.2220	
HLA B*3801	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.379231	2.313503	-2.065728	23945.8876	
HLA B*4801	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.237905	2.172078	-2.065827	17294.3688	
HLA A*2402	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.238638	2.172078	-2.066560	17323.5844	
HLA B*3901	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.091868	2.025047	-2.066820	12355.7120	
HLA A*0202	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.299734	2.232643	-2.067091	19940.3953	
HLA B*4001	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.857892	1.790637	-2.0672			
HLA A*2402	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.094621	2.027215			

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HLA B*4801	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.301390	2.233875	-2.067515	20016.5927
HLA B*4402	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.214234	2.146371	-2.067863	16376.973890
HLA B*1501	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.300763	2.232643	-2.068120	19987.7008
HLA A*2602	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.487035	2.417755	-2.069280	30692.672808
HLA A*6802	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.241706	2.172078	-2.069629	17446.4144
HLA B*1502	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.096999	2.027215	-2.069784	12502.5630
HLA A*3301	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.487627	2.417755	-2.069872	30734.544420
HLA A*0201	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.385788	2.313503	-2.072286	24310.1899
HLA B*3901	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.236963	2.164386	-2.072576	17256.8917
HLA A*0202	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.509028	2.436235	-2.072793	32287.040526
HLA A*0216	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.237461	2.164386	-2.073074	17276.6949
HLA B*4402	1:39-47	9	AGRACYQSW	1.340001	0.305812	-3.719409	1.645813	-2.073596	5240.933152
HLA A*3001	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.247519	2.172078	-2.075441	17681.4880
HLA B*5701	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.527907	1.451496	-2.076410	3372.14931
HLA B*0803	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.390083	2.313503	-2.076580	24551.7928
HLA A*0250	1:1-9	9	VAETAPLRV	1.127505	0.095337	-3.300115	1.222842	-2.077273	1995.789934
HLA A*2501	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.242310	2.164386	-2.077924	17470.6877
HLA A*0211	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.514312	2.436235	-2.078077	32682.271284
HLA B*4001	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.251614	2.172078	-2.079536	17849.0030
HLA A*2602	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.226954	2.146371	-2.080583	16863.734978
HLA B*1509	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.106181	2.025047	-2.081134	12769.7043
HLA B*1801	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.317717	2.233875	-2.083842	20783.4060
HLA B*0702	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.003259	1.919326	-2.083934	10075.330505
HLA A*0203	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.257575	2.172078	-2.085497	18095.6674
HLA B*1801	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.318393	2.232643	-2.085751	20815.8128
HLA A*2403	1:53-61	9	KTATNAGYL	1.501925	0.397625	-3.986146	1.899550	-2.086596	9686.026494
HLA A*2403	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.103127	2.016506	-2.086620	12680.211892
HLA A*6802	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-2.534474	0.446772	-2.087702	342.352933
HLA A*3201	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.525571	2.436235	-2.089336	33540.610456
HLA B*5801	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.009937	1.919326	-2.090611	10231.434722
HLA A*0203	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.325266	2.232643	-2.092623	21147.8206
HLA B*1517	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.066397	0.973692	-2.092706	1165.19190
HLA A*3101	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.024085	1.931281	-2.092804	10570.2470
HLA A*1101	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.406682	2.313503	-2.093180	25508.3473
HLA A*3001	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-3.106404	1.012095	-2.094309	1277.62819
HLA A*0216	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.408743	2.313503	-2.095240	25629.6585
HLA B*4501	1:146-154	9	LLAKLEAKF	1.509592	1.044948	-4.651151	2.554540	-2.096611	44786.8930
HLA A*2601	1:53-61	9	KTATNAGYL	1.501925	0.397625	-3.996944	1.899550	-2.097394	9929.877382
HLA A*0203	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.412377	2.313503	-2.098875	25845.0558
HLA B*1503	1:141-149	9	ATYSELLAK	0.738811	0.394589	-3.233305	1.133400	-2.099905	1711.21615
HLA A*6802	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.815813	1.715719	-2.100093	6543.53890
HLA A*0206	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.413665	2.313503	-2.100162	25921.7902
HLA B*4001	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.334032	2.232643	-2.101389	21579.0115
HLA A*3002	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-4.260514	2.158014	-2.102500	18218.550140
HLA A*0211	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.520278	2.417755	-2.102522	33134.282678
HLA A*8001	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.119051	2.016506	-2.102545	13153.802604
HLA A*0216	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-3.297352	1.194587	-2.102765	1983.132964
HLA B*5701	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.336856	2.233875	-2.102981	21719.7903
HLA A*2602	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.555546	1.451496	-2.104050	3593.73573
HLA A*2602	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.262438	2.158180	-2.104258	18299.4501
HLA A*2301	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.044328	1.939903	-2.104426	11074.606380
HLA A*3001	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.264158	2.158180	-2.105977	18372.0603
HLA A*3002	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.524023	2.417755	-2.106268	33421.247156
HLA A*2601	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.341007	2.233875	-2.107132	21928.4112
HLA A*0212	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.422252	2.313503	-2.108750	26439.4465
HLA A*2301	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-3.953215	1.843851	-2.109364	8978.73741
HLA B*4001	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-4.267738	2.158014	-2.109725	18524.158084
HLA B*3801	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.344571	2.233875	-2.110697	22109.1139
HLA B*5301	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.547304	2.436235	-2.111069	35261.736762
HLA A*0202	1:138-146	9	AARATYSEL	1.196073	0.462758	-3.770111	1.658831	-2.111279	5889.93506
HLA A*3301	1:156-164	9	DQPNAILRR	1.122083	0.599902	-3.834444	1.721985	-2.112460	6830.36803
HLA A*3001	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-4.270706	2.158014	-2.112692	18651.161306
HLA A*0202	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.270877	2.158180	-2.112697	18658.5285
HLA A*6801	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.550114	2.436235	-2.113879	35490.627908
HLA B*1501	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.260457	2.146371	-2.114087	18216.184846
HLA A*6802	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.427940	2.313503	-2.114438	26788.0106
HLA A*0203	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.046034	1.931281	-2.114753	11118.1883
HLA B*0702	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.348970	2.233875	-2.115095	22334.1574
HLA B*2705	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.349172	2.233875	-2.115297	22344.5508
HLA A*3001	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.264315	2.146371	-2.117945	18378.720745
HLA B*1501	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.291870	2.172078	-2.119792	19582.5858
HLA B*5101	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.433370	2.313503	-2.119867	27125.0234
HLA B*5801	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.353314	2.232643	-2.120671	22558.6845
HLA A*2902	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.355367	2.233875	-2.121493	22665.6000
HLA A*3301	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.040903	1.919326	-2.121577	10987.597708
HLA A*0211	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.053576	1.931281	-2.122295	11312.9501
HLA B*4801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.068415	1.945662	-2.122753	11706.1805
HLA A*2301	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.150205	2.027215	-2.122990	14132.0606
HLA B*0702	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.356234	2.232643	-2.123591	22710.8914
HLA A*6801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.081796	0.957621	-2.124175	1207.24657
HLA A*6901	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.055897	1.931281	-2.124616	11373.5793
HLA A*0301	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-3.627793	1.502929	-2.124864	4244.17030
HLA A*0203	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-3.087313	0.962074	-2.125239	1222.679338
HLA A*0219	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.439042	2.313503	-2.125539	27481.5851
HLA B*4403	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.562392	2.436235	-2.126157	36508.340440
HLA A*2403	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.170980	2.044564	-2.126415	14824.4857
HLA A*0301	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-2.963467	0.836190	-2.127276	919.319601
HLA A*2601	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.291750	2.164386	-2.127364	19577.1836
HLA B*5401	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.564295	2.436235	-2.128060	36668.671390
HLA A*2902	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-4.286485	2.158014	-2.128471	19341.271416
HLA B*5801	1:9-17	9	VQLIAKTDF	0.933457	1.224557	-4.286821	2.158014	-2.128807	19356.239886
HLA B*5701	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.154007	2.025047	-2.128960	14256.3043
HLA A*0301	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.363106	2.233875	-2.129232	23073.1252
HLA A*0201	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.581235	1.451496	-2.129739	3812.72434
HLA A*2501	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.365792	2.233875	-2.131917	23216.2400
HLA A*2902	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.160416	2.027215	-2.133201	14468.2616
HLA A*0301	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.367566	2.232643	-2.134923	23311.2599
HLA A*0250	1:30-38	9	DGGPALVEF	1.593417	0.842818	-4.571226	2.436235	-2.134991	37258.567668
HLA B*3901	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.449288	2.313503	-2.135785	28137.6539
HLA A*0202	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.160990	2.025047	-2.135942	14487.3725
HLA A*3101	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.370592	2.233875	-2.136717	23474.2585
HLA B*1501	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.167023	2.030272	-2.136751	14690.0442
HLA B*7301	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.308986	2.172078	-2.136908	20369.7658
HLA A*2602	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.450561	2.313503	-2.137059	28220.2790
HLA B*5301	1:91-99	9	HELIRHRHF	1.404658	1.013097	-4.554972	2.417755	-2.137217	35889.914030
HLA B*0803	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.371684	2.233875	-2.137810	23533.3846
HLA B*3501	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.078255	1.939903	-2.138352	11974.430361
HLA A*6801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-3.076237	0.937566	-2.138671	1191.89253
HLA B*4002	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.371917	2.232643	-2.139274	23545.9920
HLA A*2402	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.373317	2.233875	-2.139443	23622.0337
HLA B*5701	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.372504	2.232643	-2.139862	23577.8588
HLA A*2601	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.299271	2.158180	-2.141090	19919.1552
HLA B*3901	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.495230	1.354114	-2.141116	3127.73650
HLA A*0101	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.373801	2.232643	-2.141159	23648.3737
HLA B*4601	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.373827	2.232643	-2.141184	23649.7816
HLA A*3101	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.376360	2.232643		
HLA B*4402	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.376372	2.232643		

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HLA B*7301	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.561793	2.417755	-2.144038	36458.011115
HLA B*4001	1:201-209	9 SEHADVEIR	1.214047	0.687630	-4.045799	1.901677	-2.144122	11112.1751
HLA B*5401	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.561993	2.417755	-2.144238	36474.779843
HLA A*3002	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.457828	2.313503	-2.144326	28696.4557
HLA A*0211	1:70-78 9	FSVLEHASV	1.102668	0.135344	-3.383465	1.238012	-2.145453	2418.049337
HLA B*2705	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.292246	2.146371	-2.145875	19599.543521
HLA B*1517	1:166-174	9 QARQAARAV	0.923681	0.228464	-3.298052	1.152145	-2.145907	1986.33264
HLA A*3001	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.162498	2.016506	-2.145992	14537.776803
HLA A*2403	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.065474	1.919326	-2.146148	11627.160414
HLA A*0201	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.318313	2.172078	-2.146236	20811.9844
HLA A*0212	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-2.930884	0.784286	-2.146597	852.872010
HLA B*4801	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.380084	2.232643	-2.147441	23992.9585
HLA A*0212	1:154-162	9 FADQPNAIL	1.350025	0.365694	-3.863775	1.715719	-2.148056	7307.60519
HLA A*6801	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.381938	2.233875	-2.148063	24095.5889
HLA B*0801	1:188-196	9 NYRAWRHFI	1.295038	0.370458	-3.813867	1.665496	-2.148371	6514.29340
HLA B*1502	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.110960	1.962283	-2.148677	12910.994433
HLA A*3101	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.306904	2.158180	-2.148724	20272.3639
HLA A*3301	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.585718	2.436235	-2.149483	38522.794041
HLA A*2902	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.111782	1.962283	-2.149499	12935.464059
HLA B*3501	1:134-142	9 EAADAARAT	0.999569	-0.361461	-2.789431	0.638108	-2.151323	615.787357
HLA A*0211	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.178305	2.025047	-2.153258	15076.6666
HLA A*0101	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.325385	2.172078	-2.153308	21153.6562
HLA B*1501	1:196-204	9 IAMRASEHA	1.101605	-0.216191	-3.038894	0.885414	-2.153480	1093.69036
HLA B*7301	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.468962	2.313503	-2.155460	29441.6720
HLA B*1801	1:144-152	9 SELLAKLEA	1.205349	-0.282089	-3.078812	0.923260	-2.155553	1198.98054
HLA B*4601	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.314188	2.158014	-2.156174	20615.211610
HLA A*0202	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.573991	2.417755	-2.156236	37496.566261
HLA A*0201	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.389552	2.232643	-2.156910	24521.7933
HLA B*0803	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.315363	2.158014	-2.157349	20671.050100
HLA A*3101	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.316302	2.158014	-2.158289	20715.829769
HLA A*0206	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.391227	2.232643	-2.158585	24616.5626
HLA B*4402	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.330778	2.172078	-2.158700	21417.9307
HLA B*2705	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-2.727564	0.568388	-2.159176	534.028123
HLA B*1501	1:184-192	9 VVTGNYRAW	1.568491	0.458724	-4.186397	2.027215	-2.159182	15360.2031
HLA A*3002	1:191-199	9 AWRHFIAMR	1.152543	0.892021	-4.204450	2.044564	-2.159886	16012.1776
HLA A*6901	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.393955	2.232643	-2.161312	24771.6629
HLA A*8001	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.319610	2.158180	-2.161430	20874.2273
HLA A*2601	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.309200	2.146371	-2.162829	20379.796374
HLA B*4402	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.327260	2.164386	-2.162874	21245.1759
HLA B*1517	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.395957	2.232643	-2.163314	24886.1046
HLA B*4002	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.321795	2.158014	-2.163782	20979.514298
HLA A*0202	1:238-246	9 GTEVATSPL	1.240590	0.206169	-3.611173	1.446759	-2.164413	4084.81643
HLA B*1509	1:202-210	9 EHADVEIRR	1.104999	0.588801	-3.858334	1.693800	-2.164534	7216.61719
HLA A*0201	1:131-139	9 ILTEAADAA	1.112012	-0.238517	-3.038124	0.873495	-2.164629	1091.75139
HLA A*2501	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.478468	2.313503	-2.164966	30093.2080
HLA B*0801	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.323346	2.158014	-2.165333	21054.556106
HLA A*2601	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.398349	2.232643	-2.165706	25023.5371
HLA A*3301	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.099067	1.931281	-2.167785	12562.2259
HLA A*8001	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.400564	2.232643	-2.167922	25151.5215
HLA B*4001	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.332561	2.164386	-2.168174	21506.0558
HLA A*3002	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.100519	1.931281	-2.169237	12604.2956
HLA A*8001	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.403264	2.233875	-2.169389	25308.3494
HLA B*4402	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.404349	2.233875	-2.170475	25371.6834
HLA A*2301	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.403189	2.232643	-2.170546	25303.9685
HLA A*0211	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.484622	2.313503	-2.171119	30522.6185
HLA B*5801	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.343237	2.172078	-2.171159	22041.2809
HLA A*1101	1:89-97 9	CTHELIRHR	1.005015	0.652731	-3.829003	1.657746	-2.171257	6745.322177
HLA B*3501	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.344057	2.172078	-2.171979	22082.9352
HLA B*0802	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.330209	2.158180	-2.172028	21389.9089
HLA B*3901	1:124-132	9 DDADLRHIL	1.566722	0.080178	-3.819182	1.646900	-2.172282	6594.49966
HLA A*2902	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.344470	2.172078	-2.172393	22103.9713
HLA A*2601	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.189085	2.016506	-2.172579	15455.560844
HLA B*1517	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.003339	1.830609	-2.172730	10077.183894
HLA B*1503	1:160-168	9 AILRRKQAR	1.023219	0.831799	-4.028192	1.855018	-2.173174	10670.6785
HLA A*2402	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.337786	2.164386	-2.173400	21766.3708
HLA A*0203	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.115090	1.939903	-2.175188	13034.371308
HLA A*0219	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.408571	2.232643	-2.175929	25619.5388
HLA A*6801	1:33-41 9	PALVEFAGR	1.046707	0.453047	-3.676009	1.499754	-2.176255	4742.517404
HLA A*2301	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.410580	2.233875	-2.176705	25738.3153
HLA B*5701	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.096454	1.919326	-2.177128	12486.881016
HLA A*3101	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.194658	2.016506	-2.178152	15655.168543
HLA A*0250	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.596142	2.417755	-2.178387	39458.670088
HLA A*8001	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.350553	2.172078	-2.178476	22415.7423
HLA B*1509	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.098178	1.919326	-2.178853	12536.563231
HLA A*0211	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.351075	2.172078	-2.178997	22442.6797
HLA B*0803	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.351086	2.172078	-2.179009	22443.2867
HLA A*6901	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.351317	2.172078	-2.179239	22455.1886
HLA A*6802	1:124-132	9 DDADLRHIL	1.566722	0.080178	-3.826475	1.646900	-2.179575	6706.17144
HLA A*0203	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.338846	2.158180	-2.180665	21819.5425
HLA A*6802	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.414525	2.232643	-2.181882	25973.1667
HLA B*3501	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.101397	1.919326	-2.182072	12629.823748
HLA B*4402	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.341087	2.158180	-2.182907	21932.4450
HLA A*0203	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.744910	1.561696	-2.183214	5557.889788
HLA B*7301	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.620554	2.436235	-2.184319	41740.110351
HLA A*2402	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.417375	2.232643	-2.184732	26144.1681
HLA A*0301	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.084970	1.899550	-2.185420	12161.011265
HLA B*5101	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.418207	2.232643	-2.185564	26194.2848
HLA B*4601	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.877341	1.691549	-2.185792	7539.473206
HLA A*2902	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.118826	1.931281	-2.187544	13146.9729
HLA A*2403	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.359986	2.172078	-2.187909	22907.9543
HLA A*8001	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.346033	2.158014	-2.188019	22183.635299
HLA A*2601	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.360771	2.172078	-2.188693	22949.3841
HLA A*0212	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.421522	2.232643	-2.188879	26395.0002
HLA B*1509	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.979544	1.790637	-2.188906	9539.895111
HLA A*0216	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.421891	2.232643	-2.189248	26417.4284
HLA A*0301	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.347506	2.158180	-2.189325	22259.0099
HLA A*3001	1:184-192	9 VVTGNYRAW	1.568491	0.458724	-4.216959	2.027215	-2.189744	16480.0702
HLA B*3801	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.422828	2.232643	-2.190185	26474.5132
HLA A*0216	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.348972	2.158014	-2.190958	22334.278254
HLA A*0202	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-2.816018	0.625007	-2.191010	654.662614
HLA B*0802	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.364147	2.172078	-2.192070	23128.4882
HLA A*0219	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.091774	1.899550	-2.192224	12353.038625
HLA B*1509	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.123741	1.931281	-2.192460	13296.6088
HLA A*0101	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.350652	2.158180	-2.192471	22420.8361
HLA B*4801	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.351697	2.158180	-2.193517	22474.8770
HLA A*0301	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.365973	2.172078	-2.193895	23225.9130
HLA B*4002	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.630299	2.436235	-2.194064	42687.356069
HLA B*4501	1:110-118	9 PEKDSRVVV	1.317651	-0.112924	-3.398878	1.204727	-2.194151	2505.40407
HLA A*2603	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.358819	2.164386	-2.194432	22846.4440
HLA A*0216	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.125724	1.931281	-2.194443	13357.4592
HLA B*2705	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.358873	2.164386	-2.194486	22849.2869
HLA B*1801	1:27-35 9	TDADGGPAL	1.505710	0.284927	-3.985511	1.790637	-2.194874	9671.888733
HLA A*2501	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.353593	2.158180	-2.195413	22573.2119
HLA A*1101	1:132-140	9 LTEAADAAR	1.180631	0.577926	-3.954009	1.758557	-2.195453	8995.17044
HLA B*7301	1:163-171	9 RRKQARQAA	1.170385	-0.015739	-3.350243	1.154646	-2.195598	2239.97636
HLA A*3002	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.212190	2.016506	-2.1956	
HLA B*5801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.342095	2.146371	-2.1957	

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HLA A*0301	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.353835	2.158014	-2.195822	22585.793676
HLA A*0219	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.368360	2.172078	-2.196282	23353.9245
HLA A*2301	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-3.391195	1.194587	-2.196608	2461.472360
HLA B*1501	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.096501	1.899550	-2.196951	12488.232142
HLA A*0301	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.361490	2.164386	-2.197103	22987.4066
HLA B*0803	1:138-146	9 AARATYSEL	1.196073	0.462758	-3.856111	1.658831	-2.197280	7179.77865
HLA A*0301	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-2.986656	0.789295	-2.197361	969.741400
HLA B*3801	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.362120	2.164386	-2.197733	23020.7591
HLA A*0203	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.889563	1.691549	-2.198014	7754.664679
HLA B*0802	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.356086	2.158014	-2.198073	22703.152330
HLA A*6901	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.357517	2.158180	-2.199337	22778.0739
HLA A*0212	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.357555	2.158014	-2.199541	22780.045713
HLA B*3901	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.357736	2.158014	-2.199722	22789.536979
HLA A*0211	1:174-182	9 VLPNATETR	1.038504	0.740297	-3.978731	1.778801	-2.199930	9522.05483
HLA A*3101	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.372305	2.172078	-2.200227	23567.0193
HLA B*5701	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.358426	2.158014	-2.200413	22825.812747
HLA A*2902	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.217631	2.016506	-2.201125	16505.588439
HLA A*2403	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.433892	2.232643	-2.201249	27157.6200
HLA A*0101	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.366516	2.164386	-2.202129	23254.9562
HLA B*1501	1:234-242	9 TLADGTEVA	1.234837	-0.220592	-3.218804	1.014245	-2.204559	1655.02230
HLA B*0702	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.362921	2.158180	-2.204740	23063.2663
HLA A*0219	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.363323	2.158014	-2.205309	23084.611866
HLA B*4002	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-3.008407	0.803085	-2.205323	1019.547512
HLA A*1101	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.439213	2.233875	-2.205339	27492.4403
HLA A*3001	1:142-150	9 TYSELLAKL	1.344148	0.587133	-4.136842	1.931281	-2.205560	13703.8192
HLA B*5301	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.767310	1.561696	-2.205614	5852.075501
HLA A*2902	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.370282	2.164386	-2.205895	23457.5014
HLA B*1509	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.353109	2.146371	-2.206739	22548.069544
HLA A*0216	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.379849	2.172078	-2.207771	23979.9820
HLA B*1517	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.567561	1.359245	-2.208316	3694.548777
HLA A*0101	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.354745	2.146371	-2.208374	22633.129440
HLA A*3201	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.522519	2.313503	-2.209016	33305.7318
HLA A*0250	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-2.828738	0.619672	-2.209065	674.120683
HLA A*6901	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.367220	2.158014	-2.209207	23292.728927
HLA B*5801	1:154-162	9 FADQPNAIL	1.350025	0.365694	-3.925087	1.715719	-2.209368	8415.64169
HLA B*3501	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.442850	2.232643	-2.210208	27723.6428
HLA B*4501	1:30-38 9	DGGPALVEF	1.593417	0.842818	-4.646701	2.436235	-2.210466	44330.334822
HLA A*0216	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-2.830410	0.619672	-2.210738	676.722296
HLA A*0301	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.357193	2.146371	-2.210822	22761.075038
HLA A*6901	1:74-82 9	EHASVSFYI	0.978340	0.173645	-3.363518	1.151985	-2.211533	2309.500338
HLA B*1509	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.376513	2.164386	-2.212126	23796.4726
HLA B*0801	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.131781	1.919326	-2.212455	13545.056782
HLA B*3801	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.385013	2.172078	-2.212935	24266.8285
HLA A*3001	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.238194	2.025047	-2.213146	17305.8806
HLA A*6802	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.905211	1.691549	-2.213661	8039.158536
HLA A*0201	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.371886	2.158180	-2.213706	23544.3361
HLA B*3801	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.239075	2.025047	-2.214027	17341.0248
HLA B*3801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.361690	2.146371	-2.215319	22997.979624
HLA A*0201	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.373454	2.158014	-2.215440	23629.446907
HLA A*3001	1:209-217	9 RRLAIECLR	0.972846	0.851605	-4.039935	1.824451	-2.215484	10963.1350
HLA A*0301	1:191-199	9 AWRHFIAMR	1.152543	0.892021	-4.260829	2.044564	-2.216264	18231.7620
HLA B*1801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.362679	2.146371	-2.216308	23050.418673
HLA B*0802	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.380937	2.164386	-2.216550	24040.1219
HLA B*4001	1:167-175	9 ARQAARAVL	1.496924	0.533348	-4.246837	2.030272	-2.216565	17653.7698
HLA A*0206	1:138-146	9 AARATYSEL	1.196073	0.462758	-3.876434	1.658831	-2.217603	7523.74557
HLA A*2402	1:107-115	9 RYVPEKDSR	0.966438	0.877413	-4.061907	1.843851	-2.218056	11532.0667
HLA B*4002	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.382854	2.164386	-2.218467	24146.4808
HLA B*1503	1:201-209	9 SEHADVEIR	1.214047	0.687630	-4.120174	1.901677	-2.218498	13187.8613
HLA B*0803	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.377140	2.158180	-2.218959	23830.8700
HLA B*3901	1:198-206	9 MRASEHADV	0.792968	0.319530	-3.331908	1.112498	-2.219410	2147.37582
HLA B*3901	1:189-197	9 YRAWRHFIA	1.123021	-0.081757	-3.261132	1.041264	-2.219868	1824.45086
HLA B*1517	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.236493	2.016506	-2.219987	17238.230261
HLA A*2403	1:167-175	9 ARQAARAVL	1.496924	0.533348	-4.250550	2.030272	-2.220277	17805.3143
HLA A*0203	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.378721	2.158014	-2.220708	23917.792930
HLA B*4601	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.392818	2.172078	-2.220740	24706.8860
HLA B*2705	1:168-176	9 RQAARAVLP	0.787201	0.256977	-3.265587	1.044178	-2.221409	1843.26083
HLA A*6801	1:209-217	9 RRLAIECLR	0.972846	0.851605	-4.046274	1.824451	-2.221823	11124.3251
HLA A*2902	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.784456	1.561696	-2.222760	6087.745132
HLA B*1801	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.381935	2.158180	-2.223755	24095.4586
HLA B*5401	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.459003	2.233875	-2.225128	28774.1831
HLA B*1517	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.397456	2.172078	-2.225378	24972.1477
HLA A*0212	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.398398	2.172078	-2.226320	25026.3802
HLA A*2601	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.384440	2.158014	-2.226426	24234.817193
HLA A*6801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.126847	1.899550	-2.227297	13392.045354
HLA B*0702	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.385330	2.158014	-2.227317	24284.557977
HLA B*5301	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.374309	2.146371	-2.227938	23676.023851
HLA B*5301	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.541975	2.313503	-2.228472	34831.7317
HLA A*0216	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.148223	1.919326	-2.228897	14067.681465
HLA B*1801	1:184-192	9 VVTGNYRAW	1.568491	0.458724	-4.256228	2.027215	-2.229013	18039.6601
HLA B*5801	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.254339	2.025047	-2.229292	17961.3661
HLA A*2902	1:208-216	9 IRRLAIECL	1.768404	0.464239	-4.462008	2.232643	-2.229365	28973.9692
HLA A*0206	1:177-185	9 NATETRIVV	1.258391	0.095723	-3.584999	1.354114	-2.230885	3845.91146
HLA A*2501	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.377619	2.146371	-2.231249	23857.184718
HLA B*4001	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.389437	2.158180	-2.231257	24515.2938
HLA A*2403	1:96-104	9 HRHFSYSQL	1.392138	0.536582	-4.160327	1.928720	-2.231607	14465.2876
HLA B*3901	1:86-94 9	SRSCTHELI	1.200502	0.345702	-3.777986	1.546204	-2.231782	5997.717145
HLA A*0203	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.257276	2.025047	-2.232229	18083.2385
HLA A*2603	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.546343	2.313503	-2.232840	35183.8013
HLA B*5401	1:118-126	9 VPPGMEDDA	0.772465	-0.322630	-2.682717	0.449835	-2.232882	481.634024
HLA B*0801	1:203-211	9 HADVEIRRL	1.774485	0.250562	-4.258397	2.025047	-2.233350	18129.9633
HLA A*0101	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.391596	2.158014	-2.233583	24637.479699
HLA B*0801	1:57-65 9	NAGYLRHII	1.129740	0.203828	-3.567176	1.333568	-2.233608	3691.272346
HLA A*2403	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.196157	1.962283	-2.233874	15709.295860
HLA A*3001	1:107-115	9 RYVPEKDSR	0.966438	0.877413	-4.077837	1.843851	-2.233985	11962.9050
HLA A*0219	1:222-230	9 VAPAVFADF	0.948144	1.210036	-4.392724	2.158180	-2.234544	24701.5401
HLA A*6801	1:91-99 9	HELIRHRHF	1.404658	1.013097	-4.652474	2.417755	-2.234719	44923.511508
HLA A*0250	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.134408	1.899550	-2.234858	13627.229002
HLA A*6802	1:96-104	9 HRHFSYSQL	1.392138	0.536582	-4.163917	1.928720	-2.235197	14585.3577
HLA A*0250	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.407345	2.172078	-2.235267	25547.2923
HLA B*5701	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.407798	2.172078	-2.235721	25573.9804
HLA A*2301	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.252338	2.016506	-2.235832	17878.768638
HLA A*2902	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.136409	1.899550	-2.236860	13690.184952
HLA B*1503	1:218-226	9 QLAAVAPAV	1.059036	0.214314	-3.510779	1.273350	-2.237429	3241.74650
HLA B*4801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.384780	2.146371	-2.238410	24253.835264
HLA B*4601	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.385194	2.146371	-2.238823	24276.939320
HLA A*3101	1:121-129	9 GMEDDADLR	1.182603	0.492795	-3.916591	1.675398	-2.241193	8252.61336
HLA B*0702	1:139-147	9 ARATYSELL	1.529098	0.642980	-4.414189	2.172078	-2.242111	25953.0813
HLA A*6901	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.388666	2.146371	-2.242296	24471.831386
HLA B*5401	1:187-195	9 GNYRAWRHF	1.272469	1.041034	-4.555900	2.313503	-2.242398	35966.6894
HLA B*1517	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.390602	2.146371	-2.244232	24581.164167
HLA A*2602	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.184649	1.939903	-2.244746	15298.503193
HLA B*5801	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.261261	2.016506	-2.244755	18249.919302
HLA B*0803	1:96-104	9 HRHFSYSQL	1.392138	0.536582	-4.173677	1.928720	-2.244957	14916.8405
HLA B*1503	1:200-208	9 ASEHADVEI	1.329405	0.306162	-3.881006	1.635567	-2.245439	7603.37129
HLA A*8001	1:211-219	9 LAIECLRQL	1.635667	0.528719	-4.410080	2.164386	-2.245693	25708.6740
HLA A*2602	1:227-235	9 FADFEVTTL	1.891662	0.342213	-4.479592	2.233875		
HLA B*1801	1:201-209	9 SEHADVEIR	1.214047	0.687630	-4.147414	1.901677		

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HLA A*0250	1:70-78 9	FSVLEHASV	1.102668	0.135344	-3.484319	1.238012	-2.246307	3050.135627	
HLA B*2705	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.405094	2.158180	-2.246914	25415.2315
HLA A*1101	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.479791	2.232643	-2.247149	30185.0046
HLA A*0212	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.405360	2.158180	-2.247179	25430.7730
HLA B*1503	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.963102	1.715719	-2.247382	9185.48101
HLA A*0216	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.963313	1.715719	-2.247594	9189.95441
HLA A*2501	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.480867	2.232643	-2.248225	30259.8876
HLA B*0802	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.394679	2.146371	-2.248308	24812.973045	
HLA B*3501	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.007047	1.758557	-2.248490	10163.5790
HLA A*0201	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.179917	1.931281	-2.248636	15132.7228
HLA A*6901	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-3.915309	1.665496	-2.249812	8228.27276
HLA A*0202	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.563743	2.313503	-2.250240	36622.0832
HLA A*0211	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.483073	2.232643	-2.250431	30413.9955
HLA B*3801	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.282601	2.030272	-2.252329	19169.0822
HLA A*0201	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.398950	2.146371	-2.252580	25058.217096	
HLA B*1503	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.404972	1.152145	-2.252828	2540.81089
HLA B*0801	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-3.944433	1.691549	-2.252884	8798.991454	
HLA A*1101	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.411456	2.158180	-2.253276	25790.3048
HLA B*5701	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.401168	2.146371	-2.254797	25186.515117	
HLA A*0206	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.174180	1.919326	-2.254854	14934.119987	
HLA A*6802	1:28-36 9	DADGGPALV	0.931987	-0.051421	-3.135454	0.880566	-2.254887	1366.008875	
HLA A*3201	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.816593	1.561696	-2.254897	6555.302207	
HLA B*4402	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.282611	2.027215	-2.255396	19169.4970
HLA A*3201	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.186848	1.931281	-2.255567	15376.1660
HLA A*0250	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.272217	1.015721	-2.256496	1871.61726
HLA B*1501	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.176642	1.919326	-2.257316	15019.030408	
HLA A*0212	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.616901	1.359245	-2.257655	4139.049208	
HLA A*0219	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.404081	2.146371	-2.257711	25356.040848	
HLA A*2603	1:89-97 9	CTHELIRHR	1.005015	0.652731	-3.915468	1.657746	-2.257723	8231.300273	
HLA A*1101	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.430614	2.172078	-2.258537	26953.4385
HLA A*2501	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.416576	2.158014	-2.258562	26096.123799	
HLA B*4501	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.573009	2.313503	-2.259507	37411.8698
HLA A*0203	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.179165	1.919326	-2.259839	15106.548296	
HLA A*0216	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.418073	2.158180	-2.259892	26186.2087
HLA B*0702	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.407608	2.146371	-2.261237	25562.776312	
HLA A*3002	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.495190	2.233875	-2.261315	31274.4565
HLA A*2902	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.306693	2.044564	-2.262129	20262.4958
HLA B*2705	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-3.315974	1.052696	-2.263278	2070.01671
HLA B*1502	1:154-162	9	FADQPNAIL	1.350025	0.365694	-3.979074	1.715719	-2.263354	9529.57873
HLA A*3001	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.022398	1.758557	-2.263842	10529.2686
HLA A*0211	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-3.431780	1.167504	-2.264276	2702.58876
HLA B*1517	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.022859	1.758557	-2.264302	10540.4391
HLA A*0211	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.423303	2.158180	-2.265122	26503.4603
HLA A*3101	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.412262	2.146371	-2.265892	25838.205590	
HLA A*0212	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.413510	2.146371	-2.267139	25912.536453	
HLA B*4001	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.414165	2.146371	-2.267795	25951.677306	
HLA B*3801	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.425946	2.158014	-2.267932	26665.255551	
HLA B*1503	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.200804	1.931281	-2.269523	15878.2998
HLA A*1101	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.434552	2.164386	-2.270165	27198.9359
HLA A*6802	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-3.935759	1.665496	-2.270262	8624.98994
HLA B*5101	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.442860	2.172078	-2.270782	27724.2427
HLA B*4801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-3.315170	1.044178	-2.270993	2066.19034
HLA B*1502	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.506735	2.233875	-2.272860	32117.0125
HLA B*1517	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.201626	1.928720	-2.272906	15908.3933
HLA A*3002	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.446297	2.172078	-2.274219	27944.5415
HLA A*0211	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.433582	2.158014	-2.275568	27138.233598	
HLA A*3301	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.440701	2.164386	-2.276314	27586.7485
HLA B*4002	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-3.203565	0.927121	-2.276444	1597.95701
HLA A*6801	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.434820	2.158180	-2.276639	27215.7154
HLA A*0203	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.423314	2.146371	-2.276944	26504.177231	
HLA B*0802	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.307572	2.030272	-2.277299	20303.5344
HLA A*0206	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.302664	2.025047	-2.277616	20075.3706
HLA B*3901	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.223904	1.945662	-2.278242	16745.7320
HLA A*0250	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.591986	2.313503	-2.278483	39082.8481
HLA A*3101	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.181181	1.901677	-2.279504	15176.8311
HLA B*5101	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.438238	2.158014	-2.280225	27430.786232	
HLA B*3501	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.297720	2.016506	-2.281214	19848.160205	
HLA A*2301	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.454898	2.172078	-2.282821	28503.5172
HLA B*3901	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.441436	2.158180	-2.283255	27633.5006
HLA A*3001	1:200-208	9	ASEHADVEI	1.329405	0.306162	-3.919575	1.635567	-2.284008	8309.50865
HLA A*2602	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.517157	2.232643	-2.284515	32897.0880
HLA B*3801	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.204027	1.919326	-2.284702	15996.592947	
HLA A*3301	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.063693	1.778801	-2.284892	11579.5785
HLA B*1509	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.443391	2.158014	-2.285377	27758.160101	
HLA A*6802	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.444133	2.158014	-2.286120	27805.653953	
HLA A*0250	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.519018	2.232643	-2.286376	33038.3423
HLA B*1801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.217781	1.931281	-2.286500	16511.3042
HLA B*0801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.433295	2.146371	-2.286924	27120.328098	
HLA A*3002	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.451642	2.164386	-2.287256	28290.5940
HLA A*0201	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.312475	2.025047	-2.287428	20534.0692
HLA A*3001	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.734643	1.446759	-2.287883	5428.03552
HLA A*6802	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-2.926143	0.637604	-2.288538	843.61171
HLA A*2402	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.229604	1.939903	-2.289701	16966.958106	
HLA A*3301	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.603275	2.313503	-2.289773	40112.1074
HLA B*0803	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.320325	2.030272	-2.290052	20908.5854
HLA B*4801	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.230032	1.939903	-2.290129	16983.671997	
HLA B*4601	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.317980	2.027215	-2.290765	20796.0027
HLA B*0803	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.455389	2.164386	-2.291003	28535.7634
HLA A*2601	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.318750	2.027215	-2.291535	20832.9368
HLA A*0203	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.220305	1.928720	-2.291585	16607.5177
HLA A*3301	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.526875	2.233875	-2.293000	33641.4670
HLA A*2403	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.440179	2.146371	-2.293808	27553.636856	
HLA A*6802	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.440332	2.146371	-2.293961	27563.327598	
HLA B*4403	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.467186	2.172078	-2.295109	29321.5051
HLA A*2402	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.194836	1.899550	-2.295287	15661.606514	
HLA B*0702	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.313196	2.016506	-2.296690	20568.201316	
HLA B*5301	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.455035	2.158014	-2.297021	28512.462296	
HLA B*4002	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.327338	2.030272	-2.297066	21248.9690
HLA A*6802	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.322474	2.025047	-2.297427	21012.3405
HLA B*0802	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.322740	2.025047	-2.297693	21025.1896
HLA B*3801	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.455932	2.158180	-2.297752	28571.4464
HLA A*2603	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.530676	2.232643	-2.298034	33937.2301
HLA A*0212	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.229682	1.931281	-2.298400	16969.9874
HLA B*4801	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.315052	2.016506	-2.298546	20656.294062	
HLA A*3002	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.328928	2.030272	-2.298656	21326.9360
HLA B*0803	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.445118	2.146371	-2.298747	27868.753728	
HLA B*0801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.244481	1.945662	-2.298818	17558.2377
HLA A*1101	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.456888	2.158014	-2.298875	28634.425070	
HLA A*0301	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.316103	2.016506	-2.299597	20706.305980	
HLA A*6801	1:187-195	9	GNYRAWRHF	1.272469	1.041034	-4.613103	2.313503	-2.299601	41030.1756
HLA A*3002	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.135263	1.834955	-2.300308	13654.0901
HLA A*0202	1:74-82 9	EHASVSFYI	0.978340	0.173645	-3.452629	1.151985	-2.300644	2835.497687	
HLA A*3201	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.472942	2.172078	-2.300865	29712.7260
HLA B*4001	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.317461	2.016506	-2.300955	20771.154192	
HLA A*1101	1:121-129	9	GMEDDADLR	1.182603	0.492795	-3.976353	1.675398	-2.300955	9470.06585
HLA A*3101	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.220394	1.919326	-2.3010		
HLA B*1509	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.460046	2.158180		

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HLA B*4601	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.243506	1.939903	-2.303603	17518.861946	
HLA B*1501	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-3.577082	1.273350	-2.303732	3776.43068	
HLA A*6802	1:200-208	9	ASEHADVEI	1.329405	0.306162	-3.940105	1.635567	-2.304538	8711.74479	
HLA B*5301	1:57-65	9	NAGYLRHII	1.129740	0.203828	-3.638657	1.333568	-2.305089	4351.678684	
HLA A*6801	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-3.145115	0.839978	-2.305137	1396.736889	
HLA B*1801	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.479721	2.172078	-2.307643	30180.1061	
HLA A*3002	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.540321	2.232643	-2.307678	34699.3252	
HLA B*1503	1:168-176	9	RQAARAVLP	0.787201	0.256977	-3.352405	1.044178	-2.308227	2251.15275	
HLA A*2501	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.480665	2.172078	-2.308588	30245.8125	
HLA A*6801	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.473011	2.164386	-2.308624	29717.3879	
HLA A*0212	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.333975	2.025047	-2.308928	21576.2099	
HLA A*0101	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.334297	2.025047	-2.309250	21592.2072	
HLA B*4002	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.543204	2.233875	-2.309329	34930.4232	
HLA B*5401	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.542346	2.232643	-2.309704	34861.5173	
HLA A*3001	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.128313	1.818422	-2.309891	13437.330223	
HLA A*1101	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.209967	1.899550	-2.310417	16216.868379	
HLA B*4402	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.340967	2.030272	-2.310695	21926.3946	
HLA B*4001	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.335897	2.025047	-2.310850	21671.9025	
HLA B*5801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.355990	2.044564	-2.311426	22698.1172	
HLA B*1502	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.544320	2.232643	-2.311677	35020.2992	
HLA A*8001	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.211508	1.899550	-2.311959	16274.522461	
HLA B*1509	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.339616	2.027215	-2.312401	21858.2945	
HLA A*0216	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.338486	2.025047	-2.313439	21801.4897	
HLA A*3101	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.341219	2.027215	-2.314003	21939.0906	
HLA A*0203	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.344414	2.030272	-2.314142	22101.1016	
HLA A*3201	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.478607	2.164386	-2.314221	30102.8148	
HLA B*4001	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.243097	1.928720	-2.314377	17502.3788	
HLA A*0101	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.331003	2.016506	-2.314497	21429.057059	
HLA B*5301	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.548086	2.232643	-2.315443	35325.3177	
HLA A*2402	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.332211	2.016506	-2.315705	21488.727398	
HLA A*2403	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.341475	2.025047	-2.316427	21952.0314	
HLA A*3001	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.236129	1.919326	-2.316803	17223.781498	
HLA A*3001	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.443509	1.126312	-2.317196	2776.56980	
HLA B*3901	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.463643	2.146371	-2.317273	29083.270125	
HLA B*3501	1:200-208	9	ASEHADVEI	1.329405	0.306162	-3.955461	1.635567	-2.319894	9025.29442	
HLA A*0250	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.344999	2.025047	-2.319952	22130.8932	
HLA A*2402	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.011957	1.691549	-2.320408	10279.147426	
HLA A*2402	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.365468	2.044564	-2.320903	23198.9140	
HLA A*0301	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.348753	2.027215	-2.321538	22323.0442	
HLA A*3101	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.352440	2.030272	-2.322167	22513.3313	
HLA A*0216	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.349745	2.027215	-2.322530	22374.0653	
HLA A*0211	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.241885	1.919326	-2.322559	17453.589028	
HLA A*6801	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.339515	2.016506	-2.323009	21853.210314	
HLA B*5801	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.353318	2.030272	-2.323046	22558.9286	
HLA B*5301	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.495281	2.172078	-2.323204	31281.0557	
HLA B*0801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-3.478098	1.154646	-2.323452	3006.75273	
HLA A*0301	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.102332	1.778801	-2.323531	12657.0467	
HLA B*1503	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.114902	1.790637	-2.324265	13028.731368	
HLA A*1101	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.472214	2.146371	-2.325844	29662.937611	
HLA A*3301	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.150450	1.824451	-2.325999	14140.0139	
HLA A*6802	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-2.945817	0.619672	-2.326145	882.708256	
HLA A*0201	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-3.110610	0.784286	-2.326324	1290.060466	
HLA B*1501	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.371095	2.044564	-2.326531	23501.4508	
HLA A*6901	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.453104	1.126312	-2.326791	2838.59800	
HLA B*1509	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.289511	1.962283	-2.327228	19476.510803	
HLA A*0301	1:89-97	9	CTHELIRHR	1.005015	0.652731	-3.985497	1.657746	-2.327751	9671.574795	
HLA B*0702	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.267699	1.939903	-2.327796	18522.454531	
HLA A*0216	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.474251	2.146371	-2.327881	29802.394676	
HLA B*1801	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.290493	1.962283	-2.328210	19520.603528	
HLA A*0219	1:77-85	9	SVSFYITGI	0.979963	0.379282	-3.687705	1.359245	-2.328459	4871.970721	
HLA A*3101	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.354608	2.025047	-2.329561	22626.0288	
HLA B*1503	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.354634	2.025047	-2.329587	22627.3753	
HLA A*0301	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.148035	1.818422	-2.329613	14061.594414	
HLA A*3001	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.269761	1.939903	-2.329859	18610.643294	
HLA A*0101	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.229573	1.899550	-2.330024	16965.764887	
HLA A*3301	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.562834	2.232643	-2.330191	36545.4904	
HLA B*2705	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.346883	2.016506	-2.330377	22227.121852	
HLA B*0801	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.357679	2.027215	-2.330464	22786.5782	
HLA A*6901	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.376562	2.044564	-2.331998	23799.1762	
HLA A*2602	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.504238	2.172078	-2.332160	31932.8469	
HLA A*3301	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.163320	1.830609	-2.332711	14565.329596	
HLA A*6802	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.273065	1.939903	-2.333162	18752.741242	
HLA A*0202	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.325438	0.991777	-2.333661	2115.61957	
HLA A*6901	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.361624	2.027215	-2.334409	22994.4962	
HLA A*2301	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.365024	2.030272	-2.334751	23175.2060	
HLA B*1501	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.360045	2.025047	-2.334998	22911.0527	
HLA A*0301	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.365740	2.030272	-2.335468	23213.4770	
HLA A*0202	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.126776	1.790637	-2.336139	13389.872046	
HLA B*4001	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.235816	1.899550	-2.336266	17211.393182	
HLA A*1101	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.381898	2.044564	-2.337333	24093.3730	
HLA A*2603	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.277425	1.939903	-2.337523	18941.981375	
HLA A*0301	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.363245	2.025047	-2.338198	23080.4910	
HLA B*4801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.382769	2.044564	-2.338205	24141.7786	
HLA B*5101	1:52-60	9	PKTATNAGY	1.018085	1.128286	-4.484622	2.146371	-2.338251	30522.618508	
HLA B*4601	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.363550	2.025047	-2.338503	23096.7289	
HLA A*0101	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.369565	2.030272	-2.339293	23418.8280	
HLA A*0219	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.369746	2.030272	-2.339474	23428.5855	
HLA A*2603	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.573468	2.233875	-2.339593	37451.3574	
HLA A*0101	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.384621	2.044564	-2.340056	24244.9145	
HLA B*4601	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.384910	2.044564	-2.340345	24261.0529	
HLA B*0802	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.385304	2.044564	-2.340740	24283.1128	
HLA A*0203	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.385544	2.044564	-2.340980	24296.5162	
HLA B*4801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.273051	1.931281	-2.341769	18752.1325	
HLA A*6801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.287728	1.945662	-2.342065	19396.7021	
HLA A*2301	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.271277	1.928720	-2.342557	18675.6963	
HLA A*0301	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.289058	1.945662	-2.343395	19456.1858	
HLA A*2601	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.388464	2.044564	-2.343900	24460.4485	
HLA B*5701	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.389470	2.044564	-2.344906	24517.1506	
HLA A*3201	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.792304	1.446759	-2.345544	6198.74458	
HLA A*2601	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.370862	2.025047	-2.345815	23488.8672	
HLA A*2501	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.362458	2.016506	-2.345952	23038.699833	
HLA B*4002	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.518060	2.172078	-2.345982	32965.4993	
HLA B*3901	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.245557	1.899550	-2.346007	17601.796298	
HLA B*4801	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.265495	1.919326	-2.346169	18428.700856	
HLA B*0702	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.137011	1.790637	-2.346373	13709.158057	
HLA B*1502	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.275269	1.928720	-2.346549	18848.1434	
HLA B*0801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.391632	2.044564	-2.347067	24639.4790	
HLA A*0250	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.378059	2.030272	-2.347786	23881.3320	
HLA B*4501	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.519892	2.172078	-2.347815	33104.8982	
HLA A*0206	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.378188	2.030272	-2.347916	23888.4388	
HLA B*4403	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.512313	2.164386	-2.347926	32532.1539	
HLA A*0201	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.392851	2.044564	-2.348287	24708.7573	
HLA B*2705	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.373463	2.025047	-2.348416	23629.9582	
HLA B*4801	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.374649	2.025047	-2.349602	23694.6034	
HLA A*1101	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.366201	2.016506	-2.349605	23238.104269	
HLA B*3501	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-3.133362	0.783495			
HLA A*8001	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.377476	2.027215			

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HLA B*0803	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.395158	2.044564	-2.350594	24840.3721
HLA A*0212	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.381747	2.030272	-2.351475	24085.0325
HLA A*0101	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.380138	2.027215	-2.352923	23995.9440
HLA B*3901	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.012328	1.658831	-2.353497	10287.9374
HLA A*0219	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.378620	2.025047	-2.353573	23912.2296
HLA B*1503	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.197646	1.843851	-2.353795	15763.2692
HLA B*0702	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.378940	2.025047	-2.353892	23929.8294
HLA A*6901	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.384529	2.030272	-2.354257	24239.7997
HLA B*0802	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.046264	1.691549	-2.354715	11124.084390	
HLA B*4601	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.371377	2.016506	-2.354871	23516.712593	
HLA B*5701	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.385441	2.030272	-2.355168	24290.7334
HLA A*3201	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.587830	2.232643	-2.355187	38710.6056
HLA A*0201	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-2.974866	0.619672	-2.355194	943.770115	
HLA A*0206	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.802054	1.446759	-2.355295	6339.48684
HLA B*5401	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.513941	2.158180	-2.355761	32654.3476
HLA B*4001	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.383796	2.027215	-2.356581	24198.9203
HLA A*0206	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.504068	2.146371	-2.357698	31920.411102	
HLA B*7301	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.516330	2.158014	-2.358317	32834.502338	
HLA A*0201	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.388690	2.030272	-2.358418	24473.1553
HLA B*1517	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.299311	1.939903	-2.359408	19920.987274	
HLA A*3301	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.517658	2.158180	-2.359477	32935.0174
HLA A*2601	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.390039	2.030272	-2.359766	24549.2693
HLA B*2705	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-3.417754	1.057871	-2.359883	2616.69763
HLA A*0202	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.517919	2.158014	-2.359905	32954.800742	
HLA B*1509	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.259945	1.899550	-2.360396	18194.714145	
HLA A*0206	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.387875	2.027215	-2.360660	24427.2566
HLA B*1509	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.377777	2.016506	-2.361271	23865.833622	
HLA B*0801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.292657	1.931281	-2.361376	19618.1077
HLA B*5101	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.077433	1.715719	-2.361713	11951.7786
HLA B*1801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-3.290562	0.927121	-2.363440	1952.36863
HLA B*4601	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.394216	2.030272	-2.363944	24786.5427
HLA B*1502	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.528510	2.164386	-2.364124	33768.3754
HLA A*3101	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.086126	1.721985	-2.364141	12193.4229
HLA B*3501	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.293263	1.928720	-2.364543	19645.5089
HLA A*2902	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.030405	1.665496	-2.364909	10725.1963
HLA B*1517	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.395388	2.030272	-2.365116	24853.5452
HLA A*0202	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.533912	1.168653	-2.365259	3419.10218
HLA A*0250	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.524032	2.158180	-2.365852	33421.9703
HLA B*0702	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.410453	2.044564	-2.365889	25730.7974
HLA B*1501	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.328715	1.962283	-2.366432	21316.439350	
HLA B*4801	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.394507	2.027215	-2.367292	24803.1757
HLA B*4001	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.411910	2.044564	-2.367346	25817.2468
HLA B*0801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-3.408741	1.041264	-2.367477	2562.95462
HLA B*3501	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.026327	1.658831	-2.367495	10624.9414
HLA B*4403	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.514392	2.146371	-2.368021	32688.283290	
HLA A*0201	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.395872	2.027215	-2.368657	24881.2584
HLA B*5101	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-3.359411	0.990022	-2.369389	2287.76351
HLA B*0802	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.288950	1.919326	-2.369624	19451.344658	
HLA A*8001	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.400489	2.030272	-2.370217	25147.1678
HLA B*1502	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.542396	2.172078	-2.370318	34865.4780
HLA B*4801	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.161037	1.790637	-2.370399	14488.940108	
HLA A*2902	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.289875	1.919326	-2.370550	19492.849346	
HLA B*4001	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.290385	1.919326	-2.371059	19515.746334	
HLA B*5701	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.387703	2.016506	-2.371197	24417.611683	
HLA A*2603	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.271138	1.899550	-2.371589	18669.736281	
HLA A*3201	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.063655	1.691549	-2.372106	11578.576325	
HLA A*6802	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.402481	2.030272	-2.372209	25262.7976
HLA A*3001	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.275210	1.901677	-2.373533	18845.5944
HLA A*2602	1:141-149	9	ATYSELLAK	0.738811	0.394589	-3.507541	1.133400	-2.374141	3217.66969
HLA B*3501	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.305459	1.931281	-2.374178	20205.0281
HLA A*0212	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.401412	2.027215	-2.374197	25200.6897
HLA A*0212	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.419191	2.044564	-2.374627	26253.7279
HLA B*3501	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.405320	2.030272	-2.375047	25428.4343
HLA A*6901	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.337401	1.962283	-2.375118	21747.067822	
HLA B*2705	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.210413	1.834955	-2.375458	16233.5459
HLA B*4402	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.420561	2.044564	-2.375997	26336.6620
HLA A*0203	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.822833	1.446759	-2.376074	6650.17310
HLA A*2602	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-3.997418	1.621061	-2.376357	9940.73466
HLA A*2602	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.069115	1.691549	-2.377566	11725.067889	
HLA B*4402	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.402923	2.025047	-2.377876	25288.5044
HLA B*7301	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.612323	2.233875	-2.378449	40956.5481
HLA B*1501	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.307313	1.928720	-2.378593	20291.4556
HLA A*3101	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.037773	1.658831	-2.378942	10908.7059
HLA A*6901	1:134-142	9	EAADAARAT	0.999569	-0.361461	-3.018087	0.638108	-2.379980	1042.52708
HLA A*0203	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.408130	2.027215	-2.380914	25593.4955
HLA A*6802	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.425760	2.044564	-2.381196	26653.8617
HLA B*4403	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.615406	2.232643	-2.382763	41248.2826
HLA B*5101	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.408007	2.025047	-2.382960	25586.2967
HLA B*1503	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-3.172528	0.789295	-2.383234	1487.744640	
HLA B*0803	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.329142	1.945662	-2.383480	21337.4378
HLA A*2603	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.541804	2.158014	-2.383790	34817.978647	
HLA B*4402	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.346698	1.962283	-2.384415	22217.624427	
HLA B*0702	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.313878	1.928720	-2.385158	20600.4954
HLA B*0801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-3.552684	1.167504	-2.385180	3570.13357
HLA A*0216	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.415589	2.030272	-2.385317	26036.8967
HLA B*1517	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.429987	2.044564	-2.385423	26914.5339
HLA A*2301	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.532551	2.146371	-2.386181	34084.056980	
HLA B*3801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.318328	1.931281	-2.387046	20812.6600
HLA B*3501	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.349489	1.962283	-2.387206	22360.875792	
HLA A*2603	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.318501	1.931281	-2.387220	20820.9936
HLA B*4601	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.838988	1.451496	-2.387492	6902.20746
HLA A*6901	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.327559	1.939903	-2.387656	21259.777561	
HLA A*1101	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.418507	2.030272	-2.388235	26212.4298
HLA B*5401	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.560395	2.172078	-2.388317	36340.8456
HLA B*5801	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.350936	1.962283	-2.388653	22435.517527	
HLA A*0211	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.535592	2.146371	-2.389221	34323.496001	
HLA B*1801	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.419529	2.030272	-2.389257	26274.1882
HLA B*3501	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.208266	1.818422	-2.389844	16153.475031	
HLA A*2501	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.289748	1.899550	-2.390199	19487.155653	
HLA B*0803	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.353032	1.962283	-2.390749	22544.044479	
HLA B*4001	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.353321	1.962283	-2.391038	22559.050647	
HLA B*5401	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.419008	2.027215	-2.391793	26242.6519
HLA A*0202	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.422715	2.030272	-2.392443	26467.6393
HLA A*0211	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.393305	1.000751	-2.392553	2473.45948
HLA A*2603	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.844082	1.451496	-2.392585	6983.63756
HLA A*0203	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.794531	1.401827	-2.392704	6230.61697
HLA A*0219	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.419929	2.027215	-2.392714	26298.3632
HLA A*6802	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.420652	2.027215	-2.393437	26342.2192
HLA A*0219	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.325244	1.931281	-2.393963	21146.7910
HLA B*4402	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.411059	2.016506	-2.394553	25766.736320	
HLA B*4501	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.627254	2.232643	-2.394612	42389.1125
HLA A*0219	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.314131	1.919326	-2.394806	20612.535159	
HLA B*0801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.294384	1.899550	-2.394834	19696.269954	
HLA A*3101	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.324417	1.928720	-2.395697	21106.5599
HLA B*0702	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.041659	1.645813	-2.395847	11006.754611	
HLA A*0206	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.088109	1.691549	-2.3965		
HLA B*1509	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.342541	1.945662		

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HLA A*0203	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-3.307060	0.910145	-2.396915	2027.96243
HLA A*2402	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.316326	1.919326	-2.397000	20716.950503	
HLA A*3201	1:141-149	9	ATYSELLAK	0.738811	0.394589	-3.531060	1.133400	-2.397660	3396.72044
HLA B*1801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.442232	2.044564	-2.397668	27684.2256
HLA B*4402	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.188446	1.790637	-2.397808	15432.834868	
HLA A*6901	1:57-65 9	NAGYLRHII	1.129740	0.203828	-3.731861	1.333568	-2.398293	5393.378392	
HLA B*1501	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.189531	1.790637	-2.398894	15471.455457	
HLA B*4403	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.632902	2.233875	-2.399028	42943.9992
HLA A*6801	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.547804	2.146371	-2.401434	35302.392506	
HLA B*3801	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.418787	2.016506	-2.402281	26229.310204	
HLA B*5801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.333595	1.931281	-2.402313	21557.3088
HLA B*5801	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.342525	1.939903	-2.402622	22005.180521	
HLA A*2301	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.447566	2.044564	-2.403002	28026.2964
HLA A*8001	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.428124	2.025047	-2.403076	26799.3168
HLA B*4001	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.335232	1.931281	-2.403951	21638.7482
HLA B*5401	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.561964	2.158014	-2.403951	36472.412025	
HLA B*4402	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.349743	1.945662	-2.404080	22373.9443
HLA B*5101	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.431444	2.027215	-2.404228	27004.9604
HLA B*4403	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.431965	2.027215	-2.404750	27037.4127
HLA B*2705	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.336818	1.931281	-2.405537	21717.9103
HLA B*1503	1:233-241	9	TTLADGTEV	1.178752	0.144786	-3.729145	1.323538	-2.405607	5359.75435
HLA B*5401	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.552158	2.146371	-2.405787	35658.061938	
HLA A*0206	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.526074	1.119963	-2.406111	3357.94979
HLA A*0202	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.438805	1.032480	-2.406325	2746.66015
HLA A*0201	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.325945	1.919326	-2.406619	21180.910252	
HLA B*4403	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.564930	2.158180	-2.406749	36722.2713
HLA A*6901	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.336144	1.928720	-2.407424	21684.2164
HLA B*3801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.307029	1.899550	-2.407479	20278.177316	
HLA B*4402	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.347623	1.939903	-2.407721	22265.031718	
HLA A*0219	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.123783	1.715719	-2.408064	13297.9036
HLA B*4001	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-3.612845	1.204727	-2.408118	4100.58084
HLA B*1501	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.355200	1.945662	-2.409538	22656.8957
HLA A*0216	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.189146	1.778801	-2.410345	15457.7349
HLA A*0211	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.440912	2.030272	-2.410640	27600.1835
HLA A*2603	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.582875	2.172078	-2.410797	38271.4486
HLA A*3002	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.438074	2.027215	-2.410859	27420.4003
HLA B*4601	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.342306	1.931281	-2.411025	21994.1120
HLA B*1502	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.441824	2.030272	-2.411551	27658.1781
HLA B*5101	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.351484	1.939903	-2.411581	22463.815422	
HLA A*2902	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.437562	2.025047	-2.412514	27388.0810
HLA A*0250	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.570641	2.158014	-2.412628	37208.411841	
HLA A*0101	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.332058	1.919326	-2.412732	21481.172370	
HLA B*0802	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.439977	2.027215	-2.412762	27540.8204
HLA B*4402	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-3.336165	0.923260	-2.412906	2168.52945
HLA B*5301	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.353006	1.939903	-2.413103	22542.702950	
HLA B*4801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.312726	1.899550	-2.413177	20545.959013	
HLA B*3501	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.458331	2.044564	-2.413767	28729.6973
HLA A*2601	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.376343	1.962283	-2.414060	23787.205407	
HLA A*2402	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.376409	1.962283	-2.414126	23790.808892	
HLA A*0101	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.376515	1.962283	-2.414232	23796.601351	
HLA B*4801	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.377053	1.962283	-2.414770	23826.100387	
HLA B*2705	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.377208	1.962283	-2.414925	23834.609079	
HLA B*4501	1:227-235	9	FADFEVTTL	1.891662	0.342213	-4.649281	2.233875	-2.415406	44594.4432
HLA A*2902	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.233988	1.818422	-2.415566	17139.104491	
HLA B*2705	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.442984	2.027215	-2.415769	27732.1930
HLA A*0101	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.131499	1.715719	-2.415779	13536.2663
HLA A*0202	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.344938	1.928720	-2.416218	22127.7806
HLA A*0211	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.356424	1.939903	-2.416522	22720.845522	
HLA B*0801	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.379311	1.962283	-2.417028	23950.292535	
HLA B*0803	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.442331	2.025047	-2.417284	27690.5166
HLA A*2601	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.348819	1.931281	-2.417538	22326.4259
HLA B*0803	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.444864	2.027215	-2.417649	27852.4756
HLA B*4601	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.317313	1.899550	-2.417763	20764.076111	
HLA A*0219	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.462628	2.044564	-2.418064	29015.3797
HLA A*8001	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.463740	2.044564	-2.419175	29089.7216
HLA B*1801	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.338766	1.919326	-2.419440	21815.529559	
HLA A*2301	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.381930	1.962283	-2.419648	24095.197929	
HLA B*4501	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.450014	2.030272	-2.419742	28184.7297
HLA A*3201	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.566452	2.146371	-2.420081	36851.231161	
HLA B*2705	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.275344	1.855018	-2.420326	18851.4066
HLA A*2902	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.450918	2.030272	-2.420646	28243.4942
HLA A*6801	1:208-216	9	IRRLAIECL	1.768404	0.464239	-4.653320	2.232643	-2.420677	45011.0879
HLA B*5801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.366344	1.945662	-2.420682	23245.7741
HLA B*4601	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.982401	1.561696	-2.420704	9602.859474	
HLA B*7301	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.585379	2.164386	-2.420993	38492.7955
HLA A*0301	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.360905	1.939903	-2.421002	22956.462026	
HLA A*3001	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-3.480146	1.058921	-2.421226	3020.97037
HLA B*5801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.350086	1.928720	-2.421366	22391.6232
HLA B*4601	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.384045	1.962283	-2.421762	24212.801110	
HLA A*2603	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.351089	1.928720	-2.422369	22443.4082
HLA A*0101	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.362305	1.939903	-2.422403	23030.599864	
HLA A*0211	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.081474	1.658831	-2.422642	12063.5091
HLA A*3201	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.253491	1.830609	-2.422882	17926.322347	
HLA A*8001	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.354232	1.931281	-2.422951	22606.4526
HLA A*0206	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.824896	1.401827	-2.423069	6681.83578
HLA A*0211	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.451785	2.027215	-2.424570	28299.9316
HLA B*0802	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.353436	1.928720	-2.424716	22565.0314
HLA A*2602	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.582776	2.158014	-2.424763	38262.753820	
HLA B*1503	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-3.178224	0.752698	-2.425526	1507.38276
HLA A*6901	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.545584	1.119963	-2.425621	3512.24111
HLA B*1502	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-3.698996	1.273350	-2.425646	5000.30268
HLA A*2402	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.456550	2.030272	-2.426278	28612.1268
HLA A*0301	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.345807	1.919326	-2.426481	22172.117234	
HLA A*0301	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.358396	1.931281	-2.427114	22824.2074
HLA A*2501	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.367293	1.939903	-2.427391	23296.635598	
HLA A*2402	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.573999	2.146371	-2.427628	37497.174822	
HLA A*2501	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.452822	2.025047	-2.427774	28367.5291
HLA B*7301	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.574255	2.146371	-2.427884	37519.292599	
HLA A*1101	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.455352	2.027215	-2.428137	28533.2935
HLA B*0802	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.391009	1.962283	-2.428726	24604.180714	
HLA B*0802	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.360261	1.931281	-2.428980	22922.4586
HLA B*4601	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.348373	1.919326	-2.429047	22303.488874	
HLA B*0803	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.328853	1.899550	-2.429304	21323.244291	
HLA A*2601	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.369217	1.939903	-2.429315	23400.084991	
HLA B*0702	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.375211	1.945662	-2.429548	23725.2594
HLA A*2902	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.369582	1.939903	-2.429679	23419.714959	
HLA A*3001	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.421762	0.991777	-2.429985	2640.95963
HLA B*0802	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.375822	1.945662	-2.430159	23758.6542
HLA A*2501	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.474977	2.044564	-2.430413	29852.2556
HLA B*0801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-3.510671	1.080003	-2.430668	3240.93987
HLA B*1509	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.370742	1.939903	-2.430840	23482.387510	
HLA A*0201	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.370787	1.939903	-2.430884	23484.801339	
HLA A*0202	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.577321	2.146371	-2.430950	37785.112480	
HLA B*2705	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.330625	1.899550	-2.431075	21410.400644	
HLA A*2402	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.360012	1.928720	-2.431292	22909.3175
HLA B*1517	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.362648	1.931281		
HLA A*0201	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.394157	1.962283	-2.4318		

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HLA B*5101	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.448536	2.016506	-2.432030	28088.985148
HLA B*3801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.360849	1.928720	-2.432129	22953.4816
HLA A*0212	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.351869	1.919326	-2.432543	22483.754653
HLA B*4402	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.361391	1.928720	-2.432671	22982.1841
HLA B*3501	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.333371	1.899550	-2.433822	21546.232511
HLA A*0202	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-3.947652	1.513828	-2.433823	8864.447870
HLA A*0216	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.478598	2.044564	-2.434034	30102.1634
HLA B*1501	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.269024	1.834955	-2.434069	18579.0561
HLA B*0802	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.374147	1.939903	-2.434244	23667.187658
HLA A*0101	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.363238	1.928720	-2.434518	23080.1164
HLA A*0250	1:28-36 9	DADGGPALV	0.931987	-0.051421	-3.315471	0.880566	-2.434905	2067.621606
HLA B*3901	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.480040	2.044564	-2.435476	30202.3191
HLA B*3801	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.462772	2.027215	-2.435556	29024.9565
HLA B*1509	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.480141	2.044564	-2.435577	30209.3458
HLA A*0203	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.398212	1.962283	-2.435929	25015.686706
HLA A*0211	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.226789	1.790637	-2.436152	16857.350021
HLA A*0301	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.365073	1.928720	-2.436353	23177.8390
HLA A*2501	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.467332	2.030272	-2.437060	29331.3416
HLA B*0702	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-3.999162	1.561696	-2.437466	9980.718334
HLA A*0250	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.583888	2.146371	-2.437517	38360.788899
HLA B*2705	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.356850	1.919326	-2.437524	22743.104442
HLA B*5701	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.400221	1.962283	-2.437938	25131.663661
HLA A*6901	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.384148	1.945662	-2.438486	24218.5652
HLA A*0216	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.401201	1.962283	-2.438918	25188.422776
HLA B*0803	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.358617	1.919326	-2.439291	22835.817233
HLA A*1101	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.464574	2.025047	-2.439526	29145.6424
HLA A*2601	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.368459	1.928720	-2.439739	23359.2315
HLA A*0206	1:168-176	9	RQAARAVLP	0.787201	0.256977	-3.484126	1.044178	-2.439949	3048.78285
HLA B*3901	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.468058	2.027215	-2.440843	29380.4145
HLA B*1509	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.342541	1.901677	-2.440865	22006.0138
HLA A*2403	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.381040	1.939903	-2.441137	24045.845001
HLA B*4501	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.600045	2.158014	-2.442031	39814.836655
HLA A*3101	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.382748	1.939903	-2.442846	24140.603274
HLA A*0206	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.487429	2.044564	-2.442865	30720.5808
HLA B*3801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.388831	1.945662	-2.443168	24481.1004
HLA A*3002	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.468927	2.025047	-2.443880	29439.2830
HLA B*1801	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.469113	2.025047	-2.444066	29451.8675
HLA A*6802	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.445078	1.000751	-2.444327	2786.62194
HLA B*3801	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.489182	2.044564	-2.444618	30844.8128
HLA A*0202	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.489537	2.044564	-2.444973	30870.0200
HLA A*0211	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.407303	1.962283	-2.445020	25544.804700
HLA A*0101	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.390795	1.945662	-2.445133	24592.0710
HLA A*3301	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.461938	2.016506	-2.445431	28969.267293
HLA A*0301	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.347630	1.901677	-2.445954	22265.3930
HLA B*4801	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.270560	1.824451	-2.446109	18644.9065
HLA B*4601	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.376167	1.928720	-2.447447	23777.5559
HLA B*0802	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.347515	1.899550	-2.447966	22259.491645
HLA A*1101	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.226794	1.778801	-2.447993	16857.5324
HLA A*2601	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.393772	1.945662	-2.448109	24761.2122
HLA B*3801	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.388175	1.939903	-2.448273	24444.177535
HLA A*3301	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.606464	2.158014	-2.448450	40407.662799
HLA B*5101	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.479117	2.030272	-2.448845	30138.1746
HLA A*0212	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.388946	1.939903	-2.449043	24487.590856
HLA A*6802	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.895982	1.446759	-2.449222	7870.12836
HLA A*1101	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.395395	1.945662	-2.449733	24853.9486
HLA B*1501	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.381125	1.931281	-2.449843	24050.5285
HLA A*0201	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.396013	1.945662	-2.450351	24889.3360
HLA B*7301	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.608724	2.158180	-2.450543	40618.5051
HLA A*0216	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.241415	1.790637	-2.450777	17434.714845
HLA B*5701	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.382950	1.931281	-2.451669	24151.8373
HLA A*6801	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.623763	2.172078	-2.451685	42049.7084
HLA B*4001	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.397498	1.945662	-2.451836	24974.5795
HLA B*0702	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.414140	1.962283	-2.451857	25950.133000
HLA B*0803	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.383197	1.931281	-2.451916	24165.5603
HLA B*3501	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.806560	1.354114	-2.452446	6405.60887
HLA A*0219	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.392903	1.939903	-2.453000	24711.698299
HLA B*4801	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.112416	1.658831	-2.453585	12954.3723
HLA B*4403	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.393948	1.939903	-2.454046	24771.260925
HLA A*0211	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.856092	1.401827	-2.454265	7179.46792
HLA A*0206	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.417262	1.962283	-2.454979	26137.380101
HLA A*0211	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.809131	1.354114	-2.455017	6443.63235
HLA A*3002	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.417358	1.962283	-2.455075	26143.178157
HLA A*0202	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.417365	1.962283	-2.455082	26143.602456
HLA A*6901	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-3.511418	1.056254	-2.455165	3246.52021
HLA A*0212	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.384545	1.928720	-2.455825	24240.7177
HLA B*5101	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.500843	2.044564	-2.456278	31684.1917
HLA A*3101	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.010374	1.553233	-2.457141	10241.7351
HLA A*0212	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.402860	1.945662	-2.457197	25284.8109
HLA A*6802	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.275743	1.818422	-2.457321	18868.751895
HLA B*2705	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.288038	1.830609	-2.457429	19410.558387
HLA B*4001	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.173165	1.715719	-2.457445	14899.2586
HLA A*2602	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.487899	2.030272	-2.457627	30753.8378
HLA A*0212	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.420056	1.962283	-2.457773	26306.046973
HLA A*2603	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.149999	1.691549	-2.458450	14125.334357
HLA B*1501	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.360379	1.901677	-2.458702	22928.6598
HLA B*4601	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.404469	1.945662	-2.458807	25378.6845
HLA B*1503	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.450595	0.991777	-2.458818	2822.24455
HLA A*3301	1:139-147	9	ARATYSELL	1.529098	0.642980	-4.631154	2.172078	-2.459077	42771.4988
HLA B*5801	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.361304	1.901677	-2.459628	22977.5843
HLA B*5701	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.399763	1.939903	-2.459861	25105.165535
HLA A*6802	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.423148	1.962283	-2.460865	26493.998875
HLA B*1517	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.296163	1.834955	-2.461208	19777.0972
HLA B*5701	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.390295	1.928720	-2.461575	24563.7497
HLA A*0250	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.153288	1.691549	-2.461739	14232.723608
HLA B*5701	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.407725	1.945662	-2.462063	25569.6918
HLA B*4002	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.620408	2.158180	-2.462227	41726.1125
HLA A*0201	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.391298	1.928720	-2.462578	24620.5581
HLA B*4402	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.382168	1.919326	-2.462842	24108.367114
HLA A*0203	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-3.771182	1.308218	-2.462964	5904.482936
HLA B*4402	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.394503	1.931281	-2.463221	24802.9074
HLA A*0212	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.025199	1.561696	-2.463503	10597.386950
HLA A*2602	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.488755	2.025047	-2.463707	30814.4579
HLA B*4601	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.122613	1.658831	-2.463782	13262.1256
HLA B*5801	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.294391	1.830609	-2.463782	19696.589620
HLA A*2601	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.254473	1.790637	-2.463836	17966.905612
HLA A*0211	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.508702	2.044564	-2.464137	32262.7706
HLA B*1502	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.256797	1.790637	-2.466159	18063.293015
HLA A*2403	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.411945	1.945662	-2.466283	25819.3419
HLA A*0250	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.499469	1.032480	-2.466989	3158.41090
HLA A*6802	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.029118	1.561696	-2.467422	10693.447296
HLA A*8001	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.396150	1.928720	-2.467430	24897.1468
HLA B*1503	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.246306	1.778801	-2.467505	17632.1989
HLA B*3901	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.159298	1.691549	-2.467749	14431.052223
HLA A*0216	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.397042	1.928720	-2.468322	24948.3820
HLA A*0203	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.414083	1.945662	-2.468421	25946.7636
HLA B*3901	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.915187	1.446759		
HLA A*0216	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.408369	1.939903	-2.4684	

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HLA A*3201	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.499637	2.030272	-2.469365	31596.3813
HLA B*2705	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.288094	1.818422	-2.469672	19413.078766	
HLA A*0203	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.185960	1.715719	-2.470241	15344.7548
HLA A*0219	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.399061	1.928720	-2.470341	25064.5893
HLA A*0301	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-3.408139	0.937566	-2.470574	2559.40756
HLA A*6901	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-3.485170	1.014245	-2.470924	3056.11480
HLA A*8001	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.433619	1.962283	-2.471336	27140.582737	
HLA A*0202	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.250456	1.778801	-2.471655	17801.4618
HLA A*1101	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.391023	1.919326	-2.471697	24604.979362	
HLA A*0101	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.403586	1.931281	-2.472304	25327.1137
HLA A*8001	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.412547	1.939903	-2.472644	25855.124729	
HLA B*1801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.401530	1.928720	-2.472810	25207.5073
HLA A*2403	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.131800	1.658831	-2.472968	13545.6430
HLA B*1517	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.435323	1.962283	-2.473040	27247.241737	
HLA A*0203	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.252079	1.778801	-2.473278	17868.1323
HLA A*0211	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.402035	1.928720	-2.473315	25236.8438
HLA B*4001	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.165172	1.691549	-2.473623	14627.554026	
HLA A*8001	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.393288	1.919326	-2.473962	24733.632786	
HLA B*0702	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-3.454377	0.980281	-2.474096	2846.933443	
HLA B*3801	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.189916	1.715719	-2.474197	15485.1881
HLA A*0250	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.414318	1.939903	-2.474416	25960.804631	
HLA A*0301	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.232999	1.758557	-2.474442	17100.1135
HLA A*3301	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.511418	1.036697	-2.474722	3246.52021
HLA B*0802	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.330141	1.855018	-2.475123	21386.5533
HLA A*0201	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.507612	1.032480	-2.475132	3218.19195
HLA A*3301	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.621648	2.146371	-2.475278	41845.470268	
HLA B*2705	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-3.390467	0.915034	-2.475432	2457.34776
HLA A*0101	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.234364	1.758557	-2.475807	17153.9462
HLA A*3001	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.835205	1.359245	-2.475960	6842.350830	
HLA B*4001	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.112313	1.635567	-2.476746	12951.2890
HLA B*3901	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.439152	1.962283	-2.476869	27488.573649	
HLA A*2603	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.507231	2.030272	-2.476959	32153.6946
HLA B*2705	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.199235	1.721985	-2.477250	15821.0223
HLA A*2301	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.502309	2.025047	-2.477261	31791.3310
HLA A*0219	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.439545	1.962283	-2.477262	27513.419463	
HLA B*3901	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.379182	1.901677	-2.477505	23943.1673
HLA A*0206	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.312668	1.834955	-2.477713	20543.1804
HLA B*1801	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.494659	2.016506	-2.478153	31236.242699	
HLA A*6901	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.381071	1.901677	-2.479394	24047.5361
HLA A*0203	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.512095	1.032480	-2.479615	3251.58238
HLA B*2705	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.419795	1.939903	-2.479892	26290.254995	
HLA A*2902	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.315200	1.834955	-2.480245	20663.3354
HLA B*0803	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.420255	1.939903	-2.480353	26318.146343	
HLA A*1101	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.420312	1.939903	-2.480409	26321.563643	
HLA A*2902	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.409344	1.928720	-2.480624	25665.1785
HLA B*5401	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.420930	1.939903	-2.481027	26359.040640	
HLA A*0203	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.271815	1.790637	-2.481177	18698.847300	
HLA B*3801	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.443468	1.962283	-2.481185	27763.116106	
HLA A*3001	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.260053	1.778801	-2.481252	18199.2425
HLA A*2402	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.507287	2.025047	-2.482240	32157.8696
HLA A*0211	1:28-36 9	DADGGPALV	0.931987	-0.051421	-3.363692	0.880566	-2.483126	2310.425089	
HLA A*0301	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.327244	1.843851	-2.483393	21244.3713
HLA B*4501	1:211-219	9	LAIECLRQL	1.635667	0.528719	-4.647862	2.164386	-2.483475	44448.9654
HLA A*0301	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.308267	1.824451	-2.483816	20336.0731
HLA A*0101	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.385903	1.901677	-2.484227	24316.6350
HLA B*0702	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.931266	1.446759	-2.484507	8536.23538
HLA B*2705	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.329065	1.843851	-2.485213	21333.6288
HLA B*5801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.320447	1.834955	-2.485492	20914.4681
HLA A*2902	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-3.544889	1.058921	-2.485968	3506.62136
HLA A*0206	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.266559	1.778801	-2.487758	18473.9190
HLA A*0212	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.934527	1.446759	-2.487768	8600.57459
HLA B*4501	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.634270	2.146371	-2.487899	43079.423849	
HLA A*0206	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.416733	1.928720	-2.488013	26105.5843
HLA B*1503	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.210287	1.721985	-2.488302	16228.8042
HLA B*4501	1:222-230	9	VAPAVFADF	0.948144	1.210036	-4.646548	2.158180	-2.488368	44314.7491
HLA B*0801	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.319519	1.830609	-2.488910	20869.823614	
HLA B*1501	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.319716	1.830609	-2.489107	20879.309658	
HLA A*2601	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.391404	1.901677	-2.489727	24626.5526
HLA A*3001	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.280405	1.790637	-2.489767	19072.365119	
HLA B*4402	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.389501	1.899550	-2.489951	24518.874958	
HLA A*3002	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.334285	1.843851	-2.490434	21591.6231
HLA A*6802	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.436572	1.945662	-2.490910	27325.7739
HLA B*3901	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.156887	1.665496	-2.491391	14351.1738
HLA A*6901	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.138641	1.646900	-2.491742	13760.7253
HLA B*4002	1:52-60 9	PKTATNAGY	1.018085	1.128286	-4.638194	2.146371	-2.491823	43470.388976	
HLA A*0201	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.183540	1.691549	-2.491991	15259.488792	
HLA A*2403	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.270948	1.778801	-2.492147	18661.5569
HLA A*2501	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.455399	1.962283	-2.493116	28536.380958	
HLA A*0201	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.395118	1.901677	-2.493441	24838.0877
HLA B*5101	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.424818	1.931281	-2.493537	26596.1024
HLA A*3201	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.518772	2.025047	-2.493724	33019.5806
HLA A*8001	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.439718	1.945662	-2.494056	27524.4361
HLA B*0803	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.395872	1.901677	-2.494195	24881.2584
HLA A*6802	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.285214	1.790637	-2.494577	19284.747105	
HLA A*0206	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.131499	1.635567	-2.495931	13536.2663
HLA B*1517	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.441598	1.945662	-2.495936	27643.8176
HLA B*7301	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.320546	1.824451	-2.496095	20919.2207
HLA B*4601	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.398403	1.901677	-2.496726	25026.6510
HLA B*1501	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.352193	1.855018	-2.497175	22500.5464
HLA A*2902	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.442923	1.945662	-2.497261	27728.2926
HLA A*0250	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.288400	1.790637	-2.497762	19426.736507	
HLA B*1502	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.438292	1.939903	-2.498390	27434.199587	
HLA A*2602	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.156300	1.657746	-2.498554	14331.777444	
HLA A*3201	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.460876	1.962283	-2.498593	28898.516154	
HLA A*6901	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.013320	1.513828	-2.499492	10311.451328	
HLA B*0802	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.401243	1.901677	-2.499566	25190.8756
HLA B*5801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.354855	1.855018	-2.499837	22638.8849
HLA A*0250	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.527103	2.027215	-2.499888	33659.1253
HLA A*0219	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.445707	1.945662	-2.500045	27906.6219
HLA B*5101	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.420281	1.919326	-2.500955	26319.712550	
HLA B*4801	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.402841	1.901677	-2.501164	25283.7166
HLA B*0801	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.403111	1.901677	-2.501434	25299.4514
HLA B*3501	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.447143	1.945662	-2.501480	27999.0182
HLA A*3002	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.447387	1.945662	-2.501725	28014.7757
HLA B*5101	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.430577	1.928720	-2.501857	26951.1059
HLA A*6901	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.160741	1.658831	-2.501909	14479.0671
HLA B*5301	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.421458	1.919326	-2.502132	26391.145060	
HLA A*0250	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.178334	1.675398	-2.502935	15077.6454
HLA A*6801	1:9-17 9	VQLIAKTDF	0.933457	1.224557	-4.661052	2.158014	-2.503038	45819.639285	
HLA B*1501	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.220060	1.715719	-2.504341	16598.1765
HLA B*5101	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.466815	1.962283	-2.504532	29296.452963	
HLA A*0202	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.180133	1.675398	-2.504735	15140.2564
HLA A*0250	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.433551	1.928720	-2.504831	27136.3250
HLA B*1503	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.323351	1.818422	-2.504929	21054.783913	
HLA A*1101	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.436286	1.931281	-2.505005	27307.7446
HLA B*1501	1:238-246	9	GTEVATSPL	1.240590	0.206169	-3.952031	1.446759		
HLA B*4403	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-3.428749	0.923260		

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HLA B*5801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.350530	1.843851	-2.506678	22414.5297
HLA B*3901	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-3.958262	1.451496	-2.506766	9083.68288
HLA A*2403	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.409809	1.901677	-2.508133	25692.6846
HLA B*1517	1:1-9 9	VAETAPLRV	1.127505	0.095337	-3.731960	1.222842	-2.509118	5394.603989	
HLA A*2301	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.428462	1.919326	-2.509136	26820.202255	
HLA B*3901	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.333693	1.824451	-2.509242	21562.2075
HLA B*4001	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.339983	1.830609	-2.509374	21876.749448	
HLA B*0802	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.169368	1.658831	-2.510537	14769.5713
HLA B*1503	1:41-49 9	RACYQSWSK	0.781972	0.322141	-3.614828	1.104113	-2.510716	4119.346686	
HLA A*1101	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.356070	1.843851	-2.512218	22702.2925
HLA A*0201	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.074289	1.561696	-2.512593	11865.578912	
HLA B*3801	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.303556	1.790637	-2.512919	20116.683237	
HLA A*6801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.066592	1.553233	-2.513359	11657.1401
HLA B*5701	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.348859	1.834955	-2.513904	22328.4793
HLA A*3001	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-3.708667	1.194587	-2.514080	5112.893833	
HLA B*2705	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.415982	1.901677	-2.514305	26060.4304
HLA A*0202	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.542142	2.027215	-2.514927	34845.1132
HLA A*2603	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.230675	1.715719	-2.514956	17008.8657
HLA A*3002	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.434397	1.919326	-2.515071	27189.226194	
HLA B*5701	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.417098	1.901677	-2.515421	26127.4839
HLA A*1101	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.444610	1.928720	-2.515890	27836.2071
HLA A*1101	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.417788	1.901677	-2.516111	26169.0729
HLA B*5401	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.077879	1.561696	-2.516183	11964.069991	
HLA B*1502	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.561130	2.044564	-2.516566	36402.4335
HLA A*6901	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.335281	1.818422	-2.516860	21641.206716	
HLA B*4801	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.233408	1.715719	-2.517688	17116.2177
HLA A*2603	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.543126	2.025047	-2.518079	34924.1877
HLA A*2403	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.080510	1.561696	-2.518814	12036.781258	
HLA A*0216	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.143959	0.625007	-2.518952	1393.02418
HLA B*5401	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.563527	2.044564	-2.518963	36603.8606
HLA B*0801	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.235447	1.715719	-2.519728	17196.7808
HLA B*5701	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.338232	1.818422	-2.519810	21788.755553	
HLA B*1501	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.278689	1.758557	-2.520133	18997.1927
HLA B*1501	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.299071	1.778801	-2.520270	19909.9977
HLA B*1501	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.512391	0.991777	-2.520614	3253.79957
HLA B*0803	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.375634	1.855018	-2.520616	23748.3739
HLA A*0101	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.351709	1.830609	-2.521100	22475.485020	
HLA A*3001	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-3.707558	1.185494	-2.522063	5099.854878	
HLA A*2603	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.484363	1.962283	-2.522080	30504.460274	
HLA B*4403	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-3.257974	0.735649	-2.522326	1811.23359
HLA A*1101	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.347118	1.824451	-2.522667	22239.1497
HLA B*0702	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.378091	1.855018	-2.523074	23883.1408
HLA A*0211	1:1-9 9	VAETAPLRV	1.127505	0.095337	-3.746296	1.222842	-2.523454	5575.657994	
HLA A*2902	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-3.360017	0.836190	-2.523827	2290.958897	
HLA A*0250	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.568475	2.044564	-2.523911	37023.2814
HLA B*5401	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.549016	2.025047	-2.523969	35401.0769
HLA A*2902	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.199573	1.675398	-2.524175	15833.3521
HLA B*0702	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.456076	1.931281	-2.524794	28580.8766
HLA A*3001	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.028371	1.502929	-2.525442	10675.0666
HLA B*5401	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.556617	2.030272	-2.526345	36026.0840
HLA B*4601	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.242287	1.715719	-2.526567	17469.7426
HLA A*3301	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.553990	2.027215	-2.526775	35808.8466
HLA B*1509	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.370702	1.843851	-2.526851	23480.2279
HLA A*8001	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.428612	1.901677	-2.526936	26829.4899
HLA A*0206	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.192835	1.665496	-2.527338	15589.5847
HLA B*5801	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.345821	1.818422	-2.527399	22172.836938	
HLA B*4501	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.572204	2.044564	-2.527639	37342.5130
HLA A*3201	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-3.233042	0.705319	-2.527723	1710.179633	
HLA B*5101	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.428105	1.899550	-2.528555	26798.156984	
HLA B*1501	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.164194	1.635567	-2.528627	14594.6719
HLA A*2501	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.457575	1.928720	-2.528854	28679.6942
HLA A*0101	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.383946	1.855018	-2.528929	24207.3002
HLA A*0216	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.474733	1.945662	-2.529070	29835.4646
HLA A*2501	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.475043	1.945662	-2.529380	29856.7779
HLA B*5301	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.460817	1.931281	-2.529536	28894.6079
HLA A*2601	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.384600	1.855018	-2.529582	24243.7341
HLA A*6802	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.431594	1.901677	-2.529917	27014.3120
HLA A*0203	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.431747	1.901677	-2.530070	27023.8131
HLA A*3201	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.386526	1.855018	-2.531508	24351.5209
HLA A*0212	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.433267	1.901677	-2.531590	27118.5675
HLA A*2601	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.366668	1.834955	-2.531713	23263.1351
HLA B*4801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.386761	1.855018	-2.531743	24364.6983
HLA B*0702	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.433567	1.901677	-2.531891	27137.3527
HLA B*4601	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.387144	1.855018	-2.532126	24386.1929
HLA B*5301	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.548796	2.016506	-2.532290	35383.078990	
HLA A*6901	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.387534	1.855018	-2.532516	24408.1025
HLA A*2601	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.351578	1.818422	-2.533156	22468.677018	
HLA B*5801	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.357712	1.824451	-2.533261	22788.3041
HLA B*4403	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-3.189745	0.655774	-2.533971	1547.90898
HLA B*4001	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.368968	1.834955	-2.534013	23386.6700
HLA A*0203	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.199737	1.665496	-2.534241	15839.3492
HLA B*4601	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.325005	1.790637	-2.534367	21135.125258	
HLA B*3501	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.181289	1.646900	-2.534390	15180.6084
HLA B*4001	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.378585	1.843851	-2.534733	23910.2893
HLA B*1801	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.480454	1.945662	-2.534791	30231.0897
HLA A*6901	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.226709	1.691549	-2.535160	16854.249629	
HLA B*5301	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.565442	2.030272	-2.535169	36765.6055
HLA B*2705	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.156291	1.621061	-2.535229	14331.4673
HLA B*1801	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.227109	1.691549	-2.535560	16869.757295	
HLA B*1502	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.561229	2.025047	-2.536182	36410.7057
HLA B*1517	1:141-149	9	ATYSELLAK	0.738811	0.394589	-3.670037	1.133400	-2.536636	4677.74499
HLA B*1502	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.195569	1.658831	-2.536738	15688.0638
HLA A*3201	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.581749	2.044564	-2.537185	38172.4028
HLA A*0211	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.392874	1.855018	-2.537857	24710.0941
HLA B*4801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.381747	1.843851	-2.537896	24085.0325
HLA B*5401	1:10-18 9	QLIAKTDFL	1.535406	0.481100	-4.554714	2.016506	-2.538208	35868.562734	
HLA A*0101	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.373244	1.834955	-2.538290	23618.0725
HLA A*2602	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.467137	1.928720	-2.538417	29318.1742
HLA A*0203	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.159561	1.621061	-2.538500	14439.7987
HLA A*2603	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.583359	2.044564	-2.538795	38314.1235
HLA A*0203	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-3.158770	0.619672	-2.539097	1441.351187	
HLA B*4402	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.395412	1.855018	-2.540394	24854.8898
HLA A*2602	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.585095	2.044564	-2.540531	38467.6065
HLA A*6901	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-3.178200	0.637604	-2.540596	1507.30122
HLA A*0101	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.359190	1.818422	-2.540768	22865.980711	
HLA B*4001	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.396086	1.855018	-2.541069	24893.5104
HLA A*6901	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.385053	1.843851	-2.541202	24269.0604
HLA A*2402	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-3.736034	1.194587	-2.541446	5445.447511	
HLA A*0212	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.320372	1.778801	-2.541571	20910.8478
HLA A*0202	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.376686	1.834955	-2.541732	23806.0010
HLA B*3801	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.233377	1.691549	-2.541828	17115.014067	
HLA B*1503	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-3.456891	0.915034	-2.541857	2863.46093
HLA B*1503	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-3.422593	0.880633	-2.541961	2646.022184	
HLA A*2301	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.188023	1.645813	-2.542210	15417.813996	
HLA A*6801	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.569480	2.027215	-2.542265	37109.1056
HLA A*6802	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.202007	1.658831		
HLA B*0801	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.367773	1.824451		

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HLA A*2402	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.322430	1.778801	-2.543629	21010.1808
HLA B*5701	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.374398	1.830609	-2.543789	23680.891568	
HLA A*6801	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.475271	1.931281	-2.543990	29872.4496
HLA A*6901	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.378965	1.834955	-2.544011	23931.2535
HLA A*6901	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.368496	1.824451	-2.544045	23361.2535
HLA A*3301	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.219746	1.675398	-2.544347	16586.1484
HLA A*2602	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.904191	1.359245	-2.544946	8020.305602	
HLA B*1501	1:77-85 9	SVSFYITGI	0.979963	0.379282	-3.904313	1.359245	-2.545068	8022.562146	
HLA A*3301	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.570585	2.025047	-2.545537	37203.5811
HLA A*0203	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.380509	1.834955	-2.545554	24016.4636
HLA A*0201	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.401175	1.855018	-2.546157	25186.9238
HLA A*0101	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.371670	1.824451	-2.547219	23532.6208
HLA A*0250	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.402467	1.855018	-2.547450	25261.9776
HLA B*1801	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.213754	1.665496	-2.548258	16358.9095
HLA B*4403	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-3.582777	1.034236	-2.548540	3826.279311	
HLA B*1509	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.094875	1.546204	-2.548671	12441.568057	
HLA B*1503	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.951994	1.401827	-2.550167	8953.51444
HLA B*4801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.385300	1.834955	-2.550345	24282.8501
HLA A*6802	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.719188	1.168653	-2.550535	5238.26866
HLA A*2403	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.242413	1.691549	-2.550864	17474.846909	
HLA A*0202	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.172065	1.621061	-2.551004	14861.5839
HLA A*3201	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.496771	1.945662	-2.551109	31388.5298
HLA A*6901	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.381968	1.830609	-2.551359	24097.283657	
HLA B*4801	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.382459	1.830609	-2.551850	24124.545065	
HLA B*7301	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.596561	2.044564	-2.551996	39496.6855
HLA A*2902	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.382703	1.830609	-2.552094	24138.122040	
HLA A*2902	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.395948	1.843851	-2.552096	24885.5661
HLA B*5401	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-3.700077	1.147510	-2.552567	5012.76168
HLA B*5701	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.377076	1.824451	-2.552626	23827.3893
HLA B*1502	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.452185	1.899550	-2.552635	28325.970510	
HLA A*2902	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.455239	1.901677	-2.553562	28525.8851
HLA B*4601	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.388805	1.834955	-2.553850	24479.6436
HLA B*5301	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.245580	1.691549	-2.554031	17602.748561	
HLA A*3002	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.482792	1.928720	-2.554071	30394.2575
HLA A*0219	1:233-241	9	TTLADGTEV	1.178752	0.144786	-3.878483	1.323538	-2.554945	7559.32211
HLA A*6901	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-2.722781	0.167651	-2.555130	528.178328	
HLA B*0801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.390318	1.834955	-2.555363	24565.0786
HLA A*2403	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.386026	1.830609	-2.555417	24323.476653	
HLA A*0201	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.399305	1.843851	-2.555454	25078.6953
HLA A*2902	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.346122	1.790637	-2.555485	22188.196186	
HLA A*2601	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.386413	1.830609	-2.555804	24345.198253	
HLA A*2501	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.346611	1.790637	-2.555973	22213.177661	
HLA B*5701	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.411398	1.855018	-2.556380	25786.8170
HLA B*5701	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.400355	1.843851	-2.556504	25139.4145
HLA A*0216	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.458644	1.901677	-2.556967	28750.3762
HLA B*3501	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.458716	1.901677	-2.557040	28755.1983
HLA A*3001	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.279077	1.721985	-2.557093	19014.1577
HLA A*0206	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-2.782805	0.225691	-2.557115	606.464271	
HLA A*2403	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.392475	1.834955	-2.557520	24687.3791
HLA A*0216	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.412598	1.855018	-2.557581	25858.2021
HLA B*5701	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.216442	1.658831	-2.557611	16460.4677
HLA A*2902	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.412666	1.855018	-2.557649	25862.2592
HLA B*5801	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.217391	1.658831	-2.558560	16496.4830
HLA B*7301	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.586148	2.027215	-2.558933	38560.9508
HLA B*4403	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.589289	2.030272	-2.559017	38840.8741
HLA B*4002	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-3.763828	1.204727	-2.559101	5805.34432
HLA A*0201	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.389790	1.830609	-2.559180	24535.195648	
HLA B*4601	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.403132	1.843851	-2.559281	25300.6833
HLA A*3002	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-3.832673	1.273350	-2.559323	6802.56332
HLA B*4002	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.206288	1.646900	-2.559388	16080.0612
HLA A*6802	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.394761	1.834955	-2.559806	24817.6717
HLA A*8001	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.390520	1.830609	-2.559911	24576.510260	
HLA A*3001	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-3.612695	1.052696	-2.559999	4099.16133
HLA A*0219	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.339121	1.778801	-2.560319	21833.3577
HLA B*1801	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.460455	1.899550	-2.560905	28870.545239	
HLA B*5801	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.351662	1.790637	-2.561025	22473.053354	
HLA B*5301	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.605858	2.044564	-2.561293	40351.3030
HLA A*0301	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.597997	1.036697	-2.561300	3962.74962
HLA B*5401	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.380246	1.818422	-2.561824	24001.916326	
HLA B*4801	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.380580	1.818422	-2.562158	24020.361784	
HLA A*0219	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.463949	1.901677	-2.562272	29103.7311
HLA A*2601	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.406325	1.843851	-2.562474	25487.3804
HLA A*3002	1:65-73 9	IDVGHFSVL	1.609507	0.330396	-4.503183	1.939903	-2.563280	31855.374867	
HLA A*0101	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.407669	1.843851	-2.563818	25566.3721
HLA B*4501	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.189017	0.625007	-2.564010	1545.31521
HLA A*8001	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.419128	1.855018	-2.564110	26249.8934
HLA B*4002	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.589580	2.025047	-2.564533	38866.9384
HLA B*1503	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.230469	1.665496	-2.564972	17000.7702
HLA A*2402	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.111364	1.546204	-2.565160	12923.013717	
HLA A*6901	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.012140	1.446759	-2.565381	10283.4858
HLA A*3001	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.186632	1.621061	-2.565571	15368.5150
HLA A*0250	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-3.733440	1.167504	-2.565935	5413.02140
HLA A*0201	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.390499	1.824451	-2.566048	24575.3136
HLA B*4001	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.213289	1.646900	-2.566390	16341.3963
HLA B*0801	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-3.874644	1.308218	-2.566426	7492.794012	
HLA A*0202	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.201998	1.635567	-2.566430	15921.9970
HLA B*1501	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.410683	1.843851	-2.566832	25744.4427
HLA B*3901	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.402106	1.834955	-2.567151	25240.9400
HLA B*4403	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.611734	2.044564	-2.567169	40900.9717
HLA B*0702	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.402138	1.834955	-2.567183	25242.8518
HLA A*0203	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.422313	1.855018	-2.567296	26443.1656
HLA B*5401	1:79-87 9	SFYITGISR	1.120990	0.841293	-4.530028	1.962283	-2.567745	33886.595282	
HLA A*3002	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.386385	1.818422	-2.567963	24343.617846	
HLA A*2603	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.403012	1.834955	-2.568057	25293.7037
HLA A*0206	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.513821	1.945662	-2.568159	32645.3394
HLA B*1509	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.403226	1.834955	-2.568271	25306.1588
HLA A*0203	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.398964	1.830609	-2.568355	25059.030482	
HLA A*2601	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.392834	1.824451	-2.568384	24707.8216
HLA A*0201	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.359697	1.790637	-2.569060	22892.716052	
HLA A*6901	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.327946	1.758557	-2.569390	21278.7631
HLA B*1517	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.471305	1.901677	-2.569628	29600.8994
HLA A*2902	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.261503	1.691549	-2.569954	18260.091330	
HLA A*0219	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.360928	1.790637	-2.570291	22957.703979	
HLA B*0802	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.414457	1.843851	-2.570605	25969.0922
HLA B*4001	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.395360	1.824451	-2.570909	24851.9318
HLA B*4002	1:191-199	9	AWRHFIAMR	1.152543	0.892021	-4.615768	2.044564	-2.571204	41282.6618
HLA B*3901	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.402479	1.830609	-2.571870	25262.660980	
HLA A*2403	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.427351	1.855018	-2.572333	26751.6603
HLA A*0212	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.407559	1.834955	-2.572604	25559.8723
HLA A*0201	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.407704	1.834955	-2.572749	25568.4469
HLA B*4601	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.403454	1.830609	-2.572845	25319.441997	
HLA A*3001	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.288574	1.715719	-2.572854	19434.5152
HLA B*4601	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.194070	1.621061	-2.573009	15634.0096
HLA A*2602	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.408097	1.834955	-2.573142	25591.5571
HLA B*0801	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.363912	1.790637	-2.573275	23115.979341	
HLA B*0803	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.408268	1.834955		
HLA A*3002	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.404258	1.830609	-2.5736		

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HLA B*4601	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.392221	1.818422	-2.573799	24672.959306	
HLA A*2902	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.195067	1.621061	-2.574005	15669.9120	
HLA B*5101	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.519859	1.945662	-2.574197	33102.3910	
HLA B*4002	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.590767	2.016506	-2.574261	38973.267831	
HLA B*0803	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.399185	1.824451	-2.574734	25071.7769	
HLA B*5301	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.220610	1.645813	-2.574797	16619.201709	
HLA A*0301	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.365557	1.790637	-2.574920	23203.683721	
HLA B*0702	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.405773	1.830609	-2.575164	25454.998275	
HLA B*1501	1:70-78	9	FSVLEHASV	1.102668	0.135344	-3.813289	1.238012	-2.575277	6505.629736	
HLA A*0201	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.394308	1.818422	-2.575886	24791.772909	
HLA B*3501	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.406802	1.830609	-2.576193	25515.386211	
HLA A*0219	1:28-36	9	DADGGPALV	0.931987	-0.051421	-3.456778	0.880566	-2.576212	2862.717467	
HLA A*0212	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-3.770985	1.194587	-2.576397	5901.800367	
HLA B*1501	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.394888	1.818422	-2.576466	24824.922875	
HLA A*8001	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.400935	1.824451	-2.576485	25173.0293	
HLA A*0212	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.367124	1.790637	-2.576487	23287.563046	
HLA A*6802	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.335681	1.758557	-2.577124	21661.1188	
HLA B*0802	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.412493	1.834955	-2.577538	25851.9078	
HLA B*4402	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.396056	1.818422	-2.577634	24891.759828	
HLA B*0801	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.396568	1.818422	-2.578146	24921.133388	
HLA A*2301	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.357451	1.778801	-2.578650	22774.6239	
HLA B*1517	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.705053	1.126312	-2.578741	5070.52895	
HLA A*2403	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.403278	1.824451	-2.578827	25309.1709	
HLA B*4001	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.397289	1.818422	-2.578867	24962.557692	
HLA B*5801	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.357679	1.778801	-2.578878	22786.5782	
HLA A*0202	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.484310	0.905427	-2.578883	3050.06962	
HLA B*3901	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.422797	1.843851	-2.578946	26472.6513	
HLA A*2301	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.524697	1.945662	-2.579034	33473.1785	
HLA A*3301	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.270657	1.691549	-2.579107	18649.042512	
HLA B*0802	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.409770	1.830609	-2.579160	25690.321895	
HLA B*0702	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.423239	1.843851	-2.579388	26499.5893	
HLA B*1509	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.434679	1.855018	-2.579661	27206.8828	
HLA A*6801	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.604805	2.025047	-2.579758	40253.6248	
HLA A*2902	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.981635	1.401827	-2.579808	9585.93856	
HLA B*1501	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.404502	1.824451	-2.580051	25380.6067	
HLA A*3201	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.520076	1.939903	-2.580173	33118.870523	
HLA A*2301	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.479803	1.899550	-2.580253	30185.821174	
HLA A*3301	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.610937	2.030272	-2.580665	40826.0300	
HLA A*3002	1:153-161	9	KFADQPNAI	0.977018	0.424809	-3.982979	1.401827	-2.581152	9615.64778	
HLA B*4402	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.425022	1.843851	-2.581171	26608.6231	
HLA B*0803	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.425041	1.843851	-2.581190	26609.7747	
HLA A*0206	1:81-89	9	YITGISRSC	1.133968	-0.008438	-3.706726	1.125530	-2.581197	5090.097489	
HLA A*0219	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.405855	1.824451	-2.581404	25459.8185	
HLA A*2501	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.483247	1.901677	-2.581570	30426.1736	
HLA A*0101	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.372530	1.790637	-2.581893	23579.262029	
HLA A*0212	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.437073	1.855018	-2.582055	27357.2797	
HLA A*0211	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.527765	1.945662	-2.582103	33710.5145	
HLA B*1509	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.247632	1.665496	-2.582135	17686.0800	
HLA B*4601	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.407061	1.824451	-2.582610	25530.5746	
HLA B*1517	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.401758	1.818422	-2.583336	25220.738667	
HLA B*3901	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.277169	1.693800	-2.583370	18930.8149	
HLA B*1509	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.242254	1.658831	-2.583422	17468.4195	
HLA A*0101	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.219426	1.635567	-2.583859	16573.9497	
HLA B*4403	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.229757	1.645813	-2.583944	16972.925464	
HLA A*6802	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.130709	1.546204	-2.584505	13511.683534	
HLA B*0802	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.408975	1.824451	-2.584525	25643.3889	
HLA A*0301	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.276406	1.691549	-2.584857	18897.559819	
HLA A*0250	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.547560	1.962283	-2.585277	35282.535961	
HLA A*2501	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.440409	1.855018	-2.585392	27568.2488	
HLA A*2403	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.404326	1.818422	-2.585904	25370.310893	
HLA B*4501	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.527051	1.939903	-2.587149	33655.119602	
HLA A*8001	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.422116	1.834955	-2.587161	26431.1518	
HLA A*0203	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.413331	1.824451	-2.588881	25901.8846	
HLA B*3901	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.443917	1.855018	-2.588899	27791.8182	
HLA A*0202	1:81-89	9	YITGISRSC	1.133968	-0.008438	-3.715048	1.125530	-2.589518	5188.573535	
HLA B*4402	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.414130	1.824451	-2.589679	25949.5714	
HLA A*6802	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.444713	1.855018	-2.589696	27842.8338	
HLA A*3101	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.380469	1.790637	-2.589832	24014.255028	
HLA B*5401	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.305791	1.715719	-2.590071	20220.4463	
HLA B*1502	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.521875	1.931281	-2.590594	33256.3990	
HLA B*3501	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.434587	1.843851	-2.590736	27201.1431	
HLA B*0802	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.409267	1.818422	-2.590845	25660.597001	
HLA A*2402	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.536980	1.945662	-2.591318	34433.4122	
HLA A*2603	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.257467	1.665496	-2.591970	18091.1648	
HLA B*7301	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.537849	1.945662	-2.592187	34502.4052	
HLA B*3501	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.447232	1.855018	-2.592214	28004.7747	
HLA A*0201	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.371269	1.778801	-2.592467	23510.8610	
HLA B*1517	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.383350	1.790637	-2.592712	24174.059521	
HLA B*7301	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.609553	2.016506	-2.593047	40696.148009	
HLA A*0212	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.436927	1.843851	-2.593076	27348.1052	
HLA A*0211	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.284662	1.691549	-2.593113	19260.245523	
HLA A*0219	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.448381	1.855018	-2.593363	28078.9576	
HLA A*2902	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.044883	1.451496	-2.593386	11088.7547	
HLA B*1801	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.412009	1.818422	-2.593587	25823.113562	
HLA B*1502	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.372798	1.778801	-2.593997	23593.8084	
HLA A*0201	1:70-78	9	FSVLEHASV	1.102668	0.135344	-3.832090	1.238012	-2.594078	6793.442768	
HLA B*4403	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.610604	2.016506	-2.594097	40794.679353	
HLA B*1503	1:74-82	9	EHASVSFYI	0.978340	0.173645	-3.746113	1.151985	-2.594128	5573.305723	
HLA A*0216	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.429157	1.834955	-2.594203	26863.1845	
HLA B*1517	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.449499	1.855018	-2.594482	28151.3571	
HLA A*2603	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.385154	1.790637	-2.594517	24274.706719	
HLA B*3801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.429543	1.834955	-2.594588	26887.0287	
HLA B*3501	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.429569	1.834955	-2.594614	26888.6288	
HLA B*1503	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.353213	1.758557	-2.594656	22553.4374	
HLA B*0702	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.419236	1.824451	-2.594785	26256.4266	
HLA B*4501	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.541125	1.945662	-2.595462	34763.5847	
HLA A*3001	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.409765	0.814245	-2.595520	2569.00703	
HLA B*7301	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.620786	2.025047	-2.595739	41762.4714	
HLA A*6901	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.217015	1.621061	-2.595954	16482.2101	
HLA B*1801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.354590	1.758557	-2.596033	22625.0496	
HLA A*1101	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.632731	1.036697	-2.596035	4292.70871	
HLA B*4002	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.623460	2.027215	-2.596245	42020.3732	
HLA A*2501	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.431498	1.834955	-2.596543	27008.3207	
HLA B*0801	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.748772	1.152145	-2.596628	5607.54133	
HLA B*4402	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.431718	1.834955	-2.596763	27022.0588	
HLA B*1509	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.421416	1.824451	-2.596965	26388.5752	
HLA B*4601	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.376327	1.778801	-2.597526	23786.3046	
HLA B*4501	1:184-192	9	VVTGNYRAW	1.568491	0.458724	-4.624905	2.027215	-2.597690	42160.4113	
HLA A*0301	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.319932	1.721985	-2.597948	20889.7040	
HLA A*0212	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.952200	1.354114	-2.598086	8957.77796	
HLA A*3101	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.291917	1.693800	-2.598117	19584.7047	
HLA A*6802	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.441993	1.843851	-2.598141	27668.9534	
HLA A*0203	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.442451	1.843851	-2.598600	27698.1576	
HLA B*5301	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.952778	1.354114	-2.598664	8969.70720	
HLA A*0202	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.265288	1.665496	-2.59879[illegible]	18419.9295	
HLA A*2602	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.430452	1.830609	-2.5998[illegible]		
HLA B*3901	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.418970	1.818422	-2.6005[illegible]		

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HLA A*6802	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.379464	1.778801	-2.600662	23958.7159
HLA B*0801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.444535	1.843851	-2.600684	27831.3886
HLA A*8001	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.444641	1.843851	-2.600789	27838.1648
HLA B*4501	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.563348	1.962283	-2.601065	36588.813975
HLA A*0203	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.420150	1.818422	-2.601728	26311.740101
HLA B*1501	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.223016	1.621061	-2.601955	16711.5230
HLA A*0101	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.381035	1.778801	-2.602234	24045.5848
HLA B*4403	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.627461	2.025047	-2.602414	42409.2975
HLA A*2601	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.324413	1.721985	-2.602428	21106.3315
HLA B*1502	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.548128	1.945662	-2.602466	35328.7578
HLA B*5101	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-3.910887	1.308218	-2.602669	8144.922364
HLA B*5801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.361250	1.758557	-2.602694	22974.7254
HLA B*0801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.249793	1.646900	-2.602894	17774.3248
HLA A*6801	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.531757	1.928720	-2.603037	34021.7897
HLA A*0211	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.438071	1.834955	-2.603116	27420.2520
HLA B*3801	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.433838	1.830609	-2.603229	27154.241135
HLA B*0801	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.249253	1.645813	-2.603440	17752.222420
HLA B*5101	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.505229	1.901677	-2.603552	32005.8320
HLA A*0212	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.428131	1.824451	-2.603680	26799.7517
HLA B*1801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.459346	1.855018	-2.604328	28796.9192
HLA B*1503	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.958722	1.354114	-2.604608	9093.31977
HLA B*4001	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.363468	1.758557	-2.604912	23092.3560
HLA B*4002	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.567352	1.962283	-2.605069	36927.665611
HLA A*2501	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.449586	1.843851	-2.605735	28156.9927
HLA B*4402	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.436450	1.830609	-2.605841	27318.087870
HLA B*7301	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-3.955865	1.349023	-2.606842	9033.69637
HLA A*2601	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.264630	1.657746	-2.606884	18392.048772
HLA A*3301	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.508655	1.901677	-2.606978	32259.2800
HLA A*2501	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.425403	1.818422	-2.606981	26631.953210
HLA B*5301	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.058834	1.451496	-2.607338	11450.7522
HLA A*3201	1:41-49	9	RACYQSWSK	0.781972	0.322141	-3.711481	1.104113	-2.607369	5146.138353
HLA B*0802	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.398384	1.790637	-2.607747	25025.567900
HLA A*2601	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.386740	1.778801	-2.607939	24363.5121
HLA A*3001	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.301959	1.693800	-2.608159	20042.8154
HLA B*0802	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.324065	1.715719	-2.608346	21089.4392
HLA B*3801	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.510135	1.901677	-2.608458	32369.4146
HLA A*0219	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.443642	1.834955	-2.608687	27774.2327
HLA B*4002	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-3.642933	1.034236	-2.608696	4394.736933
HLA A*6802	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.439345	1.830609	-2.608736	27500.770585
HLA B*1509	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.255737	1.646900	-2.608838	18019.2748
HLA B*5401	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.537683	1.928720	-2.608963	34489.1553
HLA A*0301	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.284589	1.675398	-2.609191	19257.0157
HLA A*6901	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.388032	1.778801	-2.609231	24436.1122
HLA A*0206	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.510974	1.901677	-2.609297	32431.9911
HLA B*5101	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.400118	1.790637	-2.609480	25125.682154
HLA B*5301	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.538876	1.928720	-2.610156	34584.0695
HLA B*3801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.454584	1.843851	-2.610732	28482.8618
HLA A*3201	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.539532	1.928720	-2.610812	34636.3087
HLA B*1517	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.455028	1.843851	-2.611176	28511.9995
HLA A*0212	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.430041	1.818422	-2.611619	26917.883088
HLA B*7301	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.574109	1.962283	-2.611826	37506.710246
HLA A*8001	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.402693	1.790637	-2.612055	25275.100848
HLA A*2602	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.574379	1.962283	-2.612096	37530.051827
HLA B*0702	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.370853	1.758557	-2.612296	23488.3590
HLA B*5401	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.558038	1.945662	-2.612376	36144.1899
HLA B*1503	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-3.817673	1.204727	-2.612947	6571.63571
HLA A*2402	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.259398	1.645813	-2.613585	18171.794081
HLA B*1503	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-3.666390	1.052696	-2.613694	4638.63437
HLA B*5801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.249368	1.635567	-2.613800	17756.9288
HLA A*0212	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.444544	1.830609	-2.613935	27831.990881
HLA A*6802	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.438539	1.824451	-2.614088	27449.7876
HLA A*0216	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.438870	1.824451	-2.614419	27470.7342
HLA B*3501	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.438969	1.824451	-2.614518	27476.9767
HLA B*2705	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.280433	1.665496	-2.614936	19073.6033
HLA A*2902	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.439596	1.824451	-2.615145	27516.6942
HLA B*1502	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.470363	1.855018	-2.615345	29536.7538
HLA B*4801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.373970	1.758557	-2.615414	23657.5868
HLA B*0802	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.374786	1.758557	-2.616229	23702.0393
HLA A*2403	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.407390	1.790637	-2.616752	25549.918411
HLA B*1517	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.441349	1.824451	-2.616898	27627.9698
HLA B*4001	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.395821	1.778801	-2.617020	24878.2973
HLA A*2601	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.375984	1.758557	-2.617427	23767.5245
HLA A*1101	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.408527	1.790637	-2.617889	25616.905629
HLA A*2902	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.376614	1.758557	-2.618057	23802.0089
HLA B*5401	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.537455	1.919326	-2.618129	34471.061548
HLA A*2902	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.396995	1.778801	-2.618194	24945.6828
HLA A*2602	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-3.255926	0.637604	-2.618321	1802.70936
HLA B*3801	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.443116	1.824451	-2.618665	27740.5959
HLA B*2705	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.397522	1.778801	-2.618721	24975.9306
HLA A*0211	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.520468	1.901677	-2.618791	33148.8053
HLA A*3001	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.165115	1.546204	-2.618911	14625.654946
HLA A*3002	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.410571	1.790637	-2.619933	25737.758428
HLA A*0250	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.286267	1.665496	-2.620770	19331.5428
HLA B*0803	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.451456	1.830609	-2.620847	28278.505810
HLA B*4501	1:10-18	9	QLIAKTDFL	1.535406	0.481100	-4.637475	2.016506	-2.620969	43398.486491
HLA A*0219	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.312527	1.691549	-2.620978	20536.513319
HLA B*2705	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.278746	1.657746	-2.621000	18999.659410
HLA A*3301	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.550819	1.928720	-2.622098	35548.2747
HLA B*1509	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.314822	1.691549	-2.623273	20645.345635
HLA B*5301	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.586441	1.962283	-2.624158	38587.035993
HLA B*4601	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.382722	1.758557	-2.624166	24139.1667
HLA A*0202	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.569892	1.945662	-2.624229	37144.2546
HLA B*4801	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.403128	1.778801	-2.624326	25300.4095
HLA B*1503	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.625152	1.000751	-2.624401	4218.44101
HLA B*7301	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.544278	1.919326	-2.624952	35016.889226
HLA A*2601	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.319014	1.693800	-2.625214	20845.5634
HLA B*4501	1:203-211	9	HADVEIRRL	1.774485	0.250562	-4.650373	2.025047	-2.625326	44706.7661
HLA A*3002	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.384033	1.758557	-2.625477	24212.1461
HLA A*0216	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.444049	1.818422	-2.625627	27800.239162
HLA B*1502	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.461172	1.834955	-2.626217	28918.2214
HLA A*3001	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.301700	1.675398	-2.626302	20030.8917
HLA B*0801	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.405216	1.778801	-2.626415	25422.3822
HLA A*8001	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.444915	1.818422	-2.626494	27855.790793
HLA B*5301	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.526537	1.899550	-2.626987	33615.269781
HLA B*3801	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.482101	1.855018	-2.627083	30345.9537
HLA B*1502	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.546418	1.919326	-2.627092	35189.892744
HLA A*2602	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.529300	1.901677	-2.627623	33829.8128
HLA A*3201	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.462750	1.834955	-2.627795	29023.5433
HLA A*3001	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-3.464001	0.836190	-2.627811	2910.722511
HLA A*2602	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.573991	1.945662	-2.628329	37496.5662
HLA B*5401	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.559725	1.931281	-2.628444	36284.8578
HLA A*8001	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.407265	1.778801	-2.628464	25542.5936
HLA A*0301	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.080163	1.451496	-2.628666	12027.1477
HLA B*4501	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.557940	1.928720	-2.629220	36135.9783
HLA A*2301	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.447883	1.818422	-2.629461	28046.772492
HLA A*0101	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.321286	1.691549	-2.6297	
HLA A*0219	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.448179	1.818422	-2.6297	

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HLA A*0219	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.474197	1.843851	-2.630346	29798.6866
HLA B*2705	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.306127	1.675398	-2.630729	20236.0952
HLA B*5701	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.421693	1.790637	-2.631056	26405.426240
HLA A*0206	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.486107	1.855018	-2.631089	30627.1554
HLA B*4501	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.757644	1.126312	-2.631332	5723.26874
HLA B*2705	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.347433	1.715719	-2.631714	22255.2772
HLA B*4403	1:79-87	9	SFYITGISR	1.120990	0.841293	-4.594307	1.962283	-2.632025	39292.304043
HLA A*0219	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.193897	1.561696	-2.632200	15627.752135
HLA B*1502	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.534215	1.901677	-2.632538	34214.8561
HLA A*0212	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.391251	1.758557	-2.632694	24617.8944
HLA B*5701	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.411872	1.778801	-2.633071	25815.0122
HLA B*7301	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.573634	1.939903	-2.633732	37465.745390
HLA B*5801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.355865	1.721985	-2.633881	22691.6100
HLA A*0206	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.148415	1.513828	-2.634587	14073.923426
HLA B*4001	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.293496	1.658831	-2.634665	19656.0334
HLA A*0201	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.393535	1.758557	-2.634978	24747.6864
HLA B*1801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.357012	1.721985	-2.635027	22751.5956
HLA A*2402	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.465673	1.830609	-2.635064	29219.527720
HLA A*6801	1:167-175	9	ARQAARAVL	1.496924	0.533348	-4.665781	2.030272	-2.635509	46321.3469
HLA A*0206	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-3.943986	1.308218	-2.635769	8789.951803
HLA B*0801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.394991	1.758557	-2.636435	24830.8327
HLA A*0216	1:177-185	9	NATETRIVV	1.258391	0.095723	-3.990600	1.354114	-2.636486	9785.88879
HLA B*1801	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.471664	1.834955	-2.636709	29625.4106
HLA B*0702	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.455150	1.818422	-2.636728	28520.021512
HLA A*3201	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.480628	1.843851	-2.636776	30243.1946
HLA B*4002	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.568144	1.931281	-2.636862	36995.0510
HLA B*1503	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.522301	0.885414	-2.636887	3328.90135
HLA B*5801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.258268	1.621061	-2.637207	18124.5696
HLA B*3501	1:120-128	9	PGMEDDADL	1.278233	0.056994	-3.973172	1.335227	-2.637945	9400.95116
HLA B*7301	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-3.696153	1.057871	-2.638283	4967.67777
HLA A*0216	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.297116	1.658831	-2.638285	19820.5836
HLA A*0212	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.314601	1.675398	-2.639203	20634.8495
HLA A*0216	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.483123	1.843851	-2.639271	30417.4510
HLA A*2301	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.541555	1.901677	-2.639878	34798.0180
HLA A*2501	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.470591	1.830609	-2.639982	29552.257629
HLA A*2403	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.355809	1.715719	-2.640089	22688.6640
HLA A*3001	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.525642	0.885414	-2.640227	3354.60888
HLA A*0203	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.154566	1.513828	-2.640738	14274.671921
HLA A*0250	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.586575	1.945662	-2.640913	38598.9366
HLA B*5701	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.400219	1.758557	-2.641662	25131.5277
HLA B*0802	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.420998	1.778801	-2.642197	26363.1763
HLA A*3002	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.421061	1.778801	-2.642260	26367.0274
HLA A*0202	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.762324	1.119963	-2.642361	5785.27907
HLA A*0219	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.473006	1.830609	-2.642397	29717.066407
HLA B*0803	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.461122	1.818422	-2.642700	28914.936283
HLA B*0803	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.334259	1.691549	-2.642710	21590.338304
HLA A*0202	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-3.670248	1.027504	-2.642744	4680.02309
HLA A*2501	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.334673	1.691549	-2.643124	21610.905129
HLA A*2902	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.358948	1.715719	-2.643228	22853.2429
HLA A*2403	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.300995	1.657746	-2.643249	19998.408660
HLA A*2602	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.498458	1.855018	-2.643440	31510.6894
HLA B*5301	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.279103	1.635567	-2.643535	19015.2893
HLA B*5101	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.302560	1.658831	-2.643729	20070.5926
HLA A*3001	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.291198	1.646900	-2.644299	19552.3105
HLA B*0802	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.310210	1.665496	-2.644714	20427.2601
HLA B*1509	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.475435	1.830609	-2.644826	29883.764292
HLA A*6901	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.366889	1.721985	-2.644905	23274.9681
HLA A*2603	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.590699	1.945662	-2.645036	38967.1539
HLA B*4002	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.304200	1.658831	-2.645369	20146.5245
HLA A*2602	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.436735	1.790637	-2.646097	27335.976051
HLA B*2705	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-3.490245	0.843953	-2.646292	3092.03607
HLA B*2705	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.437028	1.790637	-2.646391	27354.467878
HLA A*6802	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.304332	1.657746	-2.646586	20152.628892
HLA A*0212	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.048581	1.401827	-2.646754	11183.5804
HLA A*2602	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.160642	1.513828	-2.646814	14475.777652
HLA A*0301	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.362726	1.715719	-2.647006	23052.9128
HLA A*2403	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.282707	1.635567	-2.647140	19173.7494
HLA B*5101	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.466282	1.818422	-2.647860	29260.497687
HLA A*0211	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.313412	1.665496	-2.647916	20578.4408
HLA B*3501	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.427940	1.778801	-2.649139	26788.0106
HLA A*2601	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.365202	1.715719	-2.649483	23184.7365
HLA A*3101	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.365428	1.715719	-2.649708	23196.7806
HLA B*1501	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.371886	1.721985	-2.649902	23544.3361
HLA A*3301	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.589876	1.939903	-2.649974	38893.440934
HLA B*1503	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.776304	1.126312	-2.649991	5974.53004
HLA B*4801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.372070	1.721985	-2.650085	23554.2732
HLA B*5701	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.366111	1.715719	-2.650392	23233.3275
HLA B*1509	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.271462	1.621061	-2.650401	18683.6796
HLA A*1101	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.203694	1.553233	-2.650461	15984.3090
HLA B*5101	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.505777	1.855018	-2.650759	32046.2009
HLA A*1101	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.372934	1.721985	-2.650950	23601.2127
HLA A*2501	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.430241	1.778801	-2.651439	26930.2638
HLA A*2301	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.486461	1.834955	-2.651506	30652.1848
HLA B*1509	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.470241	1.818422	-2.651819	29528.445936
HLA B*7301	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.583103	1.931281	-2.651822	38291.5372
HLA A*0212	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-3.819506	1.167504	-2.652002	6599.42472
HLA A*6801	1:65-73	9	IDVGHFSVL	1.609507	0.330396	-4.592839	1.939903	-2.652937	39159.674011
HLA B*4403	1:96-104	9	HRHFSYSQL	1.392138	0.536582	-4.581806	1.928720	-2.653086	38177.3593
HLA B*5401	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.552891	1.899550	-2.653341	35718.299483
HLA B*4801	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.345147	1.691549	-2.653598	22138.437256
HLA A*2403	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.412410	1.758557	-2.653854	25847.0133
HLA A*6901	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-3.988124	1.334180	-2.653944	9730.24821
HLA B*4402	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.413404	1.758557	-2.654847	25906.2289
HLA A*0212	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.346665	1.691549	-2.655116	22215.941762
HLA A*2603	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.302177	1.646900	-2.655278	20052.9019
HLA B*4403	1:3-11	9	ETAPLRVQL	1.526740	0.392586	-4.574736	1.919326	-2.655411	37560.925599
HLA B*4402	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.302426	1.646900	-2.655527	20064.4045
HLA A*0301	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.349402	1.693800	-2.655602	22356.4003
HLA A*6802	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.561114	0.905427	-2.655688	3640.10924
HLA A*2603	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.557402	1.901677	-2.655725	36091.2385
HLA A*0101	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.378155	1.721985	-2.656170	23886.6296
HLA A*2301	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.480632	1.824451	-2.656182	30243.5218
HLA B*3501	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.277414	1.621061	-2.656352	18941.4690
HLA B*7301	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-3.502443	0.846009	-2.656434	3180.11685
HLA B*1503	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.015881	1.359245	-2.656635	10372.435307
HLA B*1503	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-3.698099	1.041264	-2.656835	4989.97984
HLA A*0206	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.500944	1.843851	-2.657092	31691.5631
HLA A*0202	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.542882	0.885414	-2.657468	3490.45798
HLA A*0216	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.350278	1.691549	-2.658729	22401.558628
HLA B*5301	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.604525	1.945662	-2.658863	40227.7188
HLA B*0702	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.437886	1.778801	-2.659085	27408.5356
HLA A*8001	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.350793	1.691549	-2.659244	22428.114955
HLA B*7301	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.205484	1.546204	-2.659280	16050.337702
HLA A*2602	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.324995	1.665496	-2.659499	21134.6679
HLA A*6802	1:134-142	9	EAADAARAT	0.999569	-0.361461	-3.297643	0.638108	-2.659536	1984.46374
HLA B*5101	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.494555	1.834955		
HLA A*0203	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.295578	1.635567		

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HLA A*0202	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.786407	1.126312	-2.660094	6115.14183
HLA B*4403	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.450984	1.790637	-2.660347	28247.772823	
HLA A*3002	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.562105	1.901677	-2.660429	36484.2526
HLA B*1509	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.009777	1.349023	-2.660754	10227.6715
HLA B*4002	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.580178	1.919326	-2.660852	38034.498400	
HLA B*3901	1:70-78 9	FSVLEHASV	1.102668	0.135344	-3.899069	1.238012	-2.661057	7926.273238	
HLA B*1801	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.504935	1.843851	-2.661084	31984.1958
HLA A*0216	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.491736	1.830609	-2.661127	31026.731629	
HLA A*0201	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.320327	1.658831	-2.661496	20908.6985
HLA A*2402	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.480334	1.818422	-2.661912	30222.749984	
HLA B*4402	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.440830	1.778801	-2.662029	27594.9580
HLA A*2601	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.283675	1.621061	-2.662614	19216.5329
HLA A*0216	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.338275	1.675398	-2.662877	21790.8774
HLA A*0212	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.328381	1.665496	-2.662885	21300.0702
HLA B*4402	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.322040	1.658831	-2.663209	20991.3212
HLA B*3501	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.110072	1.446759	-2.663312	12884.6192
HLA A*2402	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.498270	1.834955	-2.663315	31497.0548
HLA B*5401	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.565223	1.901677	-2.663546	36747.1126
HLA A*0203	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.422142	1.758557	-2.663585	26432.7247
HLA B*5801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.357432	1.693800	-2.663633	22773.6382
HLA A*6901	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.357550	1.693800	-2.663750	22779.7992
HLA A*6802	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-3.626040	0.962074	-2.663966	4227.076293	
HLA A*0202	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.566121	1.901677	-2.664444	36823.1319
HLA B*2705	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.423178	1.758557	-2.664621	26495.8622
HLA A*0219	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-3.833002	1.167504	-2.665497	6807.71743
HLA B*4002	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.612114	1.945662	-2.666452	40936.8331
HLA B*5101	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.511923	1.843851	-2.668071	32502.9518
HLA B*5301	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.486619	1.818422	-2.668197	30663.297094	
HLA A*2501	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.426770	1.758557	-2.668214	26715.9375
HLA B*5101	1:1-9 9	VAETAPLRV	1.127505	0.095337	-3.891574	1.222842	-2.668732	7790.658763	
HLA B*1801	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.499475	1.830609	-2.668866	31584.589209	
HLA A*2501	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.493414	1.824451	-2.668963	31146.8091
HLA A*0201	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.391089	1.721985	-2.669104	24608.7067
HLA A*2402	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.571452	1.901677	-2.669775	37277.9229
HLA A*8001	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.335606	1.665496	-2.670109	21657.3693
HLA B*4402	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.361826	1.691549	-2.670277	23005.196914	
HLA A*3101	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.316450	1.645813	-2.670638	20722.891404	
HLA A*3201	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.495126	1.824451	-2.670676	31269.8887
HLA A*2402	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.495660	1.824451	-2.671209	31308.3131
HLA A*0206	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.495829	1.824451	-2.671378	31320.5104
HLA B*4403	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.602857	1.931281	-2.671576	40073.4996
HLA B*7301	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.571449	1.899550	-2.671900	37277.721238	
HLA B*4402	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.387696	1.715719	-2.671977	24417.2153
HLA B*0803	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.462703	1.790637	-2.672066	29020.403263	
HLA A*2601	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.331377	1.658831	-2.672545	21447.4976
HLA A*0211	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.688273	1.015721	-2.672552	4878.35324
HLA A*3201	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.574421	1.901677	-2.672745	37533.7066
HLA A*2501	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.319815	1.646900	-2.672915	20884.0542
HLA A*2301	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.219440	1.546204	-2.673236	16574.487765	
HLA A*3002	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.332432	1.658831	-2.673600	21499.6578
HLA A*0212	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.332554	1.658831	-2.673722	21505.7068
HLA B*2705	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.332610	1.658831	-2.673779	21508.4992
HLA B*0803	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.432748	1.758557	-2.674191	27086.1643
HLA A*0211	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.498841	1.824451	-2.674390	31538.4882
HLA A*0219	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.333263	1.658831	-2.674432	21540.8712
HLA B*1501	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.188385	1.513828	-2.674556	15430.664283	
HLA A*2403	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.320555	1.645813	-2.674742	20919.673469	
HLA B*1501	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.332650	1.657746	-2.674904	21510.477453	
HLA A*8001	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.433619	1.758557	-2.675062	27140.5827
HLA A*3002	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.311098	1.635567	-2.675531	20469.0753
HLA A*3002	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.391521	1.715719	-2.675802	24633.2149
HLA A*0301	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.335086	1.658831	-2.676255	21631.4915
HLA B*4402	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.398436	1.721985	-2.676451	25028.5465
HLA B*4501	1:3-11 9	ETAPLRVQL	1.526740	0.392586	-4.595994	1.919326	-2.676669	39445.223956	
HLA A*2301	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.531705	1.855018	-2.676688	34017.7408
HLA A*2501	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.392489	1.715719	-2.676770	24688.1804
HLA A*3002	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.531790	1.855018	-2.676772	34024.3666
HLA A*2403	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.128698	1.451496	-2.677202	13449.2574
HLA B*4001	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.124093	1.446759	-2.677334	13307.4031
HLA B*1503	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.124333	1.446759	-2.677574	13314.7483
HLA A*2501	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.298843	1.621061	-2.677782	19899.5525
HLA B*5801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.354333	1.675398	-2.678935	22611.7121
HLA B*1517	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-3.130101	0.451144	-2.678958	1349.27786
HLA A*2402	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.535399	1.855018	-2.680381	34308.2731
HLA A*6901	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.832748	1.152145	-2.680603	6803.74106
HLA B*5801	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.346136	1.665496	-2.680640	22188.9164
HLA B*1517	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.460126	1.778801	-2.681325	28848.6874
HLA A*2603	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.440029	1.758557	-2.681472	27544.0985
HLA B*1503	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.339243	1.657746	-2.681497	21839.500697	
HLA A*2501	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.403654	1.721985	-2.681669	25331.0875
HLA A*2601	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.328663	1.646900	-2.681763	21313.9024
HLA B*0702	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.347675	1.665496	-2.682179	22267.6818
HLA B*0801	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.228584	1.546204	-2.682380	16927.168252	
HLA B*5101	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.506965	1.824451	-2.682515	32134.0445
HLA B*0801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.404718	1.721985	-2.682734	25393.2420
HLA A*0250	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.584482	1.901677	-2.682805	38413.3293
HLA B*5301	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.341872	1.658831	-2.683041	21972.1107
HLA A*0219	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.441744	1.758557	-2.683187	27653.0912
HLA B*0803	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.399227	1.715719	-2.683508	25074.2185
HLA B*5101	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.375150	1.691549	-2.683601	23721.922593	
HLA B*4001	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.359216	1.675398	-2.683818	22867.3414
HLA A*0211	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.359225	1.675398	-2.683827	22867.8363
HLA B*0802	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.319702	1.635567	-2.684135	20878.6319
HLA A*6901	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.342391	1.657746	-2.684645	21998.395969	
HLA B*4403	1:53-61 9	KTATNAGYL	1.501925	0.397625	-4.584207	1.899550	-2.684657	38389.023040	
HLA B*5701	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.342407	1.657746	-2.684662	21999.229047	
HLA A*3201	1:81-89 9	YITGISRSC	1.133968	-0.008438	-3.810244	1.125530	-2.684715	6460.176885	
HLA A*0250	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.519756	1.834955	-2.684801	33094.5124
HLA B*1517	1:140-148	9	RATYSELLA	1.126115	-0.051132	-3.760008	1.074983	-2.685024	5754.50168
HLA B*1501	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.350795	1.665496	-2.685299	22428.2362
HLA B*5101	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.516060	1.830609	-2.685451	32814.081124	
HLA A*0206	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.516276	1.830609	-2.685667	32830.417078	
HLA A*3002	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.510511	1.824451	-2.686060	32397.4451
HLA B*5801	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.343881	1.657746	-2.686135	22073.977144	
HLA A*6901	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.322665	1.635567	-2.687097	21021.5501
HLA A*3001	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.240475	1.553233	-2.687242	17397.0276
HLA B*3501	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.807641	1.119963	-2.687678	6421.56939
HLA B*4601	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.409845	1.721985	-2.687860	25694.7696
HLA B*5401	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.309183	1.621061	-2.688122	20379.0246
HLA B*4801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.364011	1.675398	-2.688613	23121.2322
HLA B*4001	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.382823	1.693800	-2.689024	24144.7827
HLA B*0803	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.468467	1.778801	-2.689666	29408.0839
HLA B*1801	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.514183	1.824451	-2.689732	32672.5483
HLA A*2301	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.520860	1.830609	-2.690251	33178.767206	
HLA A*0201	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.365684	1.675398	-2.690286	23210.4636
HLA A*0206	1:1-9 9	VAETAPLRV	1.127505	0.095337	-3.913166	1.222842	-2.6903		
HLA B*4601	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.336336	1.645813	-2.6905		

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HLA A*0201	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.356121	1.665496	-2.690625	22704.9947
HLA B*3901	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.449335	1.758557	-2.690778	28140.6985
HLA A*0206	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.509350	1.818422	-2.690928	32310.979092
HLA B*3501	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.337337	1.645813	-2.691525	21743.891525
HLA A*0216	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.357301	1.665496	-2.691804	22766.7399
HLA A*0211	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.536240	1.843851	-2.692389	34374.7837
HLA A*0216	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.451048	1.758557	-2.692491	28251.8991
HLA A*6901	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.254346	1.561696	-2.692650	17961.657634
HLA B*3801	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.511493	1.818422	-2.693071	32470.789525
HLA A*6801	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.384677	1.691549	-2.693128	24248.062687
HLA A*0216	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.415164	1.721985	-2.693179	26011.4141
HLA A*6801	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.255000	1.561696	-2.693303	17988.691378
HLA A*0201	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.329060	1.635567	-2.693493	21333.3980
HLA B*7301	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.595616	1.901677	-2.693939	39410.8824
HLA A*2501	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.255895	1.561696	-2.694199	18025.807327
HLA A*0301	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.359874	1.665496	-2.694377	22902.0064
HLA A*0101	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.388319	1.693800	-2.694519	24452.2455
HLA A*0203	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.416536	1.721985	-2.694552	26093.7238
HLA A*2402	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.353403	1.658831	-2.694572	22563.3225
HLA B*0803	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.241067	1.546204	-2.694863	17420.761090
HLA B*0702	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.330590	1.635567	-2.695022	21408.6632
HLA B*5301	1:201-209	9	SEHADVEIR	1.214047	0.687630	-4.597021	1.901677	-2.695344	39538.5875
HLA A*6801	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.411760	1.715719	-2.696040	25808.3095
HLA A*0101	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.371628	1.675398	-2.696230	23530.3293
HLA A*2601	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.371884	1.675398	-2.696486	23544.2087
HLA B*4402	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.390447	1.693800	-2.696648	24572.3885
HLA A*8001	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.412871	1.715719	-2.697151	25874.4344
HLA B*5401	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.149073	1.451496	-2.697577	14095.2583
HLA A*0206	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.456153	1.758557	-2.697596	28585.9795
HLA B*1503	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.391674	1.693800	-2.697874	24641.8785
HLA B*5701	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.364072	1.665496	-2.698576	23124.4846
HLA B*5801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.345694	1.646900	-2.698795	22166.3604
HLA B*3501	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-3.367460	0.668648	-2.698813	2330.560954
HLA A*6802	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.393109	1.693800	-2.699310	24723.4656
HLA B*3801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.335023	1.635567	-2.699456	21628.3321
HLA B*4501	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.490124	1.790637	-2.699487	30911.799120
HLA B*4403	1:164-172	9	RKQARQAAR	1.130763	0.814899	-4.645235	1.945662	-2.699572	44180.9380
HLA B*4501	1:142-150	9	TYSELLAKL	1.344148	0.587133	-4.631112	1.931281	-2.699831	42767.3340
HLA A*2602	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.458864	1.758557	-2.700308	28765.0004
HLA A*0101	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.359491	1.658831	-2.700659	22881.8201
HLA B*1517	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.358476	1.657746	-2.700730	22828.406082
HLA B*1801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.152320	1.451496	-2.700824	14201.0359
HLA A*2601	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.392475	1.691549	-2.700926	24687.379140
HLA B*0802	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.423150	1.721985	-2.701165	26494.1422
HLA B*5701	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.423314	1.721985	-2.701330	26504.1772
HLA B*3901	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.481166	1.778801	-2.702365	30280.6850
HLA B*4001	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.368066	1.665496	-2.702570	23338.1371
HLA A*0211	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.324319	1.621061	-2.703258	21101.7647
HLA A*3301	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.602935	1.899550	-2.703385	40080.654510
HLA B*3801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.397256	1.693800	-2.703456	24960.6671
HLA A*0211	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.521899	1.818422	-2.703477	33258.198241
HLA A*0202	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.522265	1.818422	-2.703843	33286.278102
HLA B*3901	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.265709	1.561696	-2.704012	18437.775537
HLA A*0202	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.250270	1.546204	-2.704066	17793.855424
HLA B*3801	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.462753	1.758557	-2.704196	29023.7003
HLA A*1101	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.420556	1.715719	-2.704837	26336.3770
HLA B*4402	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.362775	1.657746	-2.705029	23055.531948
HLA A*0212	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.427095	1.721985	-2.705110	26735.8901
HLA A*3001	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-3.737034	1.031880	-2.705154	5458.01163
HLA B*0803	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.399230	1.693800	-2.705430	25074.3541
HLA A*2602	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.364345	1.658831	-2.705513	23139.0008
HLA A*2603	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.560630	1.855018	-2.705612	36360.5109
HLA B*0803	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.381197	1.675398	-2.705799	24054.5623
HLA B*0801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.326922	1.621061	-2.705861	21228.6318
HLA B*5101	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.485052	1.778801	-2.706251	30552.8511
HLA A*0201	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.400134	1.693800	-2.706335	25126.6336
HLA A*0202	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-3.023609	0.316807	-2.706802	1055.865591
HLA B*5401	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.561915	1.855018	-2.706898	36468.2687
HLA B*3501	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.664727	0.957621	-2.707106	4620.90145
HLA B*4601	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.109127	1.401827	-2.707300	12856.6285
HLA B*4601	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.382891	1.675398	-2.707493	24148.5710
HLA A*6802	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.429503	1.721985	-2.707518	26884.5561
HLA A*2403	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.429566	1.721985	-2.707582	26888.4833
HLA A*0219	1:81-89	9	YITGISRSC	1.133968	-0.008438	-3.833222	1.125530	-2.707693	6811.180238
HLA A*2601	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.373207	1.665496	-2.707710	23616.0282
HLA A*2603	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.366992	1.658831	-2.708161	23280.5090
HLA B*5401	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.543714	1.834955	-2.708759	34971.4537
HLA A*0202	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.563804	1.855018	-2.708786	36627.2347
HLA A*3001	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.222640	1.513828	-2.708812	16697.064082
HLA A*0101	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.355821	1.646900	-2.708921	22689.2777
HLA A*6802	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.330009	1.621061	-2.708948	21380.0752
HLA A*0203	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.063091	1.354114	-2.708977	11563.5527
HLA B*4601	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.402789	1.693800	-2.708989	25280.7076
HLA B*5301	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.499752	1.790637	-2.709115	31604.758202
HLA B*4001	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.431206	1.721985	-2.709222	26990.2089
HLA B*2705	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.401166	1.691549	-2.709617	25186.378861
HLA A*0212	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.161276	1.451496	-2.709780	14496.9374
HLA B*1503	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.223989	1.513828	-2.710161	16748.993667
HLA B*4402	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.345840	1.635567	-2.710273	22173.7965
HLA B*1501	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.524603	0.814245	-2.710358	3346.59702
HLA B*1501	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.386312	1.675398	-2.710914	24339.5356
HLA B*0803	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.356807	1.645813	-2.710995	22740.889871
HLA B*0702	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.404918	1.693800	-2.711118	25404.9216
HLA B*1801	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.489997	1.778801	-2.711196	30902.7700
HLA B*1801	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.357237	1.645813	-2.711425	22763.414721
HLA A*0211	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.542400	1.830609	-2.711791	34865.855330
HLA A*6801	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.071042	1.359245	-2.711797	11777.197109
HLA A*1101	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.163480	1.451496	-2.711984	14570.6887
HLA B*3801	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.370991	1.658831	-2.712160	23495.8573
HLA A*6901	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.387821	1.675398	-2.712422	24424.2174
HLA A*2301	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.503392	1.790637	-2.712754	31870.716291
HLA A*0301	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.358703	1.645813	-2.712891	22840.388643
HLA A*0211	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.839218	1.126312	-2.712906	6905.86777
HLA B*4801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.407317	1.693800	-2.713517	25545.6338
HLA A*0202	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.360555	1.646900	-2.713655	22937.9648
HLA B*5701	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.407982	1.693800	-2.714182	25584.7741
HLA B*0802	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.408247	1.693800	-2.714447	25600.4193
HLA B*4601	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.350041	1.635567	-2.714473	22389.3217
HLA A*2501	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.073819	1.359245	-2.714574	11852.747562
HLA B*4801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.161427	1.446759	-2.714667	14501.9576
HLA B*5801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-3.789672	1.074983	-2.714689	6161.29947
HLA A*1101	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.406588	1.691549	-2.715039	25502.828080
HLA A*0219	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.380554	1.665496	-2.715057	24018.9324
HLA A*0212	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.350884	1.635567	-2.715317	22432.8474
HLA A*2301	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.374433	1.658831	-2.715602	23682.8131
HLA A*0202	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.540866	1.824451		
HLA B*4002	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.615993	1.899550	-2.7164	

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HLA A*0101	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.337706	1.621061	-2.716645	21762.3676
HLA A*6802	1:198-206	9	MRASEHADV	0.792968	0.319530	-3.829308	1.112498	-2.716811	6750.06773
HLA B*4002	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.408489	1.691549	-2.716940	25614.688371
HLA A*3002	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.220093	1.502929	-2.717165	16599.4337
HLA A*0203	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.718008	1.000751	-2.717257	5224.06205
HLA A*6802	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-3.783517	1.066259	-2.717257	6074.58576
HLA A*0203	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.392682	1.675398	-2.717284	24699.1348
HLA B*1502	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.338763	1.621061	-2.717702	21815.4115
HLA A*0219	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.440249	1.721985	-2.718265	27558.1090
HLA B*3501	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-3.708357	0.990022	-2.718335	5109.24399
HLA A*2602	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.562329	1.843851	-2.718477	36503.0081
HLA A*2902	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.440531	1.721985	-2.718547	27576.0052
HLA A*0201	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.376294	1.657746	-2.718548	23784.503152
HLA A*0101	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.376860	1.657746	-2.719114	23815.533213
HLA A*0219	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.394928	1.675398	-2.719530	24827.2060
HLA A*0301	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.366997	1.646900	-2.720098	23280.7609
HLA A*0206	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.341411	1.621061	-2.720350	21948.8252
HLA A*0202	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.564556	1.843851	-2.720705	36690.6974
HLA B*5401	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.565167	1.843851	-2.721315	36742.3418
HLA B*3501	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.415335	1.693800	-2.721536	26021.6886
HLA A*0101	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.387292	1.665496	-2.721796	24394.5057
HLA A*2301	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.437637	1.715719	-2.721917	27392.8227
HLA B*1517	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.225178	1.502929	-2.722249	16794.9052
HLA B*4801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.358391	1.635567	-2.722824	22823.9605
HLA B*1502	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.541406	1.818422	-2.722985	34786.160117
HLA A*3101	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-3.559639	0.836190	-2.723449	3627.763285
HLA A*2402	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.174969	1.451496	-2.723473	14961.2907
HLA B*0801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.417325	1.693800	-2.723526	26141.1981
HLA A*3001	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.223481	1.499754	-2.723727	16729.433295
HLA A*2501	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.417610	1.693800	-2.723810	26158.3157
HLA B*0801	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.238055	1.513828	-2.724227	17300.357797
HLA B*0801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.538583	0.814245	-2.724338	3456.07259
HLA B*1801	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.440449	1.715719	-2.724730	27570.7843
HLA A*0202	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-3.651969	0.927116	-2.724853	4487.133625
HLA B*0802	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.176506	1.451496	-2.725009	15014.3185
HLA B*5401	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.549898	1.824451	-2.725447	35472.9682
HLA B*1501	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.419776	1.693800	-2.725976	26289.1172
HLA A*3002	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.347264	1.621061	-2.726203	22246.6102
HLA B*0801	1:70-78	9	FSVLEHASV	1.102668	0.135344	-3.964295	1.238012	-2.726283	9210.759487
HLA B*4801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.347405	1.621061	-2.726344	22253.8325
HLA B*5301	1:74-82	9	EHASVSFYI	0.978340	0.173645	-3.878398	1.151985	-2.726413	7557.850038
HLA A*0101	1:1-9	9	VAETAPLRV	1.127505	0.095337	-3.949879	1.222842	-2.727037	8910.026632
HLA A*0216	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.349045	1.621061	-2.727984	22338.0241
HLA B*3901	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.349132	1.621061	-2.728071	22342.4959
HLA B*1502	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.685811	0.957621	-2.728190	4850.77337
HLA A*0301	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.363898	1.635567	-2.728331	23115.2290
HLA A*2403	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.349559	1.621061	-2.728498	22364.5051
HLA B*5701	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.349691	1.621061	-2.728630	22371.2816
HLA A*0203	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.386667	1.657746	-2.728921	24359.426530
HLA A*2603	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.508009	1.778801	-2.729207	32211.3229
HLA A*3201	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.053223	1.323538	-2.729686	11303.7735
HLA B*5101	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.488851	1.758557	-2.730294	30821.2935
HLA A*2402	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.244201	1.513828	-2.730373	17546.937849
HLA B*7301	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.521027	1.790637	-2.730390	33191.513689
HLA A*0203	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.377483	1.646900	-2.730583	23849.7001
HLA A*3001	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.704574	0.973692	-2.730882	5064.93611
HLA B*5401	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.521915	1.790637	-2.731278	33259.457727
HLA A*0219	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.425478	1.693800	-2.731678	26636.5640
HLA B*1801	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.391352	1.658831	-2.732521	24623.6218
HLA A*3101	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.368144	1.635567	-2.732576	23342.3039
HLA B*4501	1:53-61	9	KTATNAGYL	1.501925	0.397625	-4.632313	1.899550	-2.732763	42885.725883
HLA A*8001	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.391944	1.658831	-2.733113	24657.2139
HLA B*5401	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.563748	1.830609	-2.733139	36622.479496
HLA B*4801	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.379005	1.645813	-2.733193	23933.454561
HLA A*0203	1:1-9	9	VAETAPLRV	1.127505	0.095337	-3.956044	1.222842	-2.733202	9037.411361
HLA A*0206	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.734356	1.000751	-2.733605	5424.45416
HLA B*4001	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.391566	1.657746	-2.733820	24635.747042
HLA B*4001	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.185438	1.451496	-2.733942	15326.3369
HLA B*4801	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.399441	1.665496	-2.733945	25086.5656
HLA B*4801	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.391883	1.657746	-2.734137	24653.745963
HLA A*0203	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-3.860829	1.126312	-2.734516	7258.19817
HLA A*0203	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.428436	1.693800	-2.734636	26818.6062
HLA B*1502	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.493341	1.758557	-2.734784	31141.5860
HLA A*0101	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.380615	1.645813	-2.734802	24022.311076
HLA B*0801	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.094213	1.359245	-2.734967	12422.601812
HLA B*2705	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.429042	1.693800	-2.735243	26856.0645
HLA A*0216	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.370900	1.635567	-2.735332	23490.9005
HLA A*0202	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.736250	1.000751	-2.735498	5448.15843
HLA A*3101	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.382471	1.646900	-2.735571	24125.1976
HLA A*2602	1:70-78	9	FSVLEHASV	1.102668	0.135344	-3.973698	1.238012	-2.735686	9412.350281
HLA A*8001	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.457727	1.721985	-2.735743	28689.7810
HLA B*0803	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.393619	1.657746	-2.735873	24752.506660
HLA A*2601	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.297633	1.561696	-2.735937	19844.187678
HLA A*2403	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.411362	1.675398	-2.735964	25784.7245
HLA B*4801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.382957	1.646900	-2.736058	24152.2292
HLA A*6901	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.381959	1.645813	-2.736146	24096.762208
HLA B*1509	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.515048	1.778801	-2.736246	32737.6585
HLA A*0206	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-3.930900	1.194587	-2.736313	8529.034326
HLA A*2902	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.430330	1.693800	-2.736530	26935.8006
HLA B*1509	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.298263	1.561696	-2.736567	19872.979646
HLA A*0250	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.581113	1.843851	-2.737261	38116.4800
HLA B*3501	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.459339	1.721985	-2.737354	28796.4515
HLA A*0202	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.495930	1.758557	-2.737373	31327.7972
HLA A*3001	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.299642	1.561696	-2.737946	19936.188688
HLA B*3801	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.516789	1.778801	-2.737987	32869.1586
HLA A*0250	1:198-206	9	MRASEHADV	0.792968	0.319530	-3.850496	1.112498	-2.737998	7087.54430
HLA B*0802	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.385236	1.646900	-2.738337	24279.3034
HLA B*3901	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.413844	1.675398	-2.738445	25932.4502
HLA A*0201	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.359986	1.621061	-2.738925	22907.9543
HLA A*6801	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-2.964721	0.225691	-2.739030	921.979245
HLA A*0203	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.285898	1.546204	-2.739694	19315.130563
HLA A*2301	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.375399	1.635567	-2.739831	23735.5297
HLA A*2601	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.099132	1.359245	-2.739887	12564.128988
HLA B*4002	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.564737	1.824451	-2.740286	36705.9845
HLA A*3101	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-3.871171	1.130392	-2.740780	7433.121891
HLA B*4601	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.406579	1.665496	-2.741083	25502.2762
HLA B*4402	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.406974	1.665496	-2.741477	25525.4647
HLA B*0802	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.362848	1.621061	-2.741787	23059.3988
HLA A*0212	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.435971	1.693800	-2.742171	27287.9557
HLA B*5701	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.377981	1.635567	-2.742414	23877.0689
HLA A*2402	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.458272	1.715719	-2.742553	28725.8120
HLA A*2902	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.401201	1.657746	-2.743455	25188.422776
HLA B*4601	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.390501	1.646900	-2.743602	24575.4466
HLA A*2402	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.534654	1.790637	-2.744017	34249.487068
HLA B*3501	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.409643	1.665496	-2.744146	25682.8176
HLA B*4601	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.402246	1.657746	-2.7445	
HLA B*5401	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.503140	1.758557		

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HLA A*2603	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.575197	1.830609	-2.744588	37600.774009
HLA A*0206	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.391617	1.646900	-2.744718	24638.6793
HLA A*2403	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.290935	1.546204	-2.744731	19540.467236
HLA A*2601	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.390720	1.645813	-2.744907	24587.814135
HLA B*5301	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.588859	1.843851	-2.745008	38802.4403
HLA B*0702	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.467268	1.721985	-2.745284	29327.0576
HLA A*0201	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.392715	1.646900	-2.745815	24701.0056
HLA A*0101	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.192600	1.446759	-2.745840	15581.1532
HLA A*2902	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.381735	1.635567	-2.746168	24084.3811
HLA B*7301	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.601647	1.855018	-2.746630	39962.0065
HLA B*1502	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.438534	1.691549	-2.746985	27449.490693
HLA B*0702	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.101336	1.354114	-2.747222	12628.0473
HLA A*2402	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.469355	1.721985	-2.747370	29468.2832
HLA A*2603	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.469938	1.721985	-2.747953	29507.8459
HLA B*1503	1:175-183	9	LPNATETRI	1.064730	0.080627	-3.893543	1.145357	-2.748186	7826.05779
HLA B*3901	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.470309	1.721985	-2.748324	29533.0789
HLA B*3901	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.383968	1.635567	-2.748400	24208.4788
HLA A*0203	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.200494	1.451496	-2.748997	15866.9651
HLA A*2501	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.407136	1.657746	-2.749390	25534.994770
HLA A*0202	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.580126	1.830609	-2.749517	38029.971896
HLA B*3501	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.902687	1.152145	-2.750543	7992.58468
HLA B*1517	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.472562	1.721985	-2.750577	29686.6971
HLA B*4402	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.303852	1.553233	-2.750620	20130.4003
HLA A*2402	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.312898	1.561696	-2.751202	20554.074665
HLA A*0250	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.569840	1.818422	-2.751418	37139.834072
HLA B*0802	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.409577	1.657746	-2.751831	25678.927916
HLA B*5301	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.606873	1.855018	-2.751855	40445.7172
HLA A*0219	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.398783	1.646900	-2.751884	25048.5940
HLA B*1502	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.595774	1.843851	-2.751922	39425.1699
HLA A*2902	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.411083	1.658831	-2.752252	25768.1303
HLA A*2403	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.446081	1.693800	-2.752281	27930.6367
HLA A*0211	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.510901	1.758557	-2.752344	32426.5525
HLA A*0201	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.398739	1.645813	-2.752926	25046.019470
HLA B*5701	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.428340	1.675398	-2.752942	26812.6584
HLA A*2603	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.571680	1.818422	-2.753258	37297.489975
HLA A*0212	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.400264	1.646900	-2.753364	25134.1110
HLA A*0212	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.411398	1.657746	-2.753652	25786.817048
HLA A*2602	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.572081	1.818422	-2.753659	37332.009513
HLA B*0801	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.411456	1.657746	-2.753711	25790.304879
HLA B*3501	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.429132	1.675398	-2.753733	26861.5860
HLA B*1501	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.400943	1.646900	-2.754043	25173.4379
HLA B*2705	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.390147	1.635567	-2.754579	24555.3793
HLA A*0250	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-3.314898	0.559811	-2.755087	2064.89412
HLA A*0250	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.579539	1.824451	-2.755088	37978.5721
HLA B*4002	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-3.310969	0.555227	-2.755742	2046.30068
HLA B*1502	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.421324	1.665496	-2.755828	26383.0082
HLA B*4402	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.431305	1.675398	-2.755907	26996.3422
HLA A*1101	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.414851	1.658831	-2.756020	25992.7052
HLA A*8001	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.403031	1.646900	-2.756132	25294.7984
HLA B*1509	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.514766	1.758557	-2.756209	32716.4129
HLA B*5101	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.318158	1.561696	-2.756462	20804.554802
HLA A*3001	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.757494	1.000751	-2.756742	5721.28750
HLA A*2902	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.403651	1.646900	-2.756752	25330.9505
HLA A*3201	1:54-62 9	TATNAGYLR	1.132899	0.685523	-4.575180	1.818422	-2.756758	37599.350124
HLA A*2603	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.259802	1.502929	-2.756873	18188.7108
HLA A*2501	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.422469	1.665496	-2.756972	26452.6089
HLA B*4402	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.318795	1.561696	-2.757099	20835.078312
HLA A*0250	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.731696	0.973692	-2.758005	5391.33634
HLA A*8001	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.404471	1.645813	-2.758659	25378.821855
HLA A*0206	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.480665	1.721985	-2.758681	30245.8125
HLA B*0801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.394524	1.635567	-2.758956	24804.1150
HLA A*0202	1:198-206	9	MRASEHADV	0.792968	0.319530	-3.872698	1.112498	-2.760201	7459.30593
HLA A*0219	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.396093	1.635567	-2.760526	24893.9145
HLA A*0203	1:81-89 9	YITGISRSC	1.133968	-0.008438	-3.886250	1.125530	-2.760721	7695.737566
HLA B*7301	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.604998	1.843851	-2.761146	40271.4857
HLA A*0216	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.163038	1.401827	-2.761211	14555.8770
HLA A*0301	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.261019	1.499754	-2.761265	18239.752941
HLA A*0216	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.408294	1.646900	-2.761395	25603.1894
HLA B*4001	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.407441	1.645813	-2.761628	25552.959481
HLA A*3002	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.437461	1.675398	-2.762062	27381.7106
HLA A*6901	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.308338	1.546204	-2.762134	20339.373870
HLA B*5301	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.593036	1.830609	-2.762427	39177.473413
HLA A*2301	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.521119	1.758557	-2.762562	33198.5173
HLA A*0250	1:87-95 9	RSCTHELIR	1.036000	0.794609	-4.593361	1.830609	-2.762752	39206.732852
HLA A*2601	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.398330	1.635567	-2.762762	25022.4542
HLA B*4001	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.384590	1.621061	-2.763529	24243.2095
HLA B*4001	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.309919	1.546204	-2.763715	20413.561561
HLA B*5101	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.429536	1.665496	-2.764039	26886.5923
HLA B*4801	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.325914	1.561696	-2.764218	21179.420681
HLA A*1101	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.458190	1.693800	-2.764390	28720.3734
HLA B*0702	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.422219	1.657746	-2.764474	26437.444132
HLA A*1101	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.123835	1.359245	-2.764589	13299.486461
HLA B*5301	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.599747	1.834955	-2.764792	39787.4910
HLA A*6802	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.099184	1.334180	-2.765004	12565.6244
HLA A*0212	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.003461	1.238012	-2.765449	10080.019148
HLA A*0301	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.327328	1.561696	-2.765632	21248.509270
HLA B*1502	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.411590	1.645813	-2.765778	25798.258899
HLA A*6801	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-3.555339	0.789295	-2.766045	3592.025273
HLA A*6801	1:74-82 9	EHASVSFYI	0.978340	0.173645	-3.918062	1.151985	-2.766077	8280.608961
HLA A*0206	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-3.676310	0.910145	-2.766165	4745.80257
HLA A*0201	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.168005	1.401827	-2.766178	14723.3009
HLA A*0206	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.312766	1.546204	-2.766562	20547.848673
HLA B*0803	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.488856	1.721985	-2.766871	30821.6270
HLA A*0211	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.313248	1.546204	-2.767044	20570.649438
HLA A*8001	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.461150	1.693800	-2.767351	28916.8134
HLA B*2705	1:198-206	9	MRASEHADV	0.792968	0.319530	-3.879911	1.112498	-2.767414	7584.22727
HLA B*5701	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.414358	1.646900	-2.767459	25963.1923
HLA A*3001	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.091280	1.323538	-2.767743	12339.0125
HLA B*4501	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.426738	1.658831	-2.767906	26713.9141
HLA B*1801	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.427038	1.657746	-2.769292	26732.419069
HLA A*0301	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.322606	1.553233	-2.769373	21018.7072
HLA B*1503	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.416524	1.646900	-2.769625	26093.0180
HLA B*1801	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.331325	1.561696	-2.769629	21444.945195
HLA B*0801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.445169	1.675398	-2.769771	27872.0707
HLA B*4501	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.624994	1.855018	-2.769976	42169.0793
HLA B*5301	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.594745	1.824451	-2.770294	39331.8614
HLA A*3001	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.124568	1.354114	-2.770454	13321.9534
HLA B*7301	1:198-206	9	MRASEHADV	0.792968	0.319530	-3.882984	1.112498	-2.770487	7638.08461
HLA A*2602	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.595015	1.824451	-2.770564	39356.3388
HLA A*2902	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.316810	1.546204	-2.770606	20740.051112
HLA B*1503	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.446198	1.675398	-2.770800	27938.1928
HLA B*5101	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.406469	1.635567	-2.770901	25495.7927
HLA A*0216	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.217786	1.446759	-2.771027	16511.4828
HLA A*0212	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.392205	1.621061	-2.771144	24672.0249
HLA B*0702	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.446783	1.675398	-2.771385	27975.8535
HLA A*3201	1:27-35 9	TDADGGPAL	1.505710	0.284927	-4.562272	1.790637	-2.7716	
HLA A*2301	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.333536	1.561696	-2.7718	

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HLA B*2705	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.334017	1.561696	-2.772321	21578.311118	
HLA B*7301	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.608388	1.834955	-2.773433	40587.0942	
HLA B*0802	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.448853	1.675398	-2.773455	28109.5070	
HLA A*2301	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.288111	1.513828	-2.774283	19413.813938	
HLA A*6802	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.449988	1.675398	-2.774590	28183.0525	
HLA A*1101	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.420417	1.645813	-2.774605	26327.972276	
HLA B*1503	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.274359	1.499754	-2.774605	18808.723726	
HLA B*5101	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.496618	1.721985	-2.774634	31377.4942	
HLA A*3201	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.533707	1.758557	-2.775151	34174.8981	
HLA A*8001	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.451687	1.675398	-2.776289	28293.5021	
HLA A*8001	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.434517	1.657746	-2.776771	27196.728854	
HLA B*5101	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.398118	1.621061	-2.777057	25010.2740	
HLA B*1517	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.442644	1.665496	-2.777147	27710.4475	
HLA B*1517	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.471361	1.693800	-2.777562	29604.7429	
HLA B*5101	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.424858	1.646900	-2.777958	26598.5485	
HLA A*2602	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.494302	1.715719	-2.778582	31210.5675	
HLA B*0702	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.425901	1.646900	-2.779002	26662.5148	
HLA A*2301	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.230520	1.451496	-2.779024	17002.7937	
HLA A*0216	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.899304	1.119963	-2.779341	7930.56242	
HLA A*0203	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.425194	1.645813	-2.779381	26619.133540	
HLA B*0801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.052805	1.273350	-2.779455	11292.8937	
HLA B*7301	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-3.694598	0.915034	-2.779564	4949.91861	
HLA A*0211	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.294006	1.513828	-2.780178	19679.122126	
HLA B*5701	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.665704	0.885414	-2.780290	4631.31256	
HLA A*0211	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.416118	1.635567	-2.780550	26068.6087	
HLA B*1509	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.294509	1.513828	-2.780680	19701.918159	
HLA A*2301	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.502809	1.721985	-2.780825	31827.9855	
HLA B*2705	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.295136	1.513828	-2.781308	19730.396969	
HLA B*1502	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.612542	1.830609	-2.781933	40977.159391	
HLA A*8001	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.418153	1.635567	-2.782585	26191.0258	
HLA B*1502	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.607180	1.824451	-2.782730	40474.3911	
HLA B*4002	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.234982	1.451496	-2.783486	17178.3702	
HLA A*0212	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.429757	1.645813	-2.783944	26900.268500	
HLA B*5401	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.562773	1.778801	-2.783972	36540.3504	
HLA A*2301	1:74-82	9	EHASVSFYI	0.978340	0.173645	-3.936097	1.151985	-2.784112	8631.711634	
HLA B*3501	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.117891	1.333568	-2.784323	13118.696192	
HLA B*2705	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.430161	1.645813	-2.784348	26925.310874	
HLA B*5101	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.478316	1.693800	-2.784516	30082.6278	
HLA B*7301	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.603219	1.818422	-2.784797	40106.899759	
HLA B*4002	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.410141	0.625007	-2.785134	2571.23168	
HLA A*2501	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.444084	1.658831	-2.785253	27802.4951	
HLA A*0216	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.479601	1.693800	-2.785801	30171.7804	
HLA A*2902	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.431636	1.645813	-2.785823	27016.942772	
HLA B*4002	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.641020	1.855018	-2.786002	43754.2210	
HLA A*6901	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.009039	1.222842	-2.786197	10210.312501	
HLA A*3201	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.451727	1.665496	-2.786230	28296.1043	
HLA B*1501	1:168-176	9	RQAARAVLP	0.787201	0.256977	-3.830690	1.044178	-2.786512	6771.57398	
HLA B*4402	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.407979	1.621061	-2.786918	25584.6357	
HLA B*0702	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.408346	1.621061	-2.787285	25606.2368	
HLA A*8001	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.349172	1.561696	-2.787476	22344.550823	
HLA A*0101	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.349334	1.561696	-2.787638	22352.893206	
HLA B*7301	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.618251	1.830609	-2.787642	41519.402747	
HLA A*0219	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.239216	1.451496	-2.787719	17346.6545	
HLA B*5401	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.026092	1.238012	-2.788079	10619.195020	
HLA B*0803	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.435616	1.646900	-2.788717	27265.6735	
HLA A*2603	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.632719	1.843851	-2.788868	42925.8818	
HLA B*3501	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-2.653109	-0.135764	-2.788873	449.892703	
HLA B*0801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.746578	0.957621	-2.788957	5579.27881	
HLA A*0219	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.446826	1.657746	-2.789080	27978.577067	
HLA A*3101	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.236206	1.446759	-2.789447	17226.8566	
HLA A*0211	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.511455	1.721985	-2.789471	32467.9790	
HLA A*6901	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.790260	1.000751	-2.789508	6169.63810	
HLA B*4002	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.633492	1.843851	-2.789641	43002.3517	
HLA A*0203	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.941801	1.152145	-2.789657	8745.83888	
HLA B*1509	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.447664	1.657746	-2.789918	28032.665158	
HLA B*4601	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.236854	1.446759	-2.790095	17252.5978	
HLA A*0211	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.822795	1.032480	-2.790315	6649.59750	
HLA B*4402	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.337046	1.546204	-2.790842	21729.310043	
HLA A*0216	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.448841	1.657746	-2.791096	28108.746674	
HLA B*1509	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.437209	1.645813	-2.791396	27365.865068	
HLA A*0206	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.126650	1.335227	-2.791423	13385.9609	
HLA B*4501	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.622248	1.830609	-2.791638	41903.236840	
HLA A*0203	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-3.977476	1.185494	-2.791982	9494.586445	
HLA A*2603	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.616801	1.824451	-2.792351	41381.0461	
HLA A*2501	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.438952	1.645813	-2.793140	27475.936193	
HLA B*5801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.195146	1.401827	-2.793319	15672.7945	
HLA B*4403	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.611769	1.818422	-2.793347	40904.290916	
HLA A*6802	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.439413	1.645813	-2.793600	27505.085431	
HLA B*1509	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.469071	1.675398	-2.793672	29448.9996	
HLA B*2705	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.346956	1.553233	-2.793723	22230.8497	
HLA A*2601	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.307663	1.513828	-2.793835	20307.818685	
HLA A*3301	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.962576	1.168653	-2.793923	9174.35664	
HLA B*5401	1:85-93	9	ISRSCTHEL	1.239891	0.451658	-4.485844	1.691549	-2.794294	30608.603867	
HLA A*2602	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.488350	1.693800	-2.794551	30785.7984	
HLA A*2602	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.573411	1.778801	-2.794610	37446.4952	
HLA B*1801	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.488583	1.693800	-2.794783	30802.2910	
HLA A*0211	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.453660	1.657746	-2.795914	28422.369117	
HLA B*4002	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.626568	1.830609	-2.795959	42322.203832	
HLA B*4403	1:160-168	9	AILRRKQAR	1.023219	0.831799	-4.651104	1.855018	-2.796086	44782.0475	
HLA A*0219	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.442066	1.645813	-2.796253	27673.594106	
HLA A*2603	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.358062	1.561696	-2.796366	22806.680577	
HLA B*0801	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.358318	1.561696	-2.796622	22820.133138	
HLA A*2403	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.443567	1.646900	-2.796667	27769.4250	
HLA B*4403	1:87-95	9	RSCTHELIR	1.036000	0.794609	-4.627485	1.830609	-2.796875	42411.591885	
HLA B*5801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.350368	1.553233	-2.797135	22406.1643	
HLA B*5101	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.151343	1.354114	-2.797229	14169.1122	
HLA B*1501	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.344106	1.546204	-2.797902	22085.444227	
HLA B*5101	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.445172	1.645813	-2.799359	27872.221582	
HLA B*1509	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.521530	1.721985	-2.799545	33229.9622	
HLA B*4002	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.634815	1.834955	-2.799860	43133.5265	
HLA B*5301	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-3.789926	0.990022	-2.799904	6164.90038	
HLA B*4501	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.643891	1.843851	-2.800040	44044.4333	
HLA B*4403	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.624597	1.824451	-2.800146	42130.5430	
HLA B*0803	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.421503	1.621061	-2.800442	26393.8578	
HLA A*0201	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.247719	1.446759	-2.800959	17689.6205	
HLA A*6802	1:81-89	9	YITGISRSC	1.133968	-0.008438	-3.926638	1.125530	-2.801108	8445.743672	
HLA A*0202	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.374730	0.573275	-2.801455	2369.89864	
HLA B*0803	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.437240	1.635567	-2.801672	27367.7897	
HLA A*2402	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.437291	1.635567	-2.801724	27371.0471	
HLA A*3001	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.075990	1.273350	-2.802640	11912.1446	
HLA B*1503	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-3.740286	0.937566	-2.802720	5499.03069	
HLA B*3801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.254459	1.451496	-2.802963	17966.3224	
HLA B*2705	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.450279	1.646900	-2.803380	28201.9648	
HLA B*0802	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.449194	1.645813	-2.803381	28131.565712	
HLA A*3002	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.137030	1.333568	-2.803461	13709.751390	
HLA A*0202	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.137326	1.333568	-2.8037		
HLA B*1801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.008607	1.204727			

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HLA A*3201	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.519606	1.715719	-2.803886	33083.0560
HLA A*0219	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.425006	1.621061	-2.803945	26607.6155
HLA B*4002	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.622377	1.818422	-2.803955	41915.706747
HLA B*4403	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.450893	1.646900	-2.803993	28241.8135
HLA A*2402	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.562686	1.758557	-2.804129	36533.0370
HLA B*5801	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.350548	1.546204	-2.804344	22415.499808
HLA B*1503	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-3.700721	0.896310	-2.804411	5020.197656
HLA B*3501	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.462302	1.657746	-2.804556	28993.569162
HLA A*0202	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-3.030375	0.225691	-2.804684	1072.445309
HLA B*0801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.973712	1.168653	-2.805059	9412.6558
HLA A*3101	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.159223	1.354114	-2.805109	14428.5541
HLA B*3501	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.207472	1.401827	-2.805645	16123.9647
HLA A*2501	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.043826	1.238012	-2.805813	11061.792546
HLA A*1101	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.471408	1.665496	-2.805912	29607.9463
HLA A*0202	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.463817	1.657746	-2.806071	29094.915413
HLA A*3002	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.451917	1.645813	-2.806104	28308.506495
HLA B*4001	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.368555	1.561696	-2.806859	23364.413301
HLA A*0216	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.822946	1.015721	-2.807225	6651.90021
HLA A*0250	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.566579	1.758557	-2.808022	36861.9982
HLA A*3002	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.255089	1.446759	-2.808329	17992.3897
HLA B*4501	1:209-217	9	RRLAIECLR	0.972846	0.851605	-4.632957	1.824451	-2.808506	42949.3429
HLA B*3801	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.530510	1.721985	-2.808525	33924.1972
HLA A*6802	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.260143	1.451496	-2.808646	18202.9842
HLA A*1101	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.308605	1.499754	-2.808851	20351.921588
HLA A*3002	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.466646	1.657746	-2.808900	29285.043864
HLA A*2301	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.430140	1.621061	-2.809078	26923.9999
HLA A*2601	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-3.865523	1.056254	-2.809270	7337.07726
HLA B*1517	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.484742	1.675398	-2.809343	30531.0409
HLA B*4403	1:107-115	9	RYVPEKDSR	0.966438	0.877413	-4.653242	1.843851	-2.809391	45003.0530
HLA A*3301	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.144172	1.334180	-2.809992	13937.0870
HLA B*1517	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.457821	1.646900	-2.810922	28695.9900
HLA A*0250	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.257988	1.446759	-2.811229	18112.9052
HLA B*0702	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.084707	1.273350	-2.811357	12153.6450
HLA B*1502	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.533752	1.721985	-2.811767	34178.4111
HLA A*6801	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.602604	1.790637	-2.811966	40050.092870
HLA A*3101	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.373712	1.561696	-2.812016	23643.512688
HLA B*4501	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.647396	1.834955	-2.812442	44401.3790
HLA A*2602	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-2.745448	-0.067515	-2.812964	556.478524
HLA B*5101	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.470804	1.657746	-2.813059	29566.809785
HLA A*3101	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.359683	1.546204	-2.813479	22891.972982
HLA A*2902	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.327350	1.513828	-2.813521	21249.543864
HLA B*3501	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.086953	1.273350	-2.813603	12216.6647
HLA A*0212	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.359991	1.546204	-2.813787	22908.202169
HLA B*0802	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.375993	1.561696	-2.814297	23768.038898
HLA A*3002	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.461313	1.646900	-2.814413	28927.6096
HLA B*4501	1:54-62	9	TATNAGYLR	1.132899	0.685523	-4.632985	1.818422	-2.814563	42952.131251
HLA A*1101	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.461604	1.646900	-2.814704	28947.0215
HLA A*1101	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.450301	1.635567	-2.814733	28203.3379
HLA A*0206	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.490362	1.675398	-2.814963	30928.6939
HLA A*0101	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.368639	1.553233	-2.815407	23368.9641
HLA A*2603	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.262581	1.446759	-2.815822	18305.4900
HLA B*1501	1:166-174	9	QARQAARAV	0.923681	0.228464	-3.968496	1.152145	-2.816352	9300.28636
HLA B*7301	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.510858	1.693800	-2.817059	32423.3950
HLA B*5301	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.575897	1.758557	-2.817340	37661.4408
HLA A*3201	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.151761	1.334180	-2.817581	14182.7631
HLA A*3301	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.533822	1.715719	-2.818103	34183.9586
HLA B*0801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.172342	1.354114	-2.818228	14871.0741
HLA B*4403	1:182-190	9	RIVVTGNYR	0.991278	0.843677	-4.653411	1.834955	-2.818456	45020.5856
HLA A*0201	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.332309	1.513828	-2.818481	21493.610521
HLA A*8001	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.439716	1.621061	-2.818655	27524.2872
HLA A*0101	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.365463	1.546204	-2.819259	23198.663090
HLA B*5801	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.333273	1.513828	-2.819444	21541.337432
HLA B*0801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-3.873267	1.052696	-2.820571	7469.07800
HLA B*1502	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.267381	1.446759	-2.820622	18508.9318
HLA A*6801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.467522	1.646900	-2.820623	29344.1974
HLA A*0301	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.367065	1.546204	-2.820861	23284.413680
HLA B*3801	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.486739	1.665496	-2.821242	30671.7583
HLA A*6901	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.374567	1.553233	-2.821334	23690.1173
HLA A*0211	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-3.990478	1.168653	-2.821825	9783.13627
HLA A*2501	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.497497	1.675398	-2.822099	31441.0445
HLA A*2602	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.171290	1.349023	-2.822267	14835.0758
HLA A*2501	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.457936	1.635567	-2.822369	28703.5979
HLA B*3801	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.469606	1.646900	-2.822707	29485.3461
HLA A*8001	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.369062	1.546204	-2.822858	23391.731419
HLA A*2602	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.146681	1.323538	-2.823144	14017.8453
HLA B*3901	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.480968	1.657746	-2.823222	30266.927707
HLA B*5301	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.602300	1.778801	-2.823499	40022.1526
HLA A*2601	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.376971	1.553233	-2.823738	23821.5894
HLA B*1801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.445169	1.621061	-2.824108	27872.0707
HLA A*3002	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.546409	1.721985	-2.824424	35189.1312
HLA B*4402	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-3.752259	0.927121	-2.825138	5652.74142
HLA B*3801	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.483177	1.657746	-2.825431	30421.236007
HLA B*3901	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.471361	1.645813	-2.825549	29604.742997
HLA B*5101	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.372107	1.546204	-2.825903	23556.312190
HLA A*0216	1:28-36	9	DADGGPALV	0.931987	-0.051421	-3.706552	0.880566	-2.825986	5088.060169
HLA A*2603	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.471815	1.645813	-2.826002	29635.669707
HLA B*1501	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-3.143226	0.316807	-2.826419	1390.674904
HLA A*2902	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.379832	1.553233	-2.826600	23979.0740
HLA A*0219	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.180909	1.354114	-2.826794	15167.3099
HLA A*0216	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.472841	1.645813	-2.827029	29705.814916
HLA A*0211	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.521410	1.693800	-2.827610	33220.7952
HLA B*5101	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.503176	1.675398	-2.827778	31854.8578
HLA B*4801	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.374024	1.546204	-2.827820	23660.530678
HLA A*2902	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.785589	0.957621	-2.827968	6103.64004
HLA A*0250	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.948042	1.119963	-2.828079	8872.41208
HLA B*1509	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.230064	1.401827	-2.828237	16984.9583
HLA B*2705	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.820070	0.991777	-2.828293	6607.99880
HLA B*1801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.182760	1.354114	-2.828646	15232.1060
HLA A*0211	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.276554	1.446759	-2.829794	18904.0016
HLA B*0702	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-3.984539	1.154646	-2.829893	9650.25090
HLA B*4002	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.475856	1.645813	-2.830043	29912.716854
HLA A*2402	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.523861	1.693800	-2.830061	33408.7739
HLA A*3301	1:27-35	9	TDADGGPAL	1.505710	0.284927	-4.621766	1.790637	-2.831128	41856.790767
HLA A*2602	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.553217	1.721985	-2.831233	35745.1688
HLA B*4801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.385029	1.553233	-2.831797	24267.7475
HLA A*6802	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-3.500813	0.668648	-2.832165	3168.199607
HLA A*0201	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.378531	1.546204	-2.832327	23907.314425
HLA A*3001	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.166530	1.334180	-2.832350	14673.3647
HLA A*2301	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.526217	1.693800	-2.832417	33590.5466
HLA B*1503	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.791143	0.957621	-2.833522	6182.20064
HLA A*0216	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.285350	1.451496	-2.833854	19290.7990
HLA A*2501	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.348434	1.513828	-2.834606	22306.626239
HLA A*0216	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.381508	1.546204	-2.835304	24071.745926
HLA A*0250	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.482359	1.646900	-2.835460	30364.0176
HLA B*1503	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-2.769498	-0.066090	-2.835587	588.16304
HLA A*2403	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.283020	1.446759		
HLA B*1502	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.160064	1.323538		

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HLA A*2602	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.399042	1.561696	-2.837346	25063.504579		
HLA A*0101	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.340427	1.502929	-2.837498	21899.1291	
HLA A*2602	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.484920	1.646900	-2.838021	30543.5964	
HLA B*1503	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-3.896142	1.057871	-2.838271	7873.02410	
HLA B*4402	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.352219	1.513828	-2.838391	22501.885518		
HLA B*5701	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.384757	1.546204	-2.838553	24252.523194		
HLA B*3801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.514716	1.675398	-2.839318	32712.6963	
HLA A*0201	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.194080	1.354114	-2.839966	15634.3479	
HLA A*0219	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.386705	1.546204	-2.840501	24361.535130		
HLA B*1501	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.393838	1.553233	-2.840605	24764.9632	
HLA A*0202	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.148927	1.308218	-2.840710	14090.531381		
HLA B*1509	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.476295	1.635567	-2.840728	29942.9933	
HLA B*7301	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.562961	1.721985	-2.840976	36556.1682	
HLA A*0201	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.394676	1.553233	-2.841444	24812.8388	
HLA B*0801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.288717	1.446759	-2.841958	19440.9297	
HLA A*0216	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.080308	1.238012	-2.842296	12031.182442		
HLA A*0202	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.293867	1.451496	-2.842371	19672.8418	
HLA B*5101	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.294053	1.451496	-2.842556	19681.2514	
HLA A*0203	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.176238	1.333568	-2.842670	15005.061687		
HLA B*1801	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.518116	1.675398	-2.842718	32969.7798	
HLA B*7301	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.621576	1.778801	-2.842774	41838.4530	
HLA B*1503	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.396255	1.553233	-2.843022	24903.2087	
HLA A*3201	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.389378	1.546204	-2.843174	24511.978420		
HLA A*6901	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.816964	0.973692	-2.843272	6560.90782	
HLA A*0206	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.537323	1.693800	-2.843523	34460.6199	
HLA B*1501	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.246725	1.401827	-2.844898	17649.1861	
HLA B*5401	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.567058	1.721985	-2.845074	36902.7022	
HLA A*6901	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.344997	1.499754	-2.845243	22130.773528		
HLA A*2601	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.391467	1.546204	-2.845263	24630.150058		
HLA A*0202	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.567772	1.721985	-2.845788	36963.4425	
HLA B*1502	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.521481	1.675398	-2.846082	33226.1873	
HLA A*2403	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.400085	1.553233	-2.846852	25123.7792	
HLA B*0702	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.181125	1.334180	-2.846945	15174.8607	
HLA B*5701	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.360851	1.513828	-2.847023	22953.605790		
HLA B*5401	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.540960	1.693800	-2.847160	34750.4225	
HLA A*0211	1:224-232	9	PAVFADFEV	1.069788	0.050175	-3.967618	1.119963	-2.847655	9281.48813	
HLA A*2301	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.523149	1.675398	-2.847750	33354.0552	
HLA B*0803	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.401060	1.553233	-2.847827	25180.2481	
HLA A*6901	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.351531	1.502929	-2.848602	22466.2460	
HLA A*2601	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.295855	1.446759	-2.849095	19763.0862	
HLA A*3301	1:41-49 9	RACYQSWSK	0.781972	0.322141	-3.953361	1.104113	-2.849248	8981.749509		
HLA A*2402	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.470530	1.621061	-2.849468	29548.1011	
HLA B*1503	1:140-148	9	RATYSELLA	1.126115	-0.051132	-3.924486	1.074983	-2.849502	8403.99466	
HLA A*2301	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.496792	1.646900	-2.849893	31390.0582	
HLA A*6801	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.515489	1.665496	-2.849993	32770.9719	
HLA A*2603	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.543909	1.693800	-2.850109	34987.1601	
HLA A*0301	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.365439	1.513828	-2.851611	23197.408102		
HLA A*0206	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-3.893209	1.041264	-2.851945	7820.04809	
HLA A*3002	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.303646	1.451496	-2.852149	20120.8191	
HLA B*4001	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.405515	1.553233	-2.852282	25439.8548	
HLA A*0211	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.499219	1.646900	-2.852320	31565.9699	
HLA B*4001	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.366264	1.513828	-2.852436	23241.498838		
HLA A*3201	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.511631	1.658831	-2.852800	32481.1553	
HLA B*4601	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.406050	1.553233	-2.852817	25471.2530	
HLA B*0802	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.406313	1.553233	-2.853081	25486.6909	
HLA A*3301	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.512466	1.658831	-2.853634	32543.5956	
HLA B*0802	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.300521	1.446759	-2.853761	19976.5663	
HLA B*5801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.356793	1.502929	-2.853865	22740.1517	
HLA A*0202	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.207979	1.354114	-2.853865	16142.8171	
HLA A*2603	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.203130	1.349023	-2.854107	15963.5688	
HLA A*2601	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.127650	1.273350	-2.854300	13416.8460	
HLA A*0201	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.855054	1.000751	-2.854302	7162.32110	
HLA B*4501	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.490324	1.635567	-2.854757	30926.0168	
HLA B*1501	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.358746	1.502929	-2.855817	22842.6129	
HLA A*0202	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-3.836333	0.980470	-2.855864	6860.14177	
HLA B*4601	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.402277	1.546204	-2.856073	25250.910249		
HLA A*2601	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.307858	1.451496	-2.856362	20316.9393	
HLA A*2402	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.514195	1.657746	-2.856449	32673.432106		
HLA B*5401	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.522418	1.665496	-2.856922	33297.9850	
HLA B*5301	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.522813	1.665496	-2.857316	33328.2620	
HLA B*4403	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.410705	1.553233	-2.857472	25745.6962	
HLA B*0801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.360914	1.502929	-2.857986	22956.9587	
HLA B*3801	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.504059	1.645813	-2.858246	31919.720366		
HLA B*3901	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.372079	1.513828	-2.858251	23554.782995		
HLA B*5701	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.411532	1.553233	-2.858299	25794.7699	
HLA B*5801	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.191918	1.333568	-2.858350	15556.727630		
HLA A*0203	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.745657	0.885414	-2.860243	5567.45950	
HLA A*2403	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.374196	1.513828	-2.860368	23669.876585		
HLA A*2403	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.168607	1.308218	-2.860389	14743.705855		
HLA A*3201	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.582652	1.721985	-2.860667	38251.7845	
HLA B*5401	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.519803	1.658831	-2.860972	33098.0933	
HLA B*5801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.308363	1.446759	-2.861604	20340.5842	
HLA A*0101	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-3.029572	0.167651	-2.861921	1070.462924		
HLA B*5301	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.483008	1.621061	-2.861947	30409.3888	
HLA A*2902	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.364887	1.502929	-2.861959	23167.9354	
HLA A*0250	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.584477	1.721985	-2.862493	38412.9137	
HLA B*7301	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.528101	1.665496	-2.862605	33736.6035	
HLA A*3002	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.222438	1.359245	-2.863193	16689.297572		
HLA A*3201	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.768950	0.905427	-2.863523	5874.21531	
HLA A*3001	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.172023	1.308218	-2.863805	14860.136854		
HLA A*2603	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.485244	1.621061	-2.864183	30566.4077	
HLA B*0803	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.425922	1.561696	-2.864226	26663.813029		
HLA B*1801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.500034	1.635567	-2.864467	31625.2822	
HLA A*2402	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.511500	1.646900	-2.864600	32471.3165	
HLA B*7301	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.623169	1.758557	-2.864612	41992.1943	
HLA A*2902	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.188366	1.323538	-2.864828	15429.9964	
HLA A*3101	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.378850	1.513828	-2.865022	23924.910582		
HLA A*0206	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.032623	1.167504	-2.865119	10780.1093	
HLA B*5301	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.512092	1.646900	-2.865192	32515.6145	
HLA A*2301	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.523550	1.657746	-2.865804	33384.925054		
HLA A*3101	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.267863	1.401827	-2.866036	18529.4701	
HLA B*5801	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.365952	1.499754	-2.866198	23224.782239		
HLA A*3301	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.513304	1.646900	-2.866405	32606.5088	
HLA A*1101	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.428366	1.561696	-2.866670	26814.254048		
HLA A*1101	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.413031	1.546204	-2.866827	25883.954702		
HLA B*1509	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.318746	1.451496	-2.867249	20832.7114	
HLA A*0203	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-3.899304	1.031880	-2.867424	7930.56242	
HLA B*3901	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.269360	1.401827	-2.867533	18593.4347	
HLA B*5701	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.370651	1.502929	-2.867722	23477.4335	
HLA B*4403	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.591103	1.721985	-2.869118	39003.4297	
HLA B*4601	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.382964	1.513828	-2.869136	24152.621279		
HLA B*7301	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.490728	1.621061	-2.869667	30954.8069	
HLA A*2902	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.003278	1.133400	-2.869878	10075.7665	
HLA A*0203	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.423401	1.553233	-2.870168	26509.4829	
HLA A*0202	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.564403	1.693800	-2.870604	36677.7975	
HLA B*4002	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.649553	1.778801			
HLA A*0206	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.528548	1.657746	-2.8708			

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HLA B*3901	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.424054	1.553233	-2.870822	26549.3819
HLA B*5401	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.528583	1.657746	-2.870837	33774.039152	
HLA A*0219	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.903453	1.032480	-2.870973	8006.69303
HLA A*0212	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.424322	1.553233	-2.871089	26565.7606
HLA A*0202	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.685454	0.814245	-2.871209	4846.78620
HLA A*0219	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.273048	1.401827	-2.871221	18752.0311
HLA A*0101	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.385135	1.513828	-2.871307	24273.656154	
HLA A*3101	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.231136	1.359245	-2.871890	17026.910442	
HLA B*0702	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.425920	1.553233	-2.872687	26663.6687
HLA A*0250	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.508408	1.635567	-2.872841	32240.9607
HLA A*3001	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.222189	1.349023	-2.873166	16679.7298
HLA B*4403	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.567460	1.691549	-2.875911	36936.856385	
HLA A*6901	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.279119	1.401827	-2.877292	19016.0094
HLA A*0202	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-3.484845	0.607347	-2.877499	3053.834068	
HLA A*8001	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.329779	1.451496	-2.878283	21368.7431
HLA A*6802	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.431686	1.553233	-2.878453	27020.0122
HLA B*1503	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.381982	1.502929	-2.879054	24098.0658
HLA A*3002	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.572977	1.693800	-2.879177	37409.0364
HLA B*3801	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.500495	1.621061	-2.879434	31658.8335
HLA B*4002	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.638262	1.758557	-2.879705	43477.2094
HLA B*4002	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.595456	1.715719	-2.879737	39396.3869
HLA A*3001	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.103197	1.222842	-2.880355	12682.270016	
HLA B*4402	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.085440	1.204727	-2.880713	12174.1763
HLA B*5301	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.574645	1.693800	-2.880845	37553.0016
HLA B*0801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.434228	1.553233	-2.880995	27178.6377
HLA A*2403	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.033074	1.151985	-2.881089	10791.312421	
HLA B*1517	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.189602	1.308218	-2.881384	15473.966627	
HLA B*4403	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.517087	1.635567	-2.881520	32891.7493
HLA A*2601	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.381613	1.499754	-2.881859	24077.606786	
HLA B*1501	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.205588	1.323538	-2.882050	16054.1587
HLA A*8001	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.395919	1.513828	-2.882091	24883.950677	
HLA B*4801	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.395959	1.513828	-2.882131	24886.239312	
HLA B*1503	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-3.949414	1.066259	-2.883154	8900.48769
HLA B*2705	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.330033	1.446759	-2.883273	21381.2319
HLA B*4501	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.662168	1.778801	-2.883367	45937.5333
HLA B*5301	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.605752	1.721985	-2.883767	40341.4809
HLA A*2603	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.051598	1.167504	-2.884093	11261.5353
HLA B*1501	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.789522	0.905427	-2.884095	6159.16660
HLA A*3001	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.052749	1.168653	-2.884096	11291.4275
HLA B*0802	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.430367	1.546204	-2.884163	26938.132265	
HLA A*0101	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.384036	1.499754	-2.884282	24212.277162	
HLA A*6901	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.053247	1.168653	-2.884594	11304.3851
HLA A*3001	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.218627	1.333568	-2.885059	16543.492298	
HLA B*1517	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.901075	1.015721	-2.885355	7962.97770
HLA B*3501	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.431756	1.546204	-2.885552	27024.397892	
HLA A*2601	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.388728	1.502929	-2.885799	24475.2737
HLA B*4501	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.439082	1.553233	-2.885849	27484.1127
HLA B*5801	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.245160	1.359245	-2.885915	17585.710836	
HLA B*4501	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.644702	1.758557	-2.886145	44126.7152
HLA A*3201	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.219750	1.333568	-2.886182	16586.327922	
HLA A*0216	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.054478	1.167504	-2.886974	11336.4760
HLA A*0211	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.532829	1.645813	-2.887016	34105.822060	
HLA B*5301	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.007070	1.119963	-2.887107	10164.1289
HLA A*0250	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.508354	1.621061	-2.887293	32236.9493
HLA B*4601	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.390269	1.502929	-2.887340	24562.2880
HLA B*3501	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.125409	1.238012	-2.887397	13347.779591	
HLA A*0206	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.533562	1.645813	-2.887749	34163.437390	
HLA B*4001	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.390711	1.502929	-2.887782	24587.2820
HLA A*0250	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.581799	1.693800	-2.887999	38176.7397
HLA A*0201	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.391058	1.502929	-2.888130	24606.9760
HLA B*7301	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.604079	1.715719	-2.888360	40186.3908
HLA A*2902	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.247831	1.359245	-2.888586	17694.214680	
HLA A*2902	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.162019	1.273350	-2.888669	14521.7415
HLA B*7301	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.580286	1.691549	-2.888737	38043.964649	
HLA B*1517	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.435247	1.546204	-2.889043	27242.525200	
HLA B*5401	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.565002	1.675398	-2.889604	36728.4304
HLA A*3201	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.547513	1.657746	-2.889767	35278.718676	
HLA B*3501	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.443015	1.553233	-2.889782	27734.1435
HLA A*0219	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.443207	1.553233	-2.889975	27746.4494
HLA A*0216	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.403999	1.513828	-2.890171	25351.240235	
HLA A*2402	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.565616	1.675398	-2.890217	36780.3269
HLA A*0211	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.795668	0.905427	-2.890241	6246.95251
HLA B*1502	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.341764	1.451496	-2.890267	21966.6435
HLA B*4002	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.525860	1.635567	-2.890292	33562.9363
HLA B*4501	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.584559	1.693800	-2.890760	38420.1877
HLA B*1503	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-3.733548	0.842742	-2.890806	5414.368633	
HLA A*3201	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.536651	1.645813	-2.890838	34407.342771	
HLA B*4801	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.390624	1.499754	-2.890870	24582.361029	
HLA A*0203	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.394164	1.502929	-2.891236	24783.5928
HLA A*0212	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.224835	1.333568	-2.891266	16781.645124	
HLA A*3301	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-3.731607	0.839978	-2.891629	5390.228134	
HLA B*4403	1:132-140	9	LTEAADAAR	1.180631	0.577926	-4.650204	1.758557	-2.891647	44689.3557
HLA A*0211	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.928917	1.036697	-2.892220	8490.17998
HLA B*0801	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.392459	1.499754	-2.892704	24686.444266	
HLA B*5401	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.246969	1.354114	-2.892855	17659.1189
HLA B*5101	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.045212	1.151985	-2.893226	11097.156366	
HLA B*4403	1:174-182	9	VLPNATETR	1.038504	0.740297	-4.672301	1.778801	-2.893500	47021.9894
HLA B*0702	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.397280	1.502929	-2.894351	24962.0175
HLA B*2705	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.397726	1.502929	-2.894797	24987.6886
HLA B*5401	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.541846	1.646900	-2.894946	34821.3693
HLA A*0219	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.409025	1.513828	-2.895197	25646.302423	
HLA B*5401	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.541223	1.645813	-2.895411	34771.484450	
HLA A*0219	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.342323	1.446759	-2.895563	21994.9449
HLA A*0203	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.801265	0.905427	-2.895838	6327.97387
HLA B*0702	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.410291	1.513828	-2.896463	25721.194389	
HLA A*0201	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.396248	1.499754	-2.896494	24902.804534	
HLA A*2403	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.396413	1.499754	-2.896659	24912.236819	
HLA B*4001	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.396798	1.499754	-2.897044	24934.349307	
HLA B*1501	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.397125	1.499754	-2.897371	24953.106355	
HLA B*0801	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.083020	1.185494	-2.897525	12106.528207	
HLA A*2603	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.221089	1.323538	-2.897552	16637.5530
HLA B*3901	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.231173	1.333568	-2.897605	17028.384325	
HLA A*2603	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.934419	1.036697	-2.897723	8598.43456
HLA A*0212	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.411774	1.513828	-2.897945	25809.147322	
HLA B*1517	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.412032	1.513828	-2.898204	25824.510602	
HLA A*0216	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.872017	0.973692	-2.898325	7447.61244
HLA B*4801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.401271	1.502929	-2.898343	25192.5111
HLA A*2602	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.401619	1.502929	-2.898691	25212.6895
HLA A*0202	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.066714	1.167504	-2.899210	11660.4199
HLA B*4002	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.621444	1.721985	-2.899459	41825.7798
HLA B*3501	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.223040	1.323538	-2.899502	16712.4271
HLA B*3801	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.445841	1.546204	-2.899637	27915.228632	
HLA B*1503	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-3.743622	0.843953	-2.899669	5541.43716
HLA A*0101	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.351547	1.451496	-2.900051	22467.0968
HLA A*1101	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.414353	1.513828	-2.900525	25962.911393	
HLA B*5401	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-3.569817	0.668648	-2.9011		
HLA B*4501	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.567006	1.665496		

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HLA B*5101	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.415340	1.513828	-2.901512	26021.970181	
HLA B*3801	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.463305	1.561696	-2.901609	29060.622381	
HLA A*0301	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.348535	1.446759	-2.901776	22311.8159	
HLA A*0216	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.070685	1.168653	-2.902032	11767.5166	
HLA B*3901	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-3.746597	0.843953	-2.902644	5579.52028	
HLA B*3501	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-3.540740	0.637604	-2.903135	3473.27910	
HLA B*5801	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.141968	1.238012	-2.903956	13866.542815	
HLA B*0803	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.355936	1.451496	-2.904439	22695.2931	
HLA A*3201	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.580495	1.675398	-2.905097	38062.2864	
HLA A*0202	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.551876	1.645813	-2.906063	35634.920710	
HLA A*3001	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.144482	1.238012	-2.906470	13947.043193	
HLA A*0301	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.265849	1.359245	-2.906604	18443.761288	
HLA B*4403	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.600569	1.693800	-2.906769	39862.8984	
HLA B*5801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.792276	0.885414	-2.906861	6198.34218	
HLA A*0216	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.410054	1.502929	-2.907125	25707.1441	
HLA A*8001	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-3.743594	0.836190	-2.907404	5541.077430	
HLA A*0216	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.460666	1.553233	-2.907434	28884.6054	
HLA A*6802	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.309289	1.401827	-2.907462	20383.9863	
HLA A*6802	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.410477	1.502929	-2.907548	25732.1894	
HLA B*1517	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.460843	1.553233	-2.907610	28896.3275	
HLA B*5701	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.407455	1.499754	-2.907701	25553.788926	
HLA B*0801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.309874	1.401827	-2.908047	20411.4634	
HLA A*2403	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.267485	1.359245	-2.908239	18513.338172	
HLA B*3801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.355038	1.446759	-2.908279	22648.4399	
HLA B*0702	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.310424	1.401827	-2.908597	20437.3189	
HLA B*4403	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.567693	1.658831	-2.908861	36956.6442	
HLA A*8001	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.412020	1.502929	-2.909092	25823.8120	
HLA B*4601	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.408961	1.499754	-2.909207	25642.556618	
HLA A*0250	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.567070	1.657746	-2.909324	36903.700441	
HLA A*8001	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.462645	1.553233	-2.909412	29016.4785	
HLA B*3501	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.269249	1.359245	-2.910004	18588.707660	
HLA A*2501	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.361821	1.451496	-2.910325	23004.9480	
HLA A*0250	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.312468	1.401827	-2.910641	20533.7360	
HLA B*1501	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.869137	0.957621	-2.911516	7398.37942	
HLA B*0802	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.411316	1.499754	-2.911561	25781.934876	
HLA A*0206	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.063975	1.152145	-2.911830	11587.0983	
HLA B*1502	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.547654	1.635567	-2.912086	35290.1717	
HLA A*2501	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.359751	1.446759	-2.912992	22895.5647	
HLA B*4002	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.578519	1.665496	-2.913023	37889.5071	
HLA A*6901	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.221437	1.308218	-2.913219	16650.879490	
HLA B*1801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.248487	1.334180	-2.914307	17720.9417	
HLA A*2501	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.460657	1.546204	-2.914453	28883.980398	
HLA B*4402	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.417699	1.502929	-2.914770	26163.6937	
HLA A*0219	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.414800	1.499754	-2.915046	25989.611843	
HLA B*5401	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.550692	1.635567	-2.915124	35537.8914	
HLA B*1509	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.468565	1.553233	-2.915333	29414.7666	
HLA A*2403	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.418810	1.502929	-2.915882	26230.7292	
HLA B*3501	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-3.896456	0.980281	-2.916175	7878.733528	
HLA B*4002	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.469681	1.553233	-2.916449	29490.4509	
HLA A*0203	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.084387	1.167504	-2.916883	12144.7063	
HLA B*0801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-3.973830	1.056254	-2.917576	9415.20222	
HLA B*0802	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.420572	1.502929	-2.917644	26337.3744	
HLA B*3801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.470948	1.553233	-2.917715	29576.5685	
HLA A*2501	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.420873	1.502929	-2.917945	26355.6184	
HLA B*1502	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.611853	1.693800	-2.918054	40912.2580	
HLA A*6901	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.267156	1.349023	-2.918133	18499.3217	
HLA B*5101	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.252328	1.333568	-2.918760	17878.381754	
HLA A*2501	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.320752	1.401827	-2.918925	20929.1821	
HLA B*4801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.192407	1.273350	-2.919057	15574.2427	
HLA B*5701	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.366107	1.446759	-2.919347	23233.0761	
HLA A*3201	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.613350	1.693800	-2.919550	41053.4889	
HLA A*0212	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.920398	1.000751	-2.919646	8325.25729	
HLA B*0803	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.253989	1.334180	-2.919809	17946.8937	
HLA B*0801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.065525	1.145357	-2.920168	11628.5443	
HLA B*0803	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.367007	1.446759	-2.920247	23281.2647	
HLA B*4403	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.637432	1.715719	-2.921713	43394.2606	
HLA B*4402	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.421479	1.499754	-2.921725	26392.430050	
HLA B*5401	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-3.015700	0.093967	-2.921733	1036.812610	
HLA B*5301	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.597583	1.675398	-2.922185	39589.7425	
HLA A*3201	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.569833	1.646900	-2.922933	37139.2313	
HLA A*3201	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.544329	1.621061	-2.923268	35021.0570	
HLA B*0702	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.469491	1.546204	-2.923287	29477.531030	
HLA A*3001	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.956805	1.032480	-2.924325	9053.26606	
HLA B*3501	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.273373	1.349023	-2.924349	18766.0359	
HLA B*4501	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.570531	1.645813	-2.924718	37198.952255	
HLA A*6901	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.940777	1.015721	-2.925056	8725.23428	
HLA A*6801	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.584247	1.658831	-2.925416	38392.5537	
HLA A*8001	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.372471	1.446759	-2.925712	23576.0732	
HLA A*3301	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.479213	1.553233	-2.925980	30144.8602	
HLA B*5301	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.472278	1.546204	-2.926074	29667.270704	
HLA A*0219	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.078137	1.151985	-2.926152	11971.191782	
HLA A*0216	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.426040	1.499754	-2.926286	26671.026418	
HLA A*3002	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.958892	1.032480	-2.926412	9096.86242	
HLA A*2902	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.426216	1.499754	-2.926462	26681.850161	
HLA A*0202	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-3.958624	1.031880	-2.926743	9091.25386	
HLA B*5301	1:89-97	9	CTHELIRHR	1.005015	0.652731	-4.584670	1.657746	-2.926924	38429.957880	
HLA A*0211	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-3.546646	0.619672	-2.926974	3520.839997	
HLA B*3901	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.286299	1.359245	-2.927054	19333.007085	
HLA B*1509	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-3.854349	0.927116	-2.927233	7150.706321	
HLA A*0216	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.276549	1.349023	-2.927526	18903.7971	
HLA A*8001	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.427614	1.499754	-2.927860	26767.874320	
HLA B*1801	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.481203	1.553233	-2.927970	30283.3062	
HLA B*3501	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.428039	1.499754	-2.928285	26794.097990	
HLA A*0212	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.428255	1.499754	-2.928501	26807.436994	
HLA A*2602	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.375350	1.446759	-2.928590	23732.8334	
HLA B*0801	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.965372	1.036697	-2.928675	9233.60955	
HLA B*7301	1:138-146	9	AARATYSEL	1.196073	0.462758	-4.587748	1.658831	-2.928916	38703.2766	
HLA A*3101	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.252488	1.323538	-2.928950	17884.9599	
HLA B*4402	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.380704	1.451496	-2.929208	24027.2499	
HLA B*4001	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-3.664990	0.735649	-2.929341	4623.70213	
HLA B*1502	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.577043	1.646900	-2.930144	37760.9994	
HLA B*5101	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.332333	1.401827	-2.930506	21494.7733	
HLA B*1501	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.116053	1.185494	-2.930559	13063.314341	
HLA A*3301	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.492314	1.561696	-2.930618	31068.050507	
HLA A*0212	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.433645	1.502929	-2.930716	27142.1978	
HLA B*0802	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.265020	1.334180	-2.930840	18408.5730	
HLA A*2602	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-3.987565	1.056254	-2.931311	9717.72805	
HLA A*0250	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.577513	1.645813	-2.931701	37801.878087	
HLA B*4001	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.333618	1.401827	-2.931791	21558.4750	
HLA B*4501	1:154-162	9	FADQPNAIL	1.350025	0.365694	-4.647695	1.715719	-2.931975	44431.8957	
HLA B*7301	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.383639	1.451496	-2.932142	24190.1506	
HLA A*0211	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.084331	1.151985	-2.932345	12143.129620	
HLA B*4501	1:156-164	9	DQPNAILRR	1.122083	0.599902	-4.654381	1.721985	-2.932397	45121.2869	
HLA A*2501	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.266813	1.334180	-2.932633	18484.7159	
HLA B*3501	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-3.059786	0.127125	-2.932661	1147.588023	
HLA A*3101	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.013113	1.080003			
HLA B*7301	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.580013	1.646900			

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HLA B*4801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.335122	1.401827	-2.933295	21633.2469
HLA B*1801	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.447519	1.513828	-2.933691	28023.264211	
HLA A*0219	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.268984	1.335227	-2.933757	18577.3475
HLA A*2902	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.380706	1.446759	-2.933947	24027.3799
HLA B*7301	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.591761	1.657746	-2.934015	39062.555722	
HLA B*1503	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-3.861256	0.927116	-2.934141	7265.348111	
HLA B*1503	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-3.993232	1.058921	-2.934311	9845.36223
HLA A*6802	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.434456	1.499754	-2.934702	27192.903710	
HLA A*3101	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-3.971729	1.036697	-2.935033	9369.77609
HLA A*0203	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.047895	1.112498	-2.935397	11165.9278
HLA A*0219	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.951124	1.015721	-2.935403	8935.61048
HLA A*3002	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-3.897603	0.962074	-2.935529	7899.561069	
HLA A*2403	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.259515	1.323538	-2.935978	18176.7101
HLA B*1509	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.383089	1.446759	-2.936329	24159.5474
HLA A*0203	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-3.963905	1.027504	-2.936401	9202.49155
HLA B*1509	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-3.978021	1.041264	-2.936757	9506.51052
HLA B*3501	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.451980	1.513828	-2.938152	28312.641736	
HLA B*5401	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-3.979417	1.041264	-2.938153	9537.10859
HLA A*0216	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.161135	1.222842	-2.938294	14492.232591	
HLA A*1101	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.385149	1.446759	-2.938390	24274.4440
HLA B*2705	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.438403	1.499754	-2.938649	27441.176025	
HLA A*0250	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-3.939936	1.000751	-2.939185	8708.35212
HLA A*0250	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.065629	1.126312	-2.939316	11631.3126
HLA B*0702	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.439122	1.499754	-2.939368	27486.640485	
HLA A*0250	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.391866	1.451496	-2.940370	24652.8123
HLA B*1502	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.598555	1.657746	-2.940809	39678.510876	
HLA B*1503	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.274496	1.333568	-2.940927	18814.626333	
HLA A*3301	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.392623	1.451496	-2.941127	24695.7946
HLA B*5101	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.494483	1.553233	-2.941250	31223.5714
HLA A*6901	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.973797	1.032480	-2.941317	9414.48915
HLA A*3002	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.503446	1.561696	-2.941750	31874.682129	
HLA B*5701	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.127345	1.185494	-2.941851	13407.413455	
HLA A*2602	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.577791	1.635567	-2.942223	37826.0172
HLA A*0212	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.277895	1.335227	-2.942669	18962.4872
HLA B*1801	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.488881	1.546204	-2.942677	30823.461229	
HLA B*1502	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.344531	1.401827	-2.942704	22107.0806
HLA B*4002	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.601149	1.657746	-2.943403	39916.200577	
HLA A*0202	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.278798	1.335227	-2.943571	19001.9208
HLA A*2501	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.496851	1.553233	-2.943618	31394.3039
HLA B*1503	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.138566	1.194587	-2.943979	13758.343326	
HLA B*1801	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-3.679749	0.735649	-2.944101	4783.53893
HLA B*0802	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.457929	1.513828	-2.944101	28703.132084	
HLA B*4501	1:85-93 9	ISRSCTHEL	1.239891	0.451658	-4.635724	1.691549	-2.944175	43223.926652	
HLA A*6802	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.092314	1.147510	-2.944804	12368.4187
HLA A*2602	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.590772	1.645813	-2.944959	38973.689515	
HLA A*2602	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.620474	1.675398	-2.945076	41732.4335
HLA B*3901	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.268803	1.323538	-2.945265	18569.6105
HLA A*0201	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.140117	1.194587	-2.945530	13807.555665	
HLA B*4403	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.603334	1.657746	-2.945588	40117.532888	
HLA A*6801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.006229	1.058921	-2.947309	10144.4627
HLA A*0203	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.447286	1.499754	-2.947532	28008.259557	
HLA B*4002	1:202-210	9	EHADVEIRR	1.104999	0.588801	-4.641551	1.693800	-2.947751	43807.7492
HLA A*2403	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.281589	1.333568	-2.948021	19124.438486	
HLA A*0206	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.023197	1.074983	-2.948214	10548.6536
HLA A*3002	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.494694	1.546204	-2.948490	31238.777571	
HLA B*0801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.061033	1.112498	-2.948536	11508.8820
HLA A*3002	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.052725	1.104113	-2.948613	11290.816744	
HLA B*2705	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.307950	1.359245	-2.948705	20321.226401	
HLA A*2301	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.448856	1.499754	-2.949101	28109.659081	
HLA B*4402	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.396662	1.446759	-2.949902	24926.5267
HLA A*2902	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.982386	1.032480	-2.949906	9602.54777
HLA A*2301	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.283774	1.333568	-2.950206	19220.899756	
HLA B*4601	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.908608	0.957621	-2.950987	8102.29307
HLA A*0219	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.454144	1.502929	-2.951216	28454.0617
HLA A*0301	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.225046	1.273350	-2.951696	16789.8179
HLA B*5401	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.079232	1.126312	-2.952920	12001.4093
HLA A*2603	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.589120	1.635567	-2.953552	38825.7481
HLA B*7301	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.629148	1.675398	-2.953750	42574.3483
HLA A*0250	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-3.985643	1.031880	-2.953763	9674.81931
HLA A*0211	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.945716	0.991777	-2.953939	8825.02033
HLA B*1517	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.453822	1.499754	-2.954068	28432.980666	
HLA B*1503	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.928687	0.973692	-2.954995	8485.67994
HLA B*0801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-3.882143	0.927121	-2.955022	7623.30594
HLA B*1517	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.059154	1.104113	-2.955041	11459.180217	
HLA B*0803	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.469106	1.513828	-2.955278	29451.389520	
HLA B*7301	1:39-47 9	AGRACYQSW	1.340001	0.305812	-4.601180	1.645813	-2.955367	39919.007925	
HLA A*0301	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.357959	1.401827	-2.956132	22801.2524
HLA B*4801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.305462	1.349023	-2.956439	20205.1374
HLA B*1501	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.310990	1.354114	-2.956876	20463.9821
HLA A*0201	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.180721	1.222842	-2.957879	15160.747076	
HLA B*5101	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.457786	1.499754	-2.958032	28693.661520	
HLA A*0211	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.461115	1.502929	-2.958187	28914.4670
HLA B*7301	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.594143	1.635567	-2.958576	39277.4271
HLA A*3201	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.583853	0.625007	-2.958846	3835.77159
HLA B*0803	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.318161	1.359245	-2.958915	20804.667352	
HLA A*0201	1:165-173	9	KQARQAARA	1.079552	-0.087775	-3.951698	0.991777	-2.959921	8947.41339
HLA B*4002	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.581566	1.621061	-2.960505	38156.2985
HLA B*3501	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.463580	1.502929	-2.960651	29079.0223
HLA B*4601	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.284591	1.323538	-2.961054	19257.1199
HLA B*5301	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.269886	1.308218	-2.961668	18615.980179	
HLA B*0702	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.295430	1.333568	-2.961861	19743.743889	
HLA A*3001	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-3.225918	0.263887	-2.962031	1682.35673
HLA B*4402	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.311082	1.349023	-2.962059	20468.3001
HLA B*0803	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.466432	1.502929	-2.963503	29270.6303
HLA A*0212	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.996103	1.032480	-2.963623	9910.66439
HLA A*0206	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-3.844819	0.880633	-2.964187	6995.510790	
HLA A*0203	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.298951	1.334180	-2.964771	19904.5052
HLA A*0216	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.090712	1.125530	-2.965182	12322.869013	
HLA B*4501	1:124-132	9	DDADLRHIL	1.566722	0.080178	-4.612354	1.646900	-2.965454	40959.4286
HLA B*5301	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.188643	1.222842	-2.965801	15439.849616	
HLA A*2301	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.468735	1.502929	-2.965806	29426.2263
HLA B*4403	1:188-196	9	NYRAWRHFI	1.295038	0.370458	-4.631434	1.665496	-2.965938	42799.0429
HLA B*3801	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.479862	1.513828	-2.966034	30189.903999	
HLA A*0212	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.091638	1.125530	-2.966108	12349.163176	
HLA A*2603	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.300441	1.334180	-2.966261	19972.8923
HLA B*4501	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-3.460134	0.493735	-2.966399	2884.91852
HLA A*2301	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.519782	1.553233	-2.966549	33096.4819
HLA B*5401	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-3.999914	1.032480	-2.967434	9998.01156
HLA B*4501	1:89-97 9	CTHELIRHR	1.005015	0.652731	-4.625243	1.657746	-2.967497	42193.268080	
HLA A*3001	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.303000	1.335227	-2.967773	20090.9072
HLA A*2301	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.415117	1.446759	-2.968358	26008.5999
HLA B*4403	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.530101	1.561696	-2.968405	33892.278763	
HLA A*2601	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.926229	0.957621	-2.968608	8437.79726
HLA A*2601	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.292547	1.323538	-2.969009	19613.1202
HLA B*4601	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.323294	1.354114	-2.969180	21052.0503
HLA B*5801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.293428	1.323538		
HLA A*0206	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.523179	1.553233		

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HLA A*0206	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.319108	1.349023	-2.970084	20850.0748
HLA B*1503	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.305356	1.335227	-2.970129	20200.2192
HLA B*1501	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.303996	1.333568	-2.970428	20137.044562
HLA A*2601	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.304616	1.334180	-2.970436	20165.8250
HLA A*6802	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.193549	1.222842	-2.970707	15615.244571
HLA B*5301	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.330416	1.359245	-2.971170	21400.094443
HLA A*0206	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-3.706153	0.734934	-2.971219	5083.382927
HLA A*0211	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.524638	1.553233	-2.971405	33468.6517
HLA B*4501	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.646967	1.675398	-2.971568	44357.4430
HLA B*5801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.325799	1.354114	-2.971685	21173.8070
HLA B*1801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.419424	1.446759	-2.972664	26267.7926
HLA B*1801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.475675	1.502929	-2.972746	29900.2589
HLA B*4002	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.648179	1.675398	-2.972781	44481.4399
HLA A*3201	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-3.845567	0.872645	-2.972922	7007.55583
HLA B*4402	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.374929	1.401827	-2.973102	23709.8623
HLA B*5701	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.297363	1.323538	-2.973825	19831.8457
HLA B*4501	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.520355	1.546204	-2.974151	33140.198548
HLA B*1801	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.308262	1.333568	-2.974694	20335.853095
HLA B*1501	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.323734	1.349023	-2.974711	21073.3584
HLA A*6801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.329069	1.354114	-2.974955	21333.8597
HLA B*4403	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.650665	1.675398	-2.975266	44736.7666
HLA A*0101	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.377535	1.401827	-2.975708	23852.5388
HLA A*0219	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.095942	1.119963	-2.975979	12472.1632
HLA A*6801	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.611656	1.635567	-2.976089	40893.6704
HLA A*0101	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.335392	1.359245	-2.976147	21646.710013
HLA A*3201	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.170825	1.194587	-2.976237	14819.193599
HLA A*3301	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.622210	1.645813	-2.976397	41899.609927
HLA B*4801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.311735	1.335227	-2.976508	20499.1066
HLA A*0211	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.325689	1.349023	-2.976665	21168.4240
HLA A*0201	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.285484	1.308218	-2.977266	19296.748598
HLA A*8001	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.379116	1.401827	-2.977289	23939.5407
HLA A*3001	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.182408	1.204727	-2.977681	15219.7504
HLA A*0250	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.524180	1.546204	-2.977976	33433.363303
HLA A*0203	1:173-181	9	AVLPNATET	1.134394	-0.118673	-3.993866	1.015721	-2.978145	9859.75356
HLA A*2603	1:121-129	9	GMEDDADLR	1.182603	0.492795	-4.653794	1.675398	-2.978396	45060.3028
HLA A*2403	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.332622	1.354114	-2.978508	21509.0810
HLA B*3501	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.312778	1.334180	-2.978598	20548.4044
HLA A*0101	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.332824	1.354114	-2.978710	21519.0905
HLA A*0216	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.006224	1.027504	-2.978720	10144.3529
HLA A*3101	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.312343	1.333568	-2.978775	20527.849327
HLA A*0211	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.020284	1.041264	-2.979020	10478.1272
HLA A*0201	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.952811	0.973692	-2.979119	8970.38658
HLA A*0250	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.184400	1.204727	-2.979673	15289.7328
HLA A*0216	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.314930	1.335227	-2.979703	20650.4839
HLA A*0202	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.023968	1.044178	-2.979790	10567.3882
HLA A*2501	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.147809	1.167504	-2.980305	14054.2934
HLA B*3901	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.483330	1.502929	-2.980401	30431.9352
HLA A*2402	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.314249	1.333568	-2.980681	20618.111490
HLA A*2601	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.334964	1.354114	-2.980850	21625.4071
HLA B*4601	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.219168	1.238012	-2.981155	16564.089755
HLA B*3801	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.133914	1.151985	-2.981929	13611.756215
HLA B*1509	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.336473	1.354114	-2.982359	21700.6459
HLA B*3801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.331579	1.349023	-2.982556	21457.4784
HLA A*0206	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.486107	1.502929	-2.983178	30627.1554
HLA A*3101	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.178089	1.194587	-2.983502	15069.164692
HLA B*5301	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.497821	1.513828	-2.983993	31464.526123
HLA B*0801	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-3.964432	0.980281	-2.984150	9213.650034
HLA A*2501	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.109912	1.125530	-2.984382	12879.880201
HLA A*0203	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.104644	1.119963	-2.984681	12724.6040
HLA B*5801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.333876	1.349023	-2.984853	21571.3080
HLA B*0803	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.484920	1.499754	-2.985166	30543.596460
HLA B*5401	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.485134	1.499754	-2.985380	30558.636771
HLA B*1502	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.532103	1.546204	-2.985898	34048.856494
HLA A*3001	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.002399	1.015721	-2.986679	10055.4008
HLA A*0212	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.106820	1.119963	-2.986857	12788.5086
HLA A*3301	1:200-208	9	ASEHADVEI	1.329405	0.306162	-4.622532	1.635567	-2.986964	41930.6755
HLA B*0801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.322235	1.335227	-2.987008	21000.7489
HLA A*2501	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.487086	1.499754	-2.987332	30696.325992
HLA A*0206	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.120968	1.133400	-2.987568	13211.9980
HLA A*3002	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.311284	1.323538	-2.987746	20477.8252
HLA A*2501	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.044563	1.056254	-2.988310	11080.5992
HLA A*0211	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-3.962331	0.973692	-2.988640	9169.19634
HLA A*0211	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.297250	1.308218	-2.989033	19826.696549
HLA A*0250	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-3.724338	0.734934	-2.989404	5300.756320
HLA A*2902	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.227546	1.238012	-2.989534	16886.740852
HLA A*3301	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.120569	1.130392	-2.990178	13199.852782
HLA A*3002	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.070487	1.080003	-2.990484	11762.1703
HLA A*2402	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.350377	1.359245	-2.991132	22406.649184
HLA A*2601	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.393011	1.401827	-2.991184	24717.8486
HLA A*2601	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.229489	1.238012	-2.991477	16962.461024
HLA B*1509	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.494419	1.502929	-2.991490	31219.0110
HLA B*4001	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.341179	1.349023	-2.992156	21937.0730
HLA A*0201	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.325837	1.333568	-2.992268	21175.639934
HLA A*6901	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.754552	0.762047	-2.992505	5682.66712
HLA B*5701	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.394914	1.401827	-2.993087	24826.4002
HLA A*8001	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.352393	1.359245	-2.993147	22510.895541
HLA B*1501	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.328999	1.335227	-2.993772	21330.3975
HLA A*2402	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.547109	1.553233	-2.993876	35245.9070
HLA B*4601	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.146822	1.152145	-2.994678	14022.3961
HLA B*1801	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.494454	1.499754	-2.994700	31221.544497
HLA B*4001	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-3.917992	0.923260	-2.994732	8279.26515
HLA A*2601	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.343862	1.349023	-2.994839	22073.0218
HLA B*4501	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.446828	1.451496	-2.995332	27978.7284
HLA A*0206	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.107976	1.112498	-2.995478	12822.5927
HLA A*0250	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.509952	1.513828	-2.996123	32355.758589
HLA A*3201	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.510083	1.513828	-2.996255	32365.562374
HLA A*0203	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.191749	1.194587	-2.997162	15550.669278
HLA B*3501	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-3.870997	0.873495	-2.997503	7430.14677
HLA B*4001	1:150-158	9	LEAKFADQP	0.710397	0.038013	-3.745977	0.748410	-2.997567	5571.55724
HLA A*0203	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.010045	1.012095	-2.997949	10233.9811
HLA A*3002	1:46-54	9	SWSKPNPKT	1.176779	-0.200471	-3.974520	0.976308	-2.998213	9430.189084
HLA B*3901	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.498049	1.499754	-2.998295	31481.041757
HLA B*0702	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.321842	1.323538	-2.998305	20981.7843
HLA B*5101	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.501378	1.502929	-2.998450	31723.2968
HLA A*1101	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.322606	1.323538	-2.999068	21018.7072
HLA A*0250	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.502031	1.502929	-2.999103	31771.0430
HLA A*0219	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-3.784198	0.784286	-2.999912	6084.123467
HLA A*0211	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.027774	1.027504	-3.000270	10660.4080
HLA B*4001	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.354409	1.354114	-3.000295	22615.6269
HLA B*2705	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.402481	1.401827	-3.000654	25262.7976
HLA A*0101	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.324547	1.323538	-3.001009	21112.8409
HLA A*3002	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.060197	1.058921	-3.001276	11486.7381
HLA A*0203	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.081366	1.080003	-3.001362	12060.5074
HLA B*3801	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.504536	1.502929	-3.001607	31954.7940
HLA B*5801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.337086	1.335227	-3.001859	21731.3085
HLA A*2402	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.505203	1.502929		
HLA A*2902	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.197003	1.194587	-3.0024	

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HLA A*6802	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.351881	1.349023	-3.002857	22484.3628
HLA A*0206	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.503079	1.499754	-3.003325	31847.793072
HLA A*3002	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.353119	1.349023	-3.004096	22548.5574
HLA A*3002	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.518001	1.513828	-3.004173	32961.041197
HLA B*4002	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.550421	1.546204	-3.004217	35515.788871
HLA B*0801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.353274	1.349023	-3.004251	22556.6099
HLA A*0101	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.338770	1.334180	-3.004590	21815.7659
HLA B*5401	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.551488	1.546204	-3.005284	35603.126043
HLA A*3101	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.279082	1.273350	-3.005732	19014.3635
HLA B*0801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.018033	1.012095	-3.005938	10423.9630
HLA B*5101	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.453024	1.446759	-3.006264	28380.7301
HLA B*5101	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.365829	1.359245	-3.006584	23218.249696
HLA A*0206	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.768663	0.762047	-3.006616	5870.33957
HLA A*8001	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.355720	1.349023	-3.006696	22684.0002
HLA A*2603	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.520602	1.513828	-3.006774	33159.028800
HLA A*2603	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.552987	1.546204	-3.006783	35726.222875
HLA A*0211	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.822250	0.814245	-3.008005	6641.25686
HLA A*0201	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.343613	1.335227	-3.008386	22060.3677
HLA B*5701	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.362808	1.354114	-3.008694	23057.2782
HLA B*0803	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.410533	1.401827	-3.008706	25735.5307
HLA A*2402	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.508603	1.499754	-3.008849	32255.440855
HLA A*0219	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.231780	1.222842	-3.008938	17052.168310
HLA A*2902	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.343131	1.334180	-3.008951	22035.9157
HLA B*1509	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.121514	1.112498	-3.009016	13228.5907
HLA A*2601	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.134816	1.125530	-3.009287	13640.062635
HLA A*0301	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.363607	1.354114	-3.009493	23099.7279
HLA B*1502	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.524192	1.513828	-3.010364	33434.267669
HLA B*7301	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.572232	1.561696	-3.010536	37344.937321
HLA B*5401	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.564493	1.553233	-3.011260	36685.3385
HLA A*0301	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-3.969098	0.957621	-3.011477	9313.17555
HLA B*4001	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.335105	1.323538	-3.011568	21632.4277
HLA A*2402	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.458390	1.446759	-3.011630	28733.5832
HLA A*6901	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.346881	1.335227	-3.011654	22227.0016
HLA B*0702	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.159368	1.147510	-3.011859	14433.3945
HLA B*4001	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.371118	1.359245	-3.011873	23502.722247
HLA B*7301	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-3.893411	0.880633	-3.012779	7823.687219
HLA B*1503	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-3.746085	0.732654	-3.013431	5572.943923
HLA A*0101	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.347022	1.333568	-3.013454	22234.217514
HLA B*1509	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.252230	1.238012	-3.014217	17874.319973
HLA A*2902	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.363489	1.349023	-3.014466	23093.4804
HLA B*0801	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.209286	1.194587	-3.014699	16191.446203
HLA B*5701	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.374114	1.359245	-3.014868	23665.395210
HLA B*5301	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.515562	1.499754	-3.015808	32776.468342
HLA A*0219	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.254041	1.238012	-3.016029	17949.029900
HLA A*0203	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.351326	1.335227	-3.016099	22455.6746
HLA B*1801	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-3.672043	0.655774	-3.016269	4699.40638
HLA A*6802	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-3.889812	0.873495	-3.016317	7759.11285
HLA B*4403	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.637695	1.621061	-3.016634	43420.5615
HLA A*0216	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.325014	1.308218	-3.016796	21135.582617
HLA A*6801	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.350415	1.333568	-3.016846	22408.588748
HLA A*0301	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.366064	1.349023	-3.017041	23230.8139
HLA B*5401	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.531280	1.513828	-3.017452	33984.447302
HLA A*3301	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-3.807101	0.789295	-3.017806	6413.584168
HLA A*0301	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.341557	1.323538	-3.018019	21956.1883
HLA B*4601	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.353577	1.335227	-3.018350	22572.3571
HLA A*0219	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.367535	1.349023	-3.018512	23309.6205
HLA A*0203	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.367540	1.349023	-3.018517	23309.8727
HLA B*5801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.352701	1.334180	-3.018521	22526.8545
HLA B*0802	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.421898	1.401827	-3.020071	26417.8571
HLA A*3301	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.374793	1.354114	-3.020679	23702.4239
HLA A*3201	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.523976	1.502929	-3.021047	33417.6312
HLA A*2902	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.354637	1.333568	-3.021068	22627.497776
HLA A*0301	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.355548	1.334180	-3.021368	22675.0436
HLA B*5701	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.354975	1.333568	-3.021407	22645.132008
HLA A*3002	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.574706	1.553233	-3.021473	37558.2840
HLA B*4601	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.380721	1.359245	-3.021475	24028.159899
HLA B*1502	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.036378	1.014245	-3.022132	10873.7073
HLA B*1503	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-3.932620	0.910145	-3.022475	8562.87659
HLA B*4501	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-3.868643	0.846009	-3.022634	7389.97907
HLA A*0202	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.575930	1.553233	-3.022697	37664.2933
HLA A*0250	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.576061	1.553233	-3.022829	37675.7056
HLA B*1509	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.358262	1.335227	-3.023035	22817.1704
HLA B*5801	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.175030	1.151985	-3.023045	14963.395324
HLA A*2501	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.346644	1.323538	-3.023106	22214.8601
HLA A*0203	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.098254	1.074983	-3.023270	12538.7337
HLA A*3001	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.068072	1.044178	-3.023894	11696.9381
HLA A*0201	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.143956	1.119963	-3.023993	13930.1521
HLA A*0206	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.357587	1.333568	-3.024019	22781.771104
HLA A*0202	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.527157	1.502929	-3.024228	33663.3137
HLA B*4801	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.383808	1.359245	-3.024562	24199.574878
HLA B*3901	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.650019	0.625007	-3.025012	4467.03062
HLA B*4601	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.374288	1.349023	-3.025264	23674.8711
HLA A*3201	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-3.987673	0.962074	-3.025599	9720.146663
HLA B*5701	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.333938	1.308218	-3.025720	21574.342449
HLA A*0212	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.375730	1.349023	-3.026707	23753.6420
HLA A*2602	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.573115	1.546204	-3.026911	37420.978654
HLA A*0101	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.265156	1.238012	-3.027144	18414.350046
HLA B*5801	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.335765	1.308218	-3.027548	21665.337925
HLA B*5101	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.351333	1.323538	-3.027795	22456.0390
HLA A*0211	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.528325	1.499754	-3.028570	33753.946612
HLA A*2603	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.528745	1.499754	-3.028991	33786.648758
HLA B*2705	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.383444	1.354114	-3.029329	24179.2912
HLA B*0702	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.061949	1.032480	-3.029469	11533.1897
HLA B*0702	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.389378	1.359245	-3.030133	24511.978420
HLA B*4501	1:99-107	9	FSYSQLSQR	0.929437	0.691624	-4.651461	1.621061	-3.030400	44818.8870
HLA A*0250	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.935853	0.905427	-3.030426	8626.85655
HLA A*0101	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.379539	1.349023	-3.030516	23962.8639
HLA A*6802	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.182835	1.152145	-3.030691	15234.7432
HLA A*6801	1:39-47	9	AGRACYQSW	1.340001	0.305812	-4.676612	1.645813	-3.030800	47491.108325
HLA B*4001	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.364558	1.333568	-3.030990	23150.395029
HLA B*3501	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.254337	1.222842	-3.031495	17961.268956
HLA A*0301	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.366800	1.335227	-3.031573	23270.1838
HLA B*1509	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.531520	1.499754	-3.031766	34003.205391
HLA A*0301	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.365482	1.333568	-3.031914	23199.667129
HLA B*1509	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.032694	1.000751	-3.031942	10781.8590
HLA B*0802	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.391270	1.359245	-3.032024	24618.959905
HLA A*6901	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.144125	1.112050	-3.032075	13935.5792
HLA A*0250	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.794625	0.762047	-3.032578	6231.96539
HLA A*0202	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.227696	1.194587	-3.033109	16892.588610
HLA A*0206	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-3.768771	0.735649	-3.033123	5871.80061
HLA B*1501	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.159477	1.126312	-3.033164	14436.9867
HLA A*0101	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.368487	1.335227	-3.033260	23360.7480
HLA A*0201	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.382290	1.349023	-3.033267	24115.1500
HLA B*5701	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.382358	1.349023	-3.033335	24118.9337
HLA B*4501	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.547863	1.513828	-3.034035	35307.167380
HLA B*4501	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.188723	1.154646		
HLA A*8001	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.358043	1.323538		

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HLA A*1101	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.436652	1.401827	-3.034825	27330.8005
HLA B*5801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.308410	1.273350	-3.035060	20342.7852
HLA B*5301	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.370402	1.335227	-3.035175	23463.9743
HLA B*1517	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.389848	1.354114	-3.035734	24538.5141
HLA B*4001	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.369993	1.334180	-3.035813	23441.8976
HLA A*2403	1:80-88 9	FYITGISRS	1.033042	-0.849138	-3.220223	0.183904	-3.036318	1660.439055	
HLA B*4402	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.390837	1.354114	-3.036723	24594.4659
HLA B*1801	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.396128	1.359245	-3.036883	24895.934690	
HLA A*3101	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.385986	1.349023	-3.036963	24321.2397
HLA A*2603	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.189127	1.152145	-3.036983	15457.0659
HLA B*0803	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.345314	1.308218	-3.037096	22146.942311	
HLA B*1517	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.439093	1.401827	-3.037266	27484.8561
HLA B*2705	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.141700	1.104113	-3.037588	13857.993575	
HLA B*0802	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.371203	1.333568	-3.037635	23507.299989	
HLA A*3001	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.205400	1.167504	-3.037895	16047.2121
HLA A*0212	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.206603	1.168653	-3.037950	16091.7223
HLA B*0801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.361633	1.323538	-3.038096	22994.9938
HLA B*1501	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.373103	1.334180	-3.038923	23610.4075
HLA A*3101	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.373719	1.334180	-3.039539	23643.8964
HLA B*0802	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.119578	1.080003	-3.039574	13169.7522
HLA B*3801	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.539658	1.499754	-3.039904	34646.428695	
HLA B*0802	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.394169	1.354114	-3.040055	24783.8610
HLA A*3002	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.539851	1.499754	-3.040097	34661.801638	
HLA A*0203	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.802609	0.762047	-3.040562	6347.58584
HLA B*4002	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.487415	1.446759	-3.040656	30719.5837
HLA A*2601	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.348899	1.308218	-3.040681	22330.532963	
HLA B*4801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.395160	1.354114	-3.041046	24840.5065
HLA B*1502	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.193652	1.152145	-3.041508	15618.9619
HLA B*5401	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.031641	0.990022	-3.041619	10755.7594
HLA B*1517	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.376003	1.334180	-3.041823	23768.5532
HLA A*0201	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.168184	1.126312	-3.041871	14729.3557
HLA B*4001	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.377819	1.335227	-3.042592	23868.1577
HLA B*1502	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.595945	1.553233	-3.042712	39440.7429
HLA B*1801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.367143	1.323538	-3.043605	23288.5709
HLA A*0203	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-3.360769	0.316807	-3.043963	2294.928359	
HLA A*0219	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.669158	0.625007	-3.044151	4668.29008
HLA A*3101	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.352562	1.308218	-3.044344	22519.665514	
HLA A*0206	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.213219	1.168653	-3.044566	16338.7444
HLA A*0212	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.036505	0.991777	-3.044728	10876.8844
HLA B*1509	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.378780	1.333568	-3.045212	23921.027964	
HLA B*1502	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.101576	1.056254	-3.045322	12635.0175
HLA B*5301	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.598595	1.553233	-3.045362	39682.1602
HLA A*0101	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.353901	1.308218	-3.045683	22589.215161	
HLA A*0203	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.003621	0.957621	-3.046000	10083.7279
HLA B*3901	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.090294	1.044178	-3.046116	12311.0082
HLA B*4402	1:133-141	9	TEAADAARA	1.018713	-0.271480	-3.793385	0.747233	-3.046151	6214.18967
HLA B*4402	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.405583	1.359245	-3.046337	25443.846313	
HLA A*1101	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.177413	1.130392	-3.047021	15045.704490	
HLA B*1501	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.355623	1.308218	-3.047406	22678.969376	
HLA B*1503	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.177958	1.130392	-3.047566	15064.600123	
HLA B*0702	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.396814	1.349023	-3.047791	24935.2935
HLA A*0216	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.200123	1.151985	-3.048137	15853.408475	
HLA B*4403	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.562103	1.513828	-3.048275	36484.055274	
HLA B*4403	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.594519	1.546204	-3.048315	39311.439732	
HLA A*0206	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.383171	1.334180	-3.048991	24164.1223
HLA A*6801	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.495975	1.446759	-3.049215	31331.0175
HLA A*3002	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-3.922089	0.872645	-3.049444	8357.74840
HLA A*0201	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.175011	1.125530	-3.049482	14962.747735	
HLA A*2601	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.384764	1.335227	-3.049537	24252.9168
HLA A*0201	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.384207	1.334180	-3.050027	24221.8410
HLA A*3201	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.603520	1.553233	-3.050287	40134.6820
HLA A*3301	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.183690	1.133400	-3.050290	15264.7730
HLA A*0101	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.324232	1.273350	-3.050882	21097.5412
HLA A*0301	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.130897	1.080003	-3.050894	13517.5325
HLA A*1101	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.405066	1.354114	-3.050952	25413.5816
HLA B*4002	1:17-25 9	FLAPPDVPW	1.263582	0.298114	-4.612676	1.561696	-3.050980	40989.797207	
HLA B*3901	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.386430	1.335227	-3.051203	24346.1202
HLA B*4601	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.386153	1.333568	-3.052584	24330.583406	
HLA B*5101	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.290634	1.238012	-3.052622	19526.940814	
HLA A*0301	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.361020	1.308218	-3.052802	22962.548237	
HLA A*0212	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.275889	1.222842	-3.053047	18875.081784	
HLA B*1517	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.402113	1.349023	-3.053089	25241.3497
HLA A*3002	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.080745	1.027504	-3.053241	12043.2947
HLA B*0802	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.402618	1.349023	-3.053595	25270.7256
HLA A*0212	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.387795	1.334180	-3.053615	24422.7639
HLA B*5701	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.291649	1.238012	-3.053637	19572.630052	
HLA A*2403	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.403001	1.349023	-3.053978	25293.0195
HLA B*4801	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.387910	1.333568	-3.054342	24429.238948	
HLA A*0216	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.180805	1.126312	-3.054493	15163.7000
HLA A*2501	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.362843	1.308218	-3.054625	23059.149340	
HLA B*7301	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.608038	1.553233	-3.054805	40554.3912
HLA B*1503	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.277677	1.222842	-3.054835	18952.949269	
HLA B*2705	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.328193	1.273350	-3.054843	21290.8537
HLA B*1503	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.363494	1.308218	-3.055276	23093.730286	
HLA A*2601	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.389625	1.333568	-3.056057	24525.906119	
HLA A*3001	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.818115	0.762047	-3.056068	6578.32285
HLA B*5401	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.559291	1.502929	-3.056362	36248.5610
HLA A*2902	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.083988	1.027504	-3.056483	12133.5422
HLA A*8001	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.390090	1.333568	-3.056522	24552.191316	
HLA B*5801	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.279392	1.222842	-3.056550	19027.946611	
HLA A*6801	1:86-94 9	SRSCTHELI	1.200502	0.345702	-4.602822	1.546204	-3.056618	40070.247930	
HLA B*3501	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.365073	1.308218	-3.056855	23177.839077	
HLA B*7301	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.571266	1.513828	-3.057438	37261.994425	
HLA A*2403	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.330841	1.273350	-3.057491	21421.0594
HLA B*5701	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.392769	1.335227	-3.057542	24704.0792
HLA B*4801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.392325	1.334180	-3.058145	24678.8330
HLA B*4001	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.332150	1.273350	-3.058800	21485.7050
HLA B*1509	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.418249	1.359245	-3.059003	26196.835760	
HLA A*3001	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.206866	1.147510	-3.059356	16101.4753
HLA B*4402	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.367704	1.308218	-3.059487	23318.701680	
HLA A*8001	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.393727	1.334180	-3.059547	24758.6672
HLA B*4402	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.383845	1.323538	-3.060308	24201.6696
HLA B*4002	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.574614	1.513828	-3.060786	37550.360662	
HLA A*0211	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.396284	1.335227	-3.061057	24904.8254
HLA B*4402	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.396946	1.335227	-3.061719	24942.8489
HLA A*0216	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.396627	1.334180	-3.062447	24924.5041
HLA A*6901	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.948164	0.885414	-3.062749	8874.90837
HLA B*3901	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.397538	1.334180	-3.063358	24976.8765
HLA A*0211	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.175904	1.112498	-3.063407	14993.5391
HLA A*6802	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.398779	1.335227	-3.063552	25048.3230
HLA A*0211	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.197299	1.133400	-3.063898	15750.6531
HLA B*4601	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.337946	1.273350	-3.064596	21774.3795
HLA A*6801	1:56-64 9	TNAGYLRHI	1.283670	0.230158	-4.578491	1.513828	-3.064663	37887.047540	
HLA A*6901	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.210099	1.145357	-3.064742	16221.7820
HLA B*5301	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.466702	1.401827	-3.064875	29288.8464
HLA B*2705	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.398544	1.333568	-3.0649		
HLA B*1801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.466817	1.401827		

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HLA A*3201	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.039084	0.973692	-3.065393	10941.6860
HLA A*8001	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.400689	1.335227	-3.065462	25158.7341
HLA B*0702	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.400766	1.335227	-3.065540	25163.2260
HLA B*4001	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.303613	1.238012	-3.065600	20119.295303
HLA A*3001	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.074651	1.008953	-3.065698	11875.4685
HLA B*4402	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.399620	1.333568	-3.066052	25096.882116
HLA A*0203	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.214191	1.147510	-3.066682	16375.3792
HLA B*4403	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.271554	1.204727	-3.066827	18687.6220
HLA B*1517	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.075990	1.008953	-3.067037	11912.1446
HLA B*3501	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.219327	1.151985	-3.067342	16570.184349
HLA B*1501	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.200950	1.133400	-3.067549	15883.6265
HLA A*0216	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.401170	1.333568	-3.067602	25186.651373
HLA B*1501	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.148246	1.080003	-3.068243	14068.4425
HLA A*2902	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.220253	1.151985	-3.068268	16605.541304
HLA A*3001	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-3.964643	0.896310	-3.068334	9218.137160
HLA A*8001	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.422572	1.354114	-3.068458	26458.9063
HLA A*8001	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.342123	1.273350	-3.068773	21984.8331
HLA A*2603	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.423493	1.354114	-3.069379	26515.0767
HLA A*2602	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.622997	1.553233	-3.069764	41975.6139
HLA A*3002	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.203243	1.133400	-3.069843	15967.7147
HLA B*1509	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.393741	1.323538	-3.070204	24759.4708
HLA B*4601	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.404737	1.334180	-3.070557	25394.3411
HLA B*1503	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.238079	1.167504	-3.070574	17301.2937
HLA B*4801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.394319	1.323538	-3.070782	24792.4435
HLA A*0202	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.570801	1.499754	-3.071047	37222.102309
HLA A*0219	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.404798	1.333568	-3.071230	25397.913262
HLA A*2501	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.405120	1.333568	-3.071552	25416.744025
HLA B*2705	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.395344	1.323538	-3.071806	24850.9907
HLA A*6901	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-3.856191	0.784286	-3.071905	7181.099399
HLA A*2501	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.426040	1.354114	-3.071926	26671.0264
HLA A*6901	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.266712	1.194587	-3.072125	18480.416448
HLA A*2603	1:155-163	9	ADQPNAILR	1.039644	0.513589	-4.625633	1.553233	-3.072400	42231.1764
HLA A*0201	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-3.978623	0.905427	-3.073196	9519.68551
HLA A*2603	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.475391	1.401827	-3.073564	29880.6927
HLA A*0250	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.382036	1.308218	-3.073818	24101.064499
HLA B*1503	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-2.961399	-0.112631	-3.074030	914.953395
HLA B*4001	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.119352	1.044178	-3.075174	13162.9143
HLA B*0801	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.298519	1.222842	-3.075677	19884.701759
HLA A*3002	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.228072	1.151985	-3.076087	16907.216865
HLA B*7301	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.579088	1.502929	-3.076159	37939.1443
HLA B*4001	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.110556	1.034236	-3.076319	12898.986329
HLA A*0201	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.092756	1.015721	-3.077035	12381.0045
HLA B*4601	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.385509	1.308218	-3.077291	24294.544665
HLA B*4402	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.411743	1.334180	-3.077563	25807.3322
HLA A*0216	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.078823	1.000751	-3.078072	11990.1174
HLA B*5301	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.316161	1.238012	-3.078149	20709.106640
HLA A*2902	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.432303	1.354114	-3.078189	27058.4837
HLA B*0802	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.413486	1.335227	-3.078260	25911.1346
HLA A*3301	1:86-94	9	SRSCTHELI	1.200502	0.345702	-4.625210	1.546204	-3.079006	42190.072548
HLA A*0211	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.231171	1.152145	-3.079027	17028.2922
HLA B*5401	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.964737	0.885414	-3.079323	9220.13214
HLA A*3002	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.317416	1.238012	-3.079404	20769.019279
HLA A*0250	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.579182	1.499754	-3.079427	37947.355116
HLA A*0203	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.213040	1.133400	-3.079640	16332.0280
HLA B*5701	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.414111	1.334180	-3.079931	25948.4484
HLA B*5101	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.060309	0.980281	-3.080028	11489.721348
HLA B*2705	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.155595	1.074983	-3.080612	14308.5363
HLA A*2403	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.415105	1.334180	-3.080925	26007.8963
HLA B*4501	1:17-25	9	FLAPPDVPW	1.263582	0.298114	-4.642719	1.561696	-3.081023	43925.694263
HLA B*1501	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.236020	1.154646	-3.081375	17219.4958
HLA B*1517	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.415213	1.333568	-3.081645	26014.369389
HLA B*2705	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.389987	1.308218	-3.081769	24546.347728
HLA A*0250	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.123064	1.041264	-3.081800	13275.9081
HLA A*0206	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.233899	1.151985	-3.081914	17135.581468
HLA B*1501	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.110072	1.027504	-3.082567	12884.6192
HLA B*1517	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.418169	1.335227	-3.082942	26192.0176
HLA A*2902	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.045137	0.962074	-3.083063	11095.235432
HLA A*2501	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.432275	1.349023	-3.083252	27056.7271
HLA A*0250	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.235454	1.152145	-3.083310	17197.0599
HLA A*2501	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.357057	1.273350	-3.083707	22753.9343
HLA B*4002	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.238802	1.154646	-3.084157	17330.1459
HLA A*2403	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.419670	1.335227	-3.084444	26282.7180
HLA B*1501	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.058190	0.973692	-3.084499	11433.7912
HLA A*3201	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.438950	1.354114	-3.084836	27475.7875
HLA A*3201	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.129887	1.044178	-3.085709	13486.1238
HLA A*0219	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-3.971255	0.885414	-3.085840	9359.54241
HLA B*5301	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.532984	1.446759	-3.086224	34118.0018
HLA B*0801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.152607	1.066259	-3.086347	14210.4118
HLA B*0702	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.309458	1.222842	-3.086617	20391.927752
HLA B*3801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.488590	1.401827	-3.086763	30802.7909
HLA B*0801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.291546	1.204727	-3.086819	19567.9716
HLA B*4403	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.538364	1.451496	-3.086868	34543.3066
HLA B*4501	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.078997	0.991777	-3.087221	11994.9184
HLA B*1502	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.436591	1.349023	-3.087568	27326.9565
HLA A*0202	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.436845	1.349023	-3.087822	27342.9275
HLA A*0206	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.293350	1.204727	-3.088623	19649.4416
HLA A*2602	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.588673	1.499754	-3.088919	38785.860482
HLA A*6901	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.223124	1.133400	-3.089724	16715.6822
HLA B*4801	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.398006	1.308218	-3.089788	25003.780316
HLA B*3801	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.444276	1.354114	-3.090162	27814.8314
HLA A*6901	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.238048	1.147510	-3.090538	17300.0770
HLA B*5101	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.439566	1.349023	-3.090543	27514.7590
HLA B*3501	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.216578	1.125530	-3.091049	16465.633432
HLA B*1501	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.091915	1.000751	-3.091163	12357.0489
HLA A*3201	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.399446	1.308218	-3.091228	25086.837047
HLA B*1502	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.594185	1.502929	-3.091257	39281.2521
HLA B*0802	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.414913	1.323538	-3.091375	25996.3619
HLA B*5401	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.425389	1.333568	-3.091821	26631.088769
HLA A*6801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.415472	1.323538	-3.091934	26029.8548
HLA A*3101	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.427635	1.335227	-3.092408	26769.1776
HLA A*0219	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.261543	1.168653	-3.092890	18261.7707
HLA A*0219	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.287679	1.194587	-3.093091	19394.498662
HLA A*0201	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.262140	1.168653	-3.093487	18286.8817
HLA B*1502	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.447704	1.354114	-3.093590	28035.2433
HLA B*1501	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.262382	1.168653	-3.093729	18297.0743
HLA A*0301	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.121279	1.027504	-3.093774	13221.4361
HLA B*4001	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.402263	1.308218	-3.094045	25250.090635
HLA B*1503	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.263018	1.168653	-3.094366	18323.9189
HLA A*3301	1:56-64	9	TNAGYLRHI	1.283670	0.230158	-4.608209	1.513828	-3.094381	40570.410191
HLA B*5301	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.597496	1.502929	-3.094567	39581.8188
HLA A*2301	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.453945	1.359245	-3.094699	28440.980393
HLA B*5101	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.215244	1.119963	-3.095281	16415.1152
HLA A*2602	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.368762	1.273350	-3.095412	23375.5390
HLA A*6802	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-3.881298	0.784286	-3.097011	7608.473545
HLA B*0801	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.223063	1.125530	-3.097533	16713.331269
HLA A*0216	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.210230	1.112498		
HLA A*0216	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.090825	0.991777		

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HLA B*7301	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.453207	1.354114	-3.099093	28392.7085
HLA A*2902	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.434376	1.335227	-3.099149	27187.9024
HLA A*0219	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.099931	1.000751	-3.099180	12587.2602
HLA A*3301	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.433022	1.333568	-3.099454	27103.314153
HLA B*0803	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.448649	1.349023	-3.099626	28096.2800
HLA B*5301	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.080332	0.980281	-3.100050	12031.833333
HLA A*6801	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.338418	1.238012	-3.100406	21798.069649
HLA A*0216	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.142048	1.041264	-3.100784	13869.0936
HLA A*2602	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.503152	1.401827	-3.101325	31853.1346
HLA A*0203	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.142955	1.041264	-3.101691	13898.0855
HLA A*0202	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.324573	1.222842	-3.101731	21114.097407
HLA A*0212	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.410491	1.308218	-3.102273	25733.024757
HLA B*0803	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.457027	1.354114	-3.102913	28643.5661
HLA B*1501	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.307675	1.204727	-3.102948	20308.3680
HLA A*2403	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.341376	1.238012	-3.103364	21947.044161
HLA A*3101	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.341482	1.238012	-3.103469	21952.387710
HLA B*1801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.376881	1.273350	-3.103531	23816.6927
HLA B*1509	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.376985	1.273350	-3.103635	23822.3626
HLA B*3501	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.289610	1.185494	-3.104115	19480.936668
HLA A*2602	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.212180	1.108038	-3.104142	16299.722352
HLA B*7301	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.604048	1.499754	-3.104294	40183.564719
HLA B*4601	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.290474	1.185494	-3.104980	19519.758712
HLA A*2602	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.137781	1.032480	-3.105301	13733.5057
HLA A*0206	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.137260	1.031880	-3.105380	13717.0218
HLA A*0206	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.678857	0.573275	-3.105581	4773.71524
HLA A*0203	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.171887	1.066259	-3.105627	14855.4748
HLA A*2902	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.414156	1.308218	-3.105938	25951.115730
HLA A*0219	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.440165	1.334180	-3.105985	27552.7424
HLA A*6901	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.218655	1.112498	-3.106158	16544.5663
HLA A*1101	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.414598	1.308218	-3.106380	25977.522976
HLA A*6802	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.292385	1.185494	-3.106890	19605.800370
HLA A*0250	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.442263	1.335227	-3.107036	27686.1726
HLA B*1517	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.187135	1.080003	-3.107131	15386.3177
HLA B*5401	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.554023	1.446759	-3.107264	35811.5588
HLA B*2705	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.441988	1.334180	-3.107808	27668.6540
HLA A*3001	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.227884	1.119963	-3.107921	16899.9011
HLA B*5401	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.509822	1.401827	-3.107995	32346.1327
HLA B*3501	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.275832	1.167504	-3.108328	18872.6312
HLA A*3002	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.109259	1.000751	-3.108507	12860.5240
HLA A*2301	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.432059	1.323538	-3.108521	27043.2641
HLA B*1801	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.346629	1.238012	-3.108617	22214.139048
HLA B*5101	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.443055	1.334180	-3.108875	27736.6943
HLA B*1502	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.608630	1.499754	-3.108876	40609.716394
HLA B*4402	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.221263	1.112050	-3.109213	16644.2149
HLA B*5301	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.443724	1.334180	-3.109544	27779.4922
HLA A*0219	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.417943	1.308218	-3.109726	26178.418380
HLA B*5101	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.445162	1.335227	-3.109935	27871.6184
HLA B*1801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.459012	1.349023	-3.109989	28774.8058
HLA B*1517	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.383702	1.273350	-3.110352	24193.6843
HLA B*7301	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-3.679472	0.568388	-3.111084	4780.486260
HLA B*4601	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.334008	1.222842	-3.111166	21577.844178
HLA A*8001	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.138768	1.027504	-3.111264	13764.7458
HLA A*3301	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.558114	1.446759	-3.111354	36150.4476
HLA B*4501	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.085393	0.973692	-3.111701	12172.8591
HLA A*0101	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.112680	1.000751	-3.111928	12962.2238
HLA B*0702	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.022549	0.910145	-3.112404	10532.9148
HLA B*0802	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.421933	1.308218	-3.113715	26420.001004
HLA B*4001	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.265873	1.151985	-3.113888	18444.759102
HLA A*3201	1:33-41	9	PALVEFAGR	1.046707	0.453047	-4.613799	1.499754	-3.114045	41095.930999
HLA A*2602	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.150901	1.036697	-3.114204	14154.7087
HLA A*2902	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.337126	1.222842	-3.114284	21733.307218
HLA B*5101	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.266688	1.152145	-3.114544	18479.4167
HLA A*2301	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.422781	1.308218	-3.114563	26471.648890
HLA B*3501	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.095420	0.980470	-3.114951	12457.1932
HLA B*3901	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.260819	1.145357	-3.115462	18231.3674
HLA A*0211	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.196143	1.080003	-3.116139	15708.7859
HLA A*1101	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.449725	1.333568	-3.116157	28165.981382
HLA B*1503	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.021863	0.905427	-3.116436	10516.2892
HLA B*4402	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.268629	1.151985	-3.116644	18562.178018
HLA A*3001	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.242195	1.125530	-3.116665	17466.057181
HLA B*3901	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.339614	1.222842	-3.116772	21858.176263
HLA B*0702	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.354869	1.238012	-3.116857	22639.619835
HLA A*1101	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.466014	1.349023	-3.116991	29242.4575
HLA B*1517	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.145850	1.027504	-3.118345	13991.0254
HLA B*5401	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-3.930519	0.811904	-3.118615	8521.56273
HLA A*8001	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.427151	1.308218	-3.118933	26739.361703
HLA B*5801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.245761	1.126312	-3.119449	17610.0827
HLA B*5701	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.223683	1.104113	-3.119571	16737.218482
HLA A*6901	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.305300	1.185494	-3.119805	20197.596664
HLA A*2902	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.240261	1.119963	-3.120298	17388.4652
HLA B*4501	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.623547	1.502929	-3.120618	42028.7851
HLA A*0301	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.359258	1.238012	-3.121246	22869.568363
HLA B*2705	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.359960	1.238012	-3.121948	22906.591125
HLA A*1101	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.395346	1.273350	-3.121996	24851.1252
HLA A*3001	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.149637	1.027504	-3.122133	14113.5711
HLA B*0702	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.247700	1.125530	-3.122170	17688.854962
HLA A*3001	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.211814	1.089590	-3.122224	16285.972123
HLA A*3001	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.234984	1.112498	-3.122487	17178.4631
HLA B*0803	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.327770	1.204727	-3.123043	21270.1312
HLA A*0101	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.004072	0.880566	-3.123506	10094.207388
HLA B*3801	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.482777	1.359245	-3.123532	30393.271030
HLA B*5101	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.397068	1.273350	-3.123718	24949.8667
HLA A*8001	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.346629	1.222842	-3.123788	22214.139048
HLA A*2402	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.458347	1.334180	-3.124168	28730.7853
HLA B*1501	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.249962	1.125530	-3.124433	17781.249467
HLA B*1517	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.156949	1.032480	-3.124469	14353.1926
HLA B*1509	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.458665	1.334180	-3.124485	28751.7761
HLA A*0203	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.329727	1.204727	-3.125000	21366.2000
HLA B*3901	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.191293	1.066259	-3.125034	15534.3571
HLA B*1502	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.250592	1.125530	-3.125062	17807.048314
HLA B*1502	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.460481	1.335227	-3.125254	28872.2633
HLA B*1502	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.484683	1.359245	-3.125437	30526.912034
HLA B*1503	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.459835	1.334180	-3.125655	28829.3414
HLA A*2501	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.460892	1.335227	-3.125665	28899.6105
HLA B*5701	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.399944	1.273350	-3.126594	25115.6259
HLA A*1101	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.252988	1.126312	-3.126676	17905.5807
HLA A*3101	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.349566	1.222842	-3.126725	22364.868153
HLA A*3001	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.278760	1.151985	-3.126775	19000.276137
HLA A*3001	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.272299	1.145357	-3.126942	18719.6976
HLA A*3101	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.185904	1.058921	-3.126983	15342.7626
HLA B*3801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.461799	1.334180	-3.127619	28960.0222
HLA A*2501	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.297013	1.168653	-3.128360	19815.8662
HLA A*3101	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.172558	1.044178	-3.128381	14878.4774
HLA B*0801	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.024804	0.896310	-3.128494	10587.759770
HLA B*4402	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.401997	1.273350	-3.128647	25234.6595
HLA B*1509	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.314235	1.185494	-3.1287	
HLA B*1509	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.437012	1.308218	-3.1287	

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HLA B*1501	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.233304	1.104113	-3.129192	17112.144008		
HLA A*3002	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.483494	1.354114	-3.129380	30443.4618	
HLA B*2705	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.464802	1.335227	-3.129575	29160.9409	
HLA A*0206	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.053524	0.923260	-3.130265	11311.6037	
HLA B*4801	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.368604	1.238012	-3.130592	23367.067829		
HLA B*4001	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.353563	1.222842	-3.130721	22571.624472		
HLA B*0803	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.466077	1.335227	-3.130851	29246.7291	
HLA A*2301	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.466329	1.335227	-3.131102	29263.6637	
HLA B*0803	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.404666	1.273350	-3.131316	25390.2200	
HLA B*3801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.466824	1.335227	-3.131598	29297.0869	
HLA A*0301	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.354505	1.222842	-3.131663	22620.643728		
HLA A*0250	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.168466	1.036697	-3.131769	14738.9209	
HLA A*1101	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.467081	1.335227	-3.131854	29314.3678	
HLA B*4501	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.405728	1.273350	-3.132378	25452.3819	
HLA A*6802	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.174335	1.041264	-3.133071	14939.4532	
HLA B*1501	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-3.969295	0.836190	-3.133105	9317.408707		
HLA B*1503	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.241812	1.108664	-3.133148	17450.6621	
HLA B*1501	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-3.946327	0.812136	-3.134190	8837.442087		
HLA A*2402	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.372206	1.238012	-3.134194	23561.665153		
HLA B*5701	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.357106	1.222842	-3.134264	22756.519503		
HLA B*3901	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.442559	1.308218	-3.134341	27705.051298		
HLA B*4403	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.637378	1.502929	-3.134450	43388.8615	
HLA A*0211	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.468098	1.333568	-3.134530	29383.116741		
HLA B*0702	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.442848	1.308218	-3.134630	27723.492827		
HLA A*0202	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.175970	1.041264	-3.134706	14995.8105	
HLA A*6802	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-3.302624	0.167651	-3.134974	2007.354509		
HLA B*5801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.280903	1.145357	-3.135546	19094.2516	
HLA B*3501	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.262050	1.126312	-3.135738	18283.1227	
HLA A*0201	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.303324	1.167504	-3.135819	20105.9120	
HLA B*5801	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.321424	1.185494	-3.135930	20961.589458		
HLA A*0211	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.470577	1.334180	-3.136397	29551.2983	
HLA A*1101	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.470750	1.334180	-3.136570	29563.1310	
HLA B*5301	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-3.840026	0.703256	-3.136770	6918.731570		
HLA A*0250	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.471683	1.334180	-3.137503	29626.6928	
HLA B*2705	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.332305	1.194587	-3.137718	21493.377966		
HLA B*5401	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.257791	1.119963	-3.137828	18104.6760	
HLA B*1509	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.196805	1.058921	-3.137885	15732.7693	
HLA B*3501	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-3.841154	0.703256	-3.137898	6936.721111		
HLA B*0702	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.343039	1.204727	-3.138313	22031.2669	
HLA B*3501	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.170909	1.032480	-3.138429	14822.0800	
HLA B*4501	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.493275	1.354114	-3.139161	31136.8691	
HLA A*0301	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.265974	1.126312	-3.139662	18449.0503	
HLA A*0206	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-3.985953	0.846009	-3.139944	9681.73062	
HLA B*4002	1:185-193	9	VTGNYRAWR	0.891790	0.611139	-4.643130	1.502929	-3.140201	43967.2997	
HLA B*3501	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.229945	1.089590	-3.140355	16980.272785		
HLA B*4001	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.067974	0.927121	-3.140852	11694.2807	
HLA A*6901	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.177643	1.036697	-3.140946	15053.6833	
HLA B*0803	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.464656	1.323538	-3.141118	29151.1616	
HLA B*5101	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.026778	0.885414	-3.141363	10635.9832	
HLA B*1801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.476671	1.335227	-3.141444	29968.9226	
HLA A*0202	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.158659	1.015721	-3.142938	14409.8326	
HLA A*2601	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.312205	1.168653	-3.143552	20521.2982	
HLA B*4002	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.644746	1.499754	-3.144992	44131.251131		
HLA A*8001	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.383122	1.238012	-3.145109	24161.377287		
HLA B*5701	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.220183	1.074983	-3.145199	16602.8464	
HLA B*4601	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.119502	0.973692	-3.145811	13167.4725	
HLA A*2301	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.495270	1.349023	-3.146246	31280.2096	
HLA A*6801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-3.958159	0.811904	-3.146254	9081.52091	
HLA B*3901	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.109160	0.962074	-3.147086	12857.602298		
HLA B*5401	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.420488	1.273350	-3.147138	26332.2455	
HLA B*0803	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.480834	1.333568	-3.147266	30257.595925		
HLA A*2301	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.501456	1.354114	-3.147342	31728.9608	
HLA A*3301	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.506676	1.359245	-3.147431	32112.669110		
HLA B*4501	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.647253	1.499754	-3.147499	44386.728879		
HLA A*0211	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.075045	0.927116	-3.147930	11886.266578		
HLA A*2603	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.204732	1.056254	-3.148479	16022.5759	
HLA A*2603	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.483832	1.335227	-3.148606	30467.1872	
HLA B*4501	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.189884	1.041264	-3.148620	15484.0153	
HLA B*0702	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.334191	1.185494	-3.148697	21586.951331		
HLA B*0801	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.279180	1.130392	-3.148789	19018.684349		
HLA A*3002	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.484352	1.335227	-3.149125	30503.6351	
HLA B*0801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.139196	0.990022	-3.149174	13778.3053	
HLA A*0216	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.182013	1.032480	-3.149533	15205.9241	
HLA B*1501	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.372568	1.222842	-3.149726	23581.303096		
HLA A*3001	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.186547	1.036697	-3.149851	15365.5222	
HLA B*5801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.355457	1.204727	-3.150730	22670.2600	
HLA A*2301	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.485305	1.334180	-3.151126	30570.7074	
HLA A*2403	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.306049	1.154646	-3.151404	20232.4828	
HLA B*4402	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.389879	1.238012	-3.151866	24540.240009		
HLA A*3001	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.218383	1.066259	-3.152123	16534.1870	
HLA A*3201	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.320132	1.167504	-3.152628	20899.3122	
HLA B*3501	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.209055	1.056254	-3.152802	16182.8642	
HLA A*3001	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.261167	1.108038	-3.153129	18245.970528		
HLA B*4403	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-3.647317	0.493735	-3.153582	4439.32583	
HLA A*3301	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.212753	1.058921	-3.153833	16321.2524	
HLA A*2601	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.306136	1.151985	-3.154151	20236.533113		
HLA B*4002	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.556084	1.401827	-3.154257	35981.8695	
HLA B*4403	1:33-41 9	PALVEFAGR	1.046707	0.453047	-4.654905	1.499754	-3.155151	45175.754342		
HLA B*5801	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.350231	1.194587	-3.155644	22399.134960		
HLA A*6801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.429501	1.273350	-3.156151	26884.4106	
HLA A*0101	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.289845	1.133400	-3.156445	19491.4784	
HLA B*4501	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.515698	1.359245	-3.156453	32786.754345		
HLA B*0802	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.430212	1.273350	-3.156862	26928.5156	
HLA A*8001	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.290362	1.133400	-3.156961	19514.6905	
HLA A*0203	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.309129	1.151985	-3.157144	20376.489069		
HLA A*2603	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.290568	1.133400	-3.157168	19523.9831	
HLA B*2705	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.342675	1.185494	-3.157181	22012.800758		
HLA A*3101	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.189541	1.031880	-3.157660	15471.7902	
HLA A*0301	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.352980	1.194587	-3.158393	22541.361501		
HLA A*6901	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.284185	1.125530	-3.158655	19239.105387		
HLA A*0101	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.120832	0.962074	-3.158758	13207.853096		
HLA A*6801	1:190-198	9	RAWRHFIAM	1.138328	0.313168	-4.610695	1.451496	-3.159199	40803.2873	
HLA B*1501	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.218176	1.058921	-3.159256	16526.3175	
HLA A*2601	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.382236	1.222842	-3.159394	24112.149695		
HLA B*1501	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.191918	1.032480	-3.159438	15556.7276	
HLA B*0702	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.249170	1.089590	-3.159581	17748.861424		
HLA B*4403	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.509815	1.349023	-3.160792	32345.6078	
HLA A*0250	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.141494	0.980470	-3.161024	13851.3977	
HLA B*5401	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.173320	1.012095	-3.161224	14904.5793	
HLA A*0203	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.316286	1.154646	-3.161640	20715.0452	
HLA A*3101	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.366734	1.204727	-3.162007	23266.6592	
HLA A*3002	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-3.998448	0.836190	-3.162257	9964.317472		
HLA B*3501	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.221315	1.058921	-3.162394	16646.1960	
HLA A*2603	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.495984	1.333568	-3.162416	31331.695567		
HLA A*0203	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.206659	1.044178	-3.162481	16093.8115	
HLA B*4001	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.357160	1.194587	-3.1625			
HLA A*2601	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.330192	1.167504			

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HLA A*0212	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-3.977025	0.814245	-3.162780	9484.7295
HLA B*3801	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.436309	1.273350	-3.162959	27309.2220
HLA B*0803	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.308429	1.145357	-3.163072	20343.6656
HLA A*0301	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.368421	1.204727	-3.163694	23357.2096
HLA A*3002	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.386867	1.222842	-3.164025	24370.630558	
HLA A*3201	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.402192	1.238012	-3.164180	25245.992962	
HLA B*2705	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.297826	1.133400	-3.164426	19852.9927
HLA A*0250	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.498237	1.333568	-3.164669	31494.669421	
HLA A*2403	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.223697	1.058921	-3.164777	16737.7617
HLA A*0202	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.123074	0.957621	-3.165453	13276.1954
HLA A*2902	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.291092	1.125530	-3.165563	19547.551208	
HLA B*1503	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.146103	0.980281	-3.165822	13999.202334	
HLA B*3501	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-3.260028	0.093967	-3.166061	1819.817826	
HLA A*2602	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.520238	1.354114	-3.166124	33131.2355
HLA A*3201	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.319488	1.152145	-3.167344	20868.3559
HLA A*0211	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.147847	0.980470	-3.167377	14055.5099
HLA B*0801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.082451	0.915034	-3.167417	12090.6887
HLA A*3201	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-3.956932	0.789295	-3.167638	9055.911217	
HLA B*4801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.323085	1.154646	-3.168440	21041.9166
HLA A*2902	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.148941	0.980470	-3.168472	14090.9887
HLA B*3801	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.502494	1.333568	-3.168926	31804.920989	
HLA A*3001	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.015322	0.846009	-3.169312	10359.0888
HLA A*3201	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.178785	1.008953	-3.169832	15093.3146
HLA A*0212	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.322049	1.151985	-3.170064	20991.775539	
HLA B*5401	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.529504	1.359245	-3.170259	33845.738964	
HLA A*3101	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.339064	1.168653	-3.170411	21830.5231
HLA A*2501	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.128073	0.957621	-3.170452	13429.9174
HLA A*0101	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.007112	0.836190	-3.170922	10165.118757	
HLA B*4403	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.322914	1.151985	-3.170929	21033.608416	
HLA B*0802	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.408980	1.238012	-3.170968	25643.666429	
HLA B*0801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.202876	1.031880	-3.170996	15954.2446
HLA A*2402	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.520031	1.349023	-3.171008	33115.4664
HLA B*1517	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.227546	1.056254	-3.171292	16886.7408
HLA B*3501	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.187398	1.015721	-3.171677	15395.6432
HLA B*0802	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.394524	1.222842	-3.171682	24804.115088	
HLA B*4403	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.618545	1.446759	-3.171785	41547.4891
HLA A*0202	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.305227	1.133400	-3.171827	20194.2096
HLA B*4501	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.081976	0.910145	-3.171832	12077.4833
HLA A*0203	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.317237	1.145357	-3.171881	20760.4818
HLA B*7301	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.618669	1.446759	-3.171910	41559.4035
HLA B*4403	1:133-141	9	TEAADAARA	1.018713	-0.271480	-3.919505	0.747233	-3.172271	8308.16016
HLA A*0212	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.376999	1.204727	-3.172272	23823.1359
HLA A*3101	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.319845	1.147510	-3.172335	20885.5230
HLA A*2501	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.306190	1.133400	-3.172790	20239.0512
HLA A*6901	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-3.619767	0.446772	-3.172995	4166.45759
HLA B*7301	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.506585	1.333568	-3.173017	32105.894511	
HLA A*6901	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.378098	1.204727	-3.173372	23883.5284
HLA B*0702	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.131001	0.957621	-3.173380	13520.7505
HLA A*6801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.299755	1.126312	-3.173442	19941.3662
HLA A*3201	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.522500	1.349023	-3.173477	33304.2904
HLA A*2501	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.325679	1.151985	-3.173694	21167.965948	
HLA A*0301	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.217913	1.044178	-3.173735	16516.3071
HLA A*2402	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.527885	1.354114	-3.173771	33719.8167
HLA B*0702	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.300450	1.126312	-3.174138	19973.3245
HLA B*4002	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.240421	1.066259	-3.174162	17394.8631
HLA B*4601	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.378921	1.204727	-3.174194	23928.7938
HLA B*1501	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.263895	1.089590	-3.174305	18360.931955	
HLA B*4601	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.307802	1.133400	-3.174402	20314.3016
HLA A*3001	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.283323	1.108664	-3.174659	19200.9453
HLA B*3501	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.189367	1.014245	-3.175122	15465.5976
HLA B*1801	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.327702	1.152145	-3.175557	21266.7945
HLA A*0219	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.301900	1.126312	-3.175587	20040.1049
HLA A*0212	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.191711	1.015721	-3.175991	15549.3232
HLA B*4501	1:238-246	9	GTEVATSPL	1.240590	0.206169	-4.622889	1.446759	-3.176130	41965.1694
HLA A*0201	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.328306	1.151985	-3.176321	21296.383185	
HLA A*2402	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.511577	1.335227	-3.176351	32477.1140
HLA B*5801	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.012610	0.836190	-3.176420	10294.618372	
HLA B*1509	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.381371	1.204727	-3.176644	24064.1940
HLA A*3101	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.251875	1.074983	-3.176891	17859.7245
HLA B*1801	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.485251	1.308218	-3.177034	30566.903831	
HLA B*3501	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.252082	1.074983	-3.177098	17868.2290
HLA A*3101	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.304101	1.126312	-3.177789	20141.9474
HLA A*2402	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.501667	1.323538	-3.178130	31744.4131
HLA A*6801	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.512724	1.334180	-3.178544	32562.9677
HLA A*6901	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.052053	0.873495	-3.178559	11273.3607
HLA A*3101	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.346195	1.167504	-3.178690	22191.9176
HLA A*0219	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.383594	1.204727	-3.178867	24187.6643
HLA B*1503	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.194865	1.015721	-3.179144	15662.6232
HLA A*0301	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.365143	1.185494	-3.179649	23181.601069	
HLA B*0801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.065234	0.885414	-3.179820	11620.7462
HLA A*0101	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.365792	1.185494	-3.180297	23216.240053	
HLA B*4601	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.375093	1.194587	-3.180506	23718.842802	
HLA B*1517	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.300497	1.119963	-3.180534	19975.4857
HLA A*0301	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.349395	1.168653	-3.180742	22356.0375
HLA B*4601	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.306413	1.125530	-3.180884	20249.455570	
HLA A*2403	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.314521	1.133400	-3.181121	20631.0543
HLA A*2301	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.419304	1.238012	-3.181291	26260.546274	
HLA A*0201	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.333855	1.152145	-3.181711	21570.2578
HLA B*1517	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.327096	1.145357	-3.181739	21237.1320
HLA A*0206	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.139572	0.957621	-3.181951	13790.2367
HLA A*6802	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.327866	1.145357	-3.182510	21274.8496
HLA B*3901	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.172864	0.990022	-3.182842	14888.9449
HLA B*5401	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.491085	1.308218	-3.182867	30980.271672	
HLA A*0212	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.335765	1.152145	-3.183621	21665.3379
HLA B*5701	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.335869	1.152145	-3.183724	21670.4956
HLA A*2403	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.288156	1.104113	-3.184043	19415.809546	
HLA B*0803	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.422074	1.238012	-3.184061	26428.578153	
HLA B*1801	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.218430	1.034236	-3.184193	16535.976135	
HLA B*4001	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.336343	1.152145	-3.184199	21694.1900
HLA A*1101	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.407096	1.222842	-3.184254	25532.646473	
HLA A*0202	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.264515	1.080003	-3.184512	18387.1739
HLA A*6802	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.216423	1.031880	-3.184543	16459.7553
HLA B*5401	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.508081	1.323538	-3.184544	32216.7254
HLA A*3001	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.296675	1.112050	-3.184625	19800.4352
HLA A*3201	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.200381	1.015721	-3.184660	15862.8454
HLA B*5301	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.508615	1.323538	-3.185077	32256.3133
HLA B*5801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.353758	1.168653	-3.185105	22581.7618
HLA A*0101	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.390083	1.204727	-3.185356	24551.7928
HLA A*0101	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.159430	0.973692	-3.185738	14435.4248
HLA B*7301	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.177643	0.991777	-3.185866	15053.6833
HLA B*1801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.354639	1.168653	-3.185986	22627.6201
HLA A*2601	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.319495	1.133400	-3.186095	20868.6946
HLA A*0206	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.371607	1.185494	-3.186112	23529.183734	
HLA A*2601	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.391091	1.204727	-3.186364	24608.8398
HLA B*2705	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.409295	1.222842	-3.186453	25662.262907	
HLA A*3002	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.520860	1.334180		
HLA B*5801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.354709	1.167504		

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HLA A*0201	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.392313	1.204727	-3.187586	24678.1654
HLA A*2403	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.164312	0.976308	-3.188004	14598.619839	
HLA B*4402	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.382849	1.194587	-3.188262	24146.219641	
HLA A*0212	1:130-138	9	HILTEAADA	0.912003	-0.149956	-3.950405	0.762047	-3.188358	8920.83048
HLA A*3101	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.189339	1.000751	-3.188587	15464.5936
HLA A*0216	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.116354	0.927116	-3.189238	13072.363372	
HLA A*0250	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.538446	1.349023	-3.189423	34549.8479
HLA B*0803	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.344127	1.154646	-3.189482	22086.5199
HLA B*4001	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.357101	1.167504	-3.189597	22756.2732
HLA A*0216	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.394571	1.204727	-3.189844	24806.7989
HLA B*0801	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.294433	1.104113	-3.190321	19698.507728	
HLA A*3001	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.153218	0.962074	-3.191144	14230.413872	
HLA A*3001	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.232536	1.041264	-3.191272	17081.8988
HLA B*1501	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.247603	1.056254	-3.191350	17684.9319
HLA B*3901	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.249368	1.057871	-3.191497	17756.9288
HLA A*0206	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.118657	0.927116	-3.191541	13141.853052	
HLA B*1517	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.102088	0.910145	-3.191943	12649.9275
HLA B*1501	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.267005	1.074983	-3.192022	18492.9178
HLA A*0202	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.107107	0.915034	-3.192072	12796.9519
HLA B*4501	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.344181	1.151985	-3.192196	22089.267912	
HLA B*4801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.397343	1.204727	-3.192616	24965.6639
HLA A*0206	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-3.976226	0.783495	-3.192731	9467.29973
HLA A*2402	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.415723	1.222842	-3.192881	26044.926785	
HLA A*0212	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.305412	1.112498	-3.192915	20202.8421
HLA A*1101	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.431009	1.238012	-3.192997	26977.946579	
HLA A*2602	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.528454	1.335227	-3.193227	33763.9913
HLA A*3001	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.249565	1.056254	-3.193312	17765.0000
HLA B*1503	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-3.524876	0.331331	-3.193545	3348.697833	
HLA A*6801	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.501787	1.308218	-3.193569	31753.172744	
HLA B*5801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.313859	1.119963	-3.193896	20599.6038
HLA A*3301	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.596095	1.401827	-3.194268	39454.4009
HLA B*0801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-3.322975	0.128565	-3.194411	2103.65887
HLA B*4601	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.362223	1.167504	-3.194719	23026.2395
HLA B*3501	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.298864	1.104113	-3.194752	19900.521431	
HLA B*5801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.328219	1.133400	-3.194819	21292.1208
HLA B*0801	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.346857	1.151985	-3.194872	22225.799182	
HLA B*1501	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.343115	1.147510	-3.195605	22035.0812
HLA A*0101	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.363341	1.167504	-3.195837	23085.6109
HLA B*5301	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-3.864917	0.668648	-3.196269	7326.843674	
HLA B*3801	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.519904	1.323538	-3.196366	33105.7937
HLA A*0212	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.382452	1.185494	-3.196958	24124.153535	
HLA A*0201	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.382469	1.185494	-3.196974	24125.067115	
HLA B*4402	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.420220	1.222842	-3.197378	26316.010756	
HLA B*5401	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-3.324559	0.127125	-3.197434	2111.343375	
HLA A*0203	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.306359	1.108664	-3.197695	20246.9361
HLA A*8001	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.305737	1.108038	-3.197699	20217.930510	
HLA B*4801	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.420627	1.222842	-3.197785	26340.651724	
HLA A*3101	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.349884	1.151985	-3.197898	22381.207966	
HLA B*0802	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.403135	1.204727	-3.198408	25300.8201
HLA A*3101	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.318384	1.119963	-3.198421	20815.3624
HLA B*1517	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.156131	0.957621	-3.198510	14326.1961
HLA B*3501	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.239857	1.041264	-3.198593	17372.2927
HLA A*0211	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.384151	1.185494	-3.198656	24218.696314	
HLA B*4801	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.393267	1.194587	-3.198680	24732.428560	
HLA A*3101	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.824059	0.625007	-3.199052	6668.97948
HLA A*0301	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.366750	1.167504	-3.199246	23267.5403
HLA A*2403	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.179734	0.980470	-3.199264	15126.3386
HLA A*3101	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.384980	1.185494	-3.199486	24264.990727	
HLA A*2902	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.312139	1.112498	-3.199641	20518.1899
HLA B*5701	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.404544	1.204727	-3.199817	25383.0784
HLA A*3002	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.312452	1.112498	-3.199954	20532.9584
HLA B*3501	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.012131	0.812136	-3.199995	10283.263319	
HLA B*5801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.354954	1.154646	-3.200308	22644.0294
HLA A*3201	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.352325	1.151985	-3.200339	22507.364156	
HLA A*2601	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.352571	1.152145	-3.200427	22520.1528
HLA B*5701	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.326849	1.126312	-3.200537	21225.0719
HLA B*5301	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.549634	1.349023	-3.200611	35451.4814
HLA B*0803	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.352853	1.151985	-3.200868	22534.777365	
HLA A*2402	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.474293	1.273350	-3.200943	29805.2969
HLA A*2403	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.423829	1.222842	-3.200987	26535.597081	
HLA B*1501	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.396027	1.194587	-3.201440	24890.143941	
HLA A*0101	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.370559	1.168653	-3.201906	23472.4807
HLA B*5801	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.306183	1.104113	-3.202070	20238.722779	
HLA B*3901	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.082775	0.880566	-3.202209	12099.718645	
HLA B*4001	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.371118	1.168653	-3.202465	23502.7222
HLA A*2601	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.397139	1.194587	-3.202552	24953.916330	
HLA B*1502	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.536980	1.334180	-3.202800	34433.4122
HLA A*0201	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.088381	0.885414	-3.202967	12256.9141
HLA A*0203	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.776435	0.573275	-3.203160	5976.34032
HLA A*3101	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.357806	1.154646	-3.203160	22793.2359
HLA A*0202	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.240722	1.036697	-3.204025	17406.9126
HLA A*0250	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.334485	1.130392	-3.204093	21601.554145	
HLA A*0202	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.114395	0.910145	-3.204250	13013.5157
HLA A*6801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-3.362075	0.157520	-3.204555	2301.84166
HLA B*5801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.205644	1.000751	-3.204893	16056.2432
HLA A*0202	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.539320	1.334180	-3.205140	34619.4488
HLA B*1501	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.357620	1.151985	-3.205635	22783.496625	
HLA A*2403	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.410533	1.204727	-3.205806	25735.5307
HLA A*2403	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.391340	1.185494	-3.205846	24622.955804	
HLA A*6802	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.410785	1.204727	-3.206058	25750.4322
HLA B*4001	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.360891	1.154646	-3.206245	22955.7168
HLA A*0212	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.332730	1.126312	-3.206417	21514.4343
HLA A*6901	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.247878	1.041264	-3.206614	17696.1292
HLA A*2602	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.332941	1.126312	-3.206629	21524.9120
HLA B*0702	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.222358	1.015721	-3.206637	16686.2280
HLA B*5401	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.374323	1.167504	-3.206818	23676.7923
HLA A*2603	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.515092	1.308218	-3.206874	32741.024108	
HLA B*5701	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.401650	1.194587	-3.207063	25214.463144	
HLA B*3501	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.354620	1.147510	-3.207110	22626.6409
HLA B*4601	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.375838	1.168653	-3.207186	23759.5539
HLA A*6802	1:133-141	9	TEAADAARA	1.018713	-0.271480	-3.954522	0.747233	-3.207288	9005.78520
HLA A*8001	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.311465	1.104113	-3.207352	20486.357349	
HLA B*1509	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.316152	1.108664	-3.207488	20708.6585
HLA B*0801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.208510	1.000751	-3.207759	16162.5659
HLA A*0301	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.362622	1.154646	-3.207977	23047.4260
HLA A*2902	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.316053	1.108038	-3.208015	20703.953718	
HLA A*2602	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.542358	1.334180	-3.208178	34862.4603
HLA B*4501	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.610131	1.401827	-3.208304	40750.3438
HLA B*5801	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.360952	1.152145	-3.208807	22958.9459
HLA B*4501	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.782220	0.573275	-3.208945	6056.47253
HLA A*0201	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.284291	1.074983	-3.209307	19243.7896
HLA A*0301	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.361499	1.152145	-3.209355	22987.9040
HLA A*3101	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.361523	1.152145	-3.209378	22989.1477
HLA B*1503	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.289389	1.080003	-3.209386	19471.0325
HLA B*4001	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.394942	1.185494	-3.209447	24828.011970	
HLA B*5401	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.558567	1.349023		
HLA B*4402	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.364408	1.154646		

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HLA B*7301	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.052551	0.842742	-3.209810	11286.297575	
HLA B*7301	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.612164	1.401827	-3.210337	40941.4841	
HLA B*4402	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.336654	1.126312	-3.210341	21709.6875	
HLA B*1509	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.343749	1.133400	-3.210349	22067.2907	
HLA B*3901	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.362655	1.152145	-3.210511	23049.1717	
HLA A*0219	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.396025	1.185494	-3.210531	24890.009288	
HLA B*1501	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.120776	0.910145	-3.210631	13206.1383	
HLA B*3501	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.344139	1.133400	-3.210739	22087.1170	
HLA A*2601	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.396241	1.185494	-3.210747	24902.400373	
HLA A*0101	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.405456	1.194587	-3.210869	25436.414385	
HLA B*0801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.286043	1.074983	-3.211060	19321.6101	
HLA A*0301	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.363637	1.151985	-3.211652	23101.352549	
HLA A*3001	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.094988	0.883157	-3.211831	12444.7992	
HLA A*0202	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.364100	1.152145	-3.211956	23125.9858	
HLA B*4801	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.397703	1.185494	-3.212208	24986.336873	
HLA B*4002	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.535838	1.323538	-3.212300	34342.9986	
HLA B*4403	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.139435	0.927121	-3.212314	13785.9104	
HLA B*1501	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.357905	1.145357	-3.212548	22798.4155	
HLA A*0201	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.345953	1.133400	-3.212553	22179.5553	
HLA B*5401	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-3.996070	0.783495	-3.212575	9909.91380	
HLA A*3001	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.270462	1.057871	-3.212591	18640.6705	
HLA B*3501	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.320656	1.108038	-3.212618	20924.540479	
HLA B*5401	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.123111	0.910145	-3.212967	13277.3446	
HLA B*5801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.360769	1.147510	-3.213259	22949.2600	
HLA B*1517	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.175425	0.962074	-3.213351	14977.001158	
HLA B*5801	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.338914	1.125530	-3.213384	21822.966060	
HLA B*4001	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-3.869639	0.655774	-3.213865	7406.94961	
HLA B*1503	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.028117	0.814245	-3.213872	10668.8314	
HLA A*0250	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.124164	0.910145	-3.214019	13309.5631	
HLA A*3301	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.294151	1.080003	-3.214148	19685.7238	
HLA A*8001	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.419184	1.204727	-3.214457	26253.3018	
HLA A*0211	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.419250	1.204727	-3.214523	26257.2789	
HLA A*2403	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.230375	1.015721	-3.214654	16997.0917	
HLA B*1501	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.095293	0.880633	-3.214661	12453.554563	
HLA A*0201	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.327180	1.112498	-3.214683	21241.2685	
HLA A*0216	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.366891	1.152145	-3.214747	23275.0940	
HLA A*0219	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.367178	1.152145	-3.215034	23290.4608	
HLA B*3901	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.382605	1.167504	-3.215100	24132.6381	
HLA A*2603	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.574560	1.359245	-3.215315	37545.688657	
HLA B*5401	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.549773	1.334180	-3.215593	35462.7987	
HLA A*0211	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.361154	1.145357	-3.215797	22969.6301	
HLA B*1501	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.383317	1.167504	-3.215812	24172.2286	
HLA A*1101	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.291424	1.074983	-3.216440	19562.4676	
HLA B*1502	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.454595	1.238012	-3.216583	28483.632270	
HLA B*3901	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.371330	1.154646	-3.216684	23514.1682	
HLA B*5101	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.384202	1.167504	-3.216698	24221.5789	
HLA A*0101	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.369180	1.151985	-3.217195	23398.059608	
HLA A*2301	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.490566	1.273350	-3.217216	30943.2542	
HLA A*0301	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.364789	1.147510	-3.217279	23162.6719	
HLA A*0219	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.329793	1.112498	-3.217295	21369.4368	
HLA B*4001	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.337509	1.119963	-3.217546	21752.4803	
HLA A*0203	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.144910	0.927116	-3.217794	13960.782212	
HLA A*0101	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.370016	1.152145	-3.217872	23443.1658	
HLA B*4801	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.370331	1.152145	-3.218187	23460.1665	
HLA B*5401	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.370369	1.152145	-3.218224	23462.1972	
HLA A*0206	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.307823	1.089590	-3.218233	20315.290747	
HLA A*3001	1:46-54	9	SWSKPNPKT	1.176779	-0.200471	-4.194832	0.976308	-3.218524	15661.437060	
HLA A*6801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.251057	1.032480	-3.218577	17826.1326	
HLA A*6802	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.413313	1.194587	-3.218725	25900.763677	
HLA A*2602	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.552510	1.333568	-3.218942	35687.009606	
HLA B*0802	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.371466	1.152145	-3.219321	23521.5475	
HLA A*8001	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.414083	1.194587	-3.219496	25946.763922	
HLA A*6901	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.199916	0.980281	-3.219634	15845.862936	
HLA B*4002	1:77-85	9	SVSFYITGI	0.979963	0.379282	-4.578947	1.359245	-3.219701	37926.831570	
HLA A*2603	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.457730	1.238012	-3.219717	28689.936254	
HLA B*1501	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.350377	1.130392	-3.219985	22406.649184	
HLA A*6802	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.294988	1.074983	-3.220004	19723.6735	
HLA A*0301	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.365869	1.145357	-3.220513	23220.3851	
HLA B*1502	1:57-65	9	NAGYLRHII	1.129740	0.203828	-4.554134	1.333568	-3.220565	35820.665640	
HLA A*0216	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.354019	1.133400	-3.220618	22595.3262	
HLA A*2501	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.425774	1.204727	-3.221047	26654.7269	
HLA A*0202	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.296045	1.074983	-3.221062	19771.7483	
HLA A*0101	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.375888	1.154646	-3.221242	23762.2533	
HLA A*3002	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-3.281554	0.060047	-3.221507	1912.290627	
HLA A*3301	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.545067	1.323538	-3.221529	35080.5981	
HLA B*0802	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.416144	1.194587	-3.221557	26070.160131	
HLA B*4402	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.407509	1.185494	-3.222015	25556.968717	
HLA A*1101	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.195753	0.973692	-3.222061	15694.6851	
HLA A*2902	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.348511	1.126312	-3.222199	22310.6089	
HLA B*5701	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.367768	1.145357	-3.222411	23322.1080	
HLA B*1503	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.342471	1.119963	-3.222508	22002.4426	
HLA B*4403	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.624639	1.401827	-3.222812	42134.6457	
HLA A*0212	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.312726	1.089590	-3.223137	20545.959013	
HLA A*3002	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.215117	0.991777	-3.223340	16410.3204	
HLA B*5801	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.354056	1.130392	-3.223665	22597.282141	
HLA B*0801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.332716	1.108664	-3.224052	21513.7360	
HLA A*1101	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.429031	1.204727	-3.224304	26855.3380	
HLA B*7301	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.497715	1.273350	-3.224365	31456.8671	
HLA A*2501	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.409927	1.185494	-3.224432	25699.635363	
HLA A*8001	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.392031	1.167504	-3.224526	24662.1499	
HLA A*2902	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.393591	1.168653	-3.224938	24750.8998	
HLA B*4402	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.377333	1.152145	-3.225188	23841.4440	
HLA A*3101	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.370585	1.145357	-3.225228	23473.8775	
HLA B*4801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.370676	1.145357	-3.225320	23478.8307	
HLA B*3801	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.378051	1.152145	-3.225907	23880.9444	
HLA B*4002	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.574936	1.349023	-3.225913	37578.2016	
HLA B*2705	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.351852	1.125530	-3.226323	22482.903227	
HLA A*0101	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.346597	1.119963	-3.226634	22212.4566	
HLA B*3801	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.534950	1.308218	-3.226732	34272.841054	
HLA B*5401	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.562122	1.335227	-3.226895	36485.6343	
HLA A*0211	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.137232	0.910145	-3.227087	13716.1313	
HLA A*0206	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.107769	0.880566	-3.227203	12816.489712	
HLA A*3301	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.465577	1.238012	-3.227565	29213.047388	
HLA A*6802	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.160203	-0.067515	-3.227718	1446.11555	
HLA A*2501	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.450921	1.222842	-3.228079	28243.647057	
HLA A*0101	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.373895	1.145357	-3.228538	23653.4916	
HLA B*4801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.362380	1.133400	-3.228980	23034.5871	
HLA A*0219	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.265831	1.036697	-3.229134	18442.9630	
HLA B*1501	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-3.982006	0.752698	-3.229308	9594.13577	
HLA A*3001	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-3.528269	0.298936	-3.229333	3374.959903	
HLA B*5101	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.355710	1.126312	-3.229398	22683.5093	
HLA A*0101	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.376954	1.147510	-3.229444	23820.6873	
HLA B*5801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.203196	0.973692	-3.229504	15965.9871	
HLA B*0803	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.452361	1.222842	-3.229519	28337.465869	
HLA B*1501	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.103065	0.873495	-3.229571	12678.4284	
HLA A*2602	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.537901	1.308218	-3.2296		
HLA B*7301	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.553347	1.323538			

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HLA B*0802	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.415312	1.185494	-3.229817	26020.280925	
HLA B*1503	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-3.921991	0.692096	-3.229895	8355.849615	
HLA A*0301	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.305138	1.074983	-3.230154	20190.0586
HLA A*8001	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.382236	1.151985	-3.230251	24112.149695	
HLA A*0301	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.338348	1.108038	-3.230309	21794.532182	
HLA A*2403	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.286645	1.056254	-3.230391	19348.3878
HLA A*2403	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.397935	1.167504	-3.230431	24999.7226
HLA A*0219	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.375862	1.145357	-3.230505	23760.8393
HLA A*3201	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.066714	0.836190	-3.230524	11660.419963	
HLA B*5701	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.231415	1.000751	-3.230664	17037.8755
HLA B*0803	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.425318	1.194587	-3.230731	26626.766983	
HLA A*0216	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.416240	1.185494	-3.230746	26075.943276	
HLA A*0203	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.361217	1.130392	-3.230826	22972.985495	
HLA B*4801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.306317	1.074983	-3.231334	20244.9646
HLA B*4002	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.585513	1.354114	-3.231399	38504.6671
HLA B*0802	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.383538	1.151985	-3.231552	24184.524104	
HLA A*0201	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.379264	1.147510	-3.231754	23947.7013
HLA A*3301	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.540229	1.308218	-3.232012	34692.004947	
HLA A*0206	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.344769	1.112050	-3.232719	22119.1632
HLA B*4501	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.566346	1.333568	-3.232778	36842.261004	
HLA A*6901	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.299327	1.066259	-3.233068	19921.7416
HLA B*0803	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.385290	1.152145	-3.233146	24282.3246
HLA B*1509	1:90-98 9	THELIRHRH	1.009752	-0.303509	-3.939551	0.706243	-3.233308	8700.629312	
HLA A*6901	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.388030	1.154646	-3.233384	24435.9800
HLA A*0301	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.358967	1.125530	-3.233437	22854.232001	
HLA A*2301	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.353441	1.119963	-3.233478	22565.2756
HLA B*5401	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.419048	1.185494	-3.233553	26245.065574	
HLA A*3301	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.381075	1.147510	-3.233565	24047.7963
HLA A*6801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.381230	1.147510	-3.233720	24056.3842
HLA A*2902	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.419252	1.185494	-3.233758	26257.420994	
HLA B*1801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.401276	1.167504	-3.233772	25192.7836
HLA B*1517	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.246137	1.012095	-3.234042	17625.3322
HLA B*0803	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.419691	1.185494	-3.234197	26283.997735	
HLA B*5401	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.107877	0.873495	-3.234383	12819.6795
HLA A*0201	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.261940	1.027504	-3.234436	18278.4746
HLA A*3201	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.569769	1.335227	-3.234543	37133.8068
HLA B*2705	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.235339	1.000751	-3.234588	17192.5018
HLA A*2601	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.343368	1.108664	-3.234704	22047.9594
HLA B*4402	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.382356	1.147510	-3.234846	24118.8032
HLA A*2301	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.457746	1.222842	-3.234904	28691.022740	
HLA B*4501	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.584014	1.349023	-3.234991	38371.9970
HLA B*4801	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.387172	1.151985	-3.235187	24387.776100	
HLA A*3001	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.215568	0.980281	-3.235287	16427.374731	
HLA B*3501	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.404110	1.168653	-3.235457	25357.6869
HLA A*0101	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.366006	1.130392	-3.235614	23227.672220	
HLA B*3901	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.430367	1.194587	-3.235780	26938.132265	
HLA B*1509	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.390835	1.154646	-3.236189	24594.3328
HLA B*1501	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.348688	1.112498	-3.236190	22319.6630
HLA A*2402	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.340563	1.104113	-3.236450	21906.001633	
HLA B*7301	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.388443	1.151985	-3.236458	24459.257577	
HLA B*4601	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.388516	1.151985	-3.236531	24463.359899	
HLA A*0212	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.277907	1.041264	-3.236643	18963.0002
HLA A*0202	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.303432	1.066259	-3.237172	20110.9161
HLA B*1501	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.133501	0.896310	-3.237191	13598.802079	
HLA B*2705	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.389355	1.152145	-3.237210	24510.6523
HLA A*3001	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.271542	1.034236	-3.237306	18687.116573	
HLA A*2601	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.382734	1.145357	-3.237377	24139.8196
HLA B*7301	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.572685	1.335227	-3.237458	37383.9498
HLA B*3901	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.442279	1.204727	-3.237552	27687.2211
HLA B*3501	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.350069	1.112498	-3.237572	22390.7753
HLA A*6901	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.327333	1.089590	-3.237743	21248.739175	
HLA B*4001	1:133-141	9	TEAADAARA	1.018713	-0.271480	-3.985093	0.747233	-3.237860	9662.57957
HLA B*5101	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.442644	1.204727	-3.237917	27710.4475
HLA A*3301	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.389930	1.151985	-3.237945	24543.160902	
HLA A*2902	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.252201	1.014245	-3.237956	17873.1596
HLA B*4001	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.371518	1.133400	-3.238117	23524.3472
HLA A*0101	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.363748	1.125530	-3.238218	23107.227156	
HLA B*1501	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.358431	1.119963	-3.238468	22826.0597
HLA A*6901	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.347482	1.108664	-3.238818	22257.8058
HLA A*3201	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.462238	1.222842	-3.239397	28989.334467	
HLA B*5701	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.391394	1.151985	-3.239409	24626.019767	
HLA B*2705	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.391448	1.151985	-3.239463	24629.084110	
HLA A*0201	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.281131	1.041264	-3.239867	19104.2742
HLA B*5101	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.434528	1.194587	-3.239941	27197.464521	
HLA A*2601	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.366525	1.126312	-3.240212	23255.4594
HLA B*3501	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-3.896118	0.655774	-3.240344	7872.59819
HLA A*2403	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.392823	1.152145	-3.240678	24707.1533
HLA B*5801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.352769	1.112050	-3.240719	22530.3890
HLA A*0101	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.315771	1.074983	-3.240788	20690.5173
HLA A*0211	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.272670	1.031880	-3.240790	18735.7053
HLA A*0101	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.353481	1.112498	-3.240983	22567.3510
HLA B*5701	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.388650	1.147510	-3.241140	24470.9046
HLA A*2602	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-3.688038	0.446772	-3.241266	4875.71482
HLA A*0101	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.367613	1.126312	-3.241300	23313.7822
HLA B*4501	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.565012	1.323538	-3.241474	36729.2252
HLA B*0803	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.321509	1.080003	-3.241505	20965.6722
HLA A*2601	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.389019	1.147510	-3.241509	24491.6979
HLA A*6802	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.814798	0.573275	-3.241522	6528.26404
HLA A*0211	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.127082	0.885414	-3.241667	13399.2922
HLA B*5801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.354359	1.112498	-3.241862	22613.0577
HLA A*0203	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.122637	0.880566	-3.242071	13262.843173	
HLA B*4601	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.387459	1.145357	-3.242102	24403.8775
HLA A*2501	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.301334	1.058921	-3.242413	20013.9939
HLA B*4001	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.368750	1.126312	-3.242437	23374.9067
HLA A*0201	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.387861	1.145357	-3.242504	24426.4637
HLA A*2501	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.279340	1.036697	-3.242644	19025.6820
HLA B*4001	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.354940	1.112050	-3.242890	22643.2944
HLA A*2301	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.376388	1.133400	-3.242988	23789.6505
HLA B*4001	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.390689	1.147510	-3.243180	24586.0849
HLA A*6901	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.347294	1.104113	-3.243182	22248.174913	
HLA B*0801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.376790	1.133400	-3.243390	23811.6683
HLA B*0802	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.376853	1.133400	-3.243453	23815.1466
HLA A*0201	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.398168	1.154646	-3.243522	25013.1155
HLA B*0702	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.373973	1.130392	-3.243581	23657.714827	
HLA B*4601	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.363621	1.119963	-3.243658	23100.4777
HLA B*7301	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.603320	1.359245	-3.244075	40116.230721	
HLA A*6801	1:153-161	9	KFADQPNAI	0.977018	0.424809	-4.645923	1.401827	-3.244096	44251.0247
HLA B*5701	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.398847	1.154646	-3.244201	25052.2530
HLA A*6802	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.356401	1.112050	-3.244351	22719.6163
HLA B*7301	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.088527	0.843953	-3.244574	12261.0259
HLA A*3001	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.258991	1.014245	-3.244746	18154.7948
HLA B*1517	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.392273	1.147510	-3.244763	24675.8959
HLA B*5801	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.352957	1.108038	-3.244918	22540.142072	
HLA A*2403	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-3.255404	0.010485	-3.244919	1800.545615	
HLA B*7301	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.449833	1.204727	-3.245106	28172.9914
HLA B*0702	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.439904	1.194587	-3.2453		
HLA A*0101	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.301876	1.056254		

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HLA A*2601	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.400548	1.154646	-3.245902	25150.5691
HLA A*8001	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.431577	1.185494	-3.246083	27013.289052	
HLA B*4601	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.400785	1.154646	-3.246140	25164.3151
HLA B*0702	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.413700	1.167504	-3.246196	25923.8938
HLA A*0206	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.393763	1.147510	-3.246253	24760.6764
HLA B*2705	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.391702	1.145357	-3.246345	24643.4783
HLA B*4001	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.372121	1.125530	-3.246592	23557.076824	
HLA A*3002	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.441246	1.194587	-3.246658	27621.394234	
HLA B*0702	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.303089	1.056254	-3.246835	20095.0379
HLA B*1517	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-3.758109	0.511259	-3.246850	5729.402553	
HLA A*0301	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.366823	1.119963	-3.246860	23271.4427
HLA B*5701	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.414478	1.167504	-3.246973	25970.3566
HLA B*1503	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.259146	1.012095	-3.247051	18161.2782
HLA B*0702	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.415784	1.168653	-3.247131	26048.5904
HLA B*0702	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.322181	1.074983	-3.247197	20998.1360
HLA B*5801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.184898	0.937566	-3.247332	15307.2786
HLA B*2705	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.452180	1.204727	-3.247453	28325.6640
HLA A*3002	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.555694	1.308218	-3.247476	35949.570817	
HLA A*3201	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.280092	1.032480	-3.247612	19058.6471
HLA A*0101	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.314141	1.066259	-3.247881	20612.9812
HLA A*6802	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-3.951298	0.703401	-3.247897	8939.188413	
HLA B*4402	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.381811	1.133400	-3.248410	24088.5508
HLA B*5401	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-3.868126	0.619672	-3.248454	7381.188934	
HLA B*0801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.374790	1.126312	-3.248478	23702.2957
HLA A*6802	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.264426	1.015721	-3.248705	18383.3944
HLA B*5801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.357651	1.108664	-3.248987	22785.0990
HLA A*2601	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.369067	1.119963	-3.249104	23391.9845
HLA A*3101	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.241086	0.991777	-3.249309	17421.5150
HLA B*1801	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.434923	1.185494	-3.249429	27222.194482	
HLA B*1503	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.035123	0.785066	-3.250057	10842.339874	
HLA B*0801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.309160	1.058921	-3.250239	20377.9221
HLA B*4402	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.395924	1.145357	-3.250567	24884.2199
HLA B*4801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.131302	0.880633	-3.250669	13530.116467	
HLA B*4601	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.377236	1.126312	-3.250924	23836.1564
HLA A*2902	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.355325	1.104113	-3.251212	22663.393007	
HLA A*6901	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.326215	1.074983	-3.251231	21194.0917
HLA B*4801	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.381717	1.130392	-3.251325	24083.338784	
HLA A*0201	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.283513	1.031880	-3.251633	19209.3611
HLA A*0101	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.341235	1.089590	-3.251645	21939.921453	
HLA B*4601	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.307915	1.056254	-3.251661	20319.5774
HLA A*0211	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.035522	0.783495	-3.252027	10852.3159
HLA A*0301	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.311079	1.058921	-3.252159	20468.1894
HLA B*4801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.419687	1.167504	-3.252182	26283.7133
HLA A*0212	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.385659	1.133400	-3.252259	24302.9576
HLA B*5701	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.421407	1.168653	-3.252754	26388.0042
HLA B*4801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.365287	1.112498	-3.252789	23189.2523
HLA A*0301	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.365378	1.112498	-3.252881	23194.1454
HLA A*0206	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.398302	1.145357	-3.252945	25020.8298
HLA A*8001	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.365470	1.112498	-3.252972	23199.0396
HLA A*3101	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.261949	1.008953	-3.252997	18278.8701
HLA A*2403	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.398410	1.145357	-3.253053	25027.0571
HLA A*8001	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.398833	1.145357	-3.253476	25051.4399
HLA A*3101	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.280980	1.027504	-3.253476	19097.6608
HLA A*2902	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.458568	1.204727	-3.253841	28745.3995
HLA B*1509	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.406015	1.152145	-3.253871	25469.1862
HLA B*4001	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.366600	1.112498	-3.254103	23259.4857
HLA A*2601	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.384510	1.130392	-3.254119	24238.750743	
HLA A*0203	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.263112	1.008953	-3.254160	18327.8846
HLA B*1501	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.286588	1.031880	-3.254708	19345.8758
HLA B*4001	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.400205	1.145357	-3.254848	25130.7119
HLA A*2603	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.528353	1.273350	-3.255003	33756.1379
HLA A*0201	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.363917	1.108664	-3.255253	23116.2294
HLA B*1509	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.401112	1.145357	-3.255755	25183.2451
HLA A*6802	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.264757	1.008953	-3.255804	18397.4225
HLA A*3001	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.170928	0.915034	-3.255894	14822.7215
HLA B*0803	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.424642	1.168653	-3.255989	26585.3135
HLA B*2705	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.128656	0.872645	-3.256011	13447.9478
HLA A*0211	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.481998	0.225691	-3.256307	3033.876233	
HLA B*4801	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.360618	1.104113	-3.256506	22941.315612	
HLA A*0301	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.368604	1.112050	-3.256554	23367.0678
HLA A*2403	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.382175	1.125530	-3.256645	24108.758388	
HLA A*3301	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.424642	1.167504	-3.257137	26585.3135
HLA B*4801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.383787	1.126312	-3.257474	24198.3966
HLA B*4601	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.405204	1.147510	-3.257695	25421.6945
HLA A*0216	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.388192	1.130392	-3.257800	24445.103234	
HLA B*4002	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.495982	1.238012	-3.257969	31331.526066	
HLA A*0101	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.362420	1.104113	-3.258308	23036.705730	
HLA B*2705	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.425868	1.167504	-3.258364	26660.4955
HLA B*3501	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.463098	1.204727	-3.258371	29046.7907
HLA B*0802	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.403807	1.145357	-3.258450	25339.9966
HLA A*2902	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.425997	1.167504	-3.258493	26668.4293
HLA A*0301	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.367328	1.108664	-3.258664	23298.5261
HLA A*2902	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.325108	1.066259	-3.258849	21140.1567
HLA A*2603	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.048341	0.789295	-3.259047	11177.410977	
HLA B*1517	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.426636	1.167504	-3.259132	26707.7005
HLA A*3101	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.367765	1.108038	-3.259727	23321.981852	
HLA A*2601	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.371830	1.112050	-3.259780	23541.2794
HLA B*5701	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.379774	1.119963	-3.259811	23975.8311
HLA A*0216	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.405303	1.145357	-3.259946	25427.4714
HLA B*0801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.372081	1.112050	-3.260031	23554.9104
HLA B*1502	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.568249	1.308218	-3.260032	37004.058408	
HLA A*6901	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.390483	1.130392	-3.260091	24574.383053	
HLA B*0702	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.340267	1.080003	-3.260264	21891.0745
HLA B*4402	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.372977	1.112498	-3.260479	23603.5111
HLA A*2902	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.301884	1.041264	-3.260620	20039.3460
HLA B*1503	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.386162	1.125530	-3.260632	24331.109914	
HLA B*7301	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.594878	1.334180	-3.260698	39343.9917
HLA B*3501	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.455476	1.194587	-3.260889	28541.475909	
HLA B*4001	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.365338	1.104113	-3.261226	23192.012427	
HLA A*6802	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.370075	1.108664	-3.261411	23446.3366
HLA B*2705	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.387987	1.126312	-3.261675	24433.6006
HLA B*1801	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.484547	1.222842	-3.261705	30517.334998	
HLA A*0212	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.407129	1.145357	-3.261772	25534.5803
HLA A*2902	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.337105	1.074983	-3.262121	21732.2490
HLA B*0803	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.392574	1.130392	-3.262182	24692.989129	
HLA A*0301	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.254036	0.991777	-3.262260	17948.8356
HLA A*0202	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.447864	1.185494	-3.262370	28045.558679	
HLA B*4801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.431810	1.168653	-3.263157	27027.7606
HLA A*0212	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.417852	1.154646	-3.263206	26172.8956
HLA B*0802	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.430903	1.167504	-3.263399	26971.3797
HLA A*0216	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.243898	0.980470	-3.263429	17534.6965
HLA A*0216	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.025814	0.762047	-3.263767	10612.4182
HLA B*0801	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.353474	1.089590	-3.263884	22566.984770	
HLA A*2602	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.458519	1.194587	-3.263932	28742.134030	
HLA A*3101	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.376463	1.112498	-3.263966	23793.7693
HLA B*5801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.323193	1.058921		
HLA A*0212	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.296379	1.031880		

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HLA A*0101	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.373183	1.108664	-3.264519	23614.7507
HLA B*4403	1:77-85 9	SVSFYITGI	0.979963	0.379282	-4.624005	1.359245	-3.264760	42073.145900	
HLA A*1101	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.459459	1.194587	-3.264872	28804.398077	
HLA B*4402	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.432588	1.167504	-3.265083	27076.2019
HLA B*0802	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.369213	1.104113	-3.265100	23399.831808	
HLA B*5101	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.377638	1.112498	-3.265140	23858.2172
HLA A*2501	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.417577	1.152145	-3.265432	26156.3346
HLA B*4001	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.355247	1.089590	-3.265658	22659.347356	
HLA A*0202	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.324784	1.058921	-3.265863	21124.3801
HLA A*0216	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.345939	1.080003	-3.265935	22178.8353
HLA A*3101	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.391514	1.125530	-3.265984	24632.815130	
HLA A*2403	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.392322	1.126312	-3.266010	24678.6995
HLA B*3801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.420758	1.154646	-3.266113	26348.6329
HLA A*8001	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.418329	1.152145	-3.266184	26201.6547
HLA B*5101	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.451814	1.185494	-3.266319	28301.768878	
HLA B*5801	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.355919	1.089590	-3.266330	22694.433676	
HLA A*0202	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.146897	0.880566	-3.266331	14024.823888	
HLA A*3001	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.189794	0.923260	-3.266535	15480.8325
HLA A*2902	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.323149	1.056254	-3.266895	21044.9904
HLA B*3901	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.019720	0.752698	-3.267022	10464.5315
HLA B*1517	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.461656	1.194587	-3.267068	28950.466933	
HLA B*4601	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.379597	1.112498	-3.267100	23966.1051
HLA A*0101	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.276065	1.008953	-3.267112	18882.7417
HLA A*2402	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.452634	1.185494	-3.267139	28355.254546	
HLA A*0219	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.308608	1.041264	-3.267344	20352.0316
HLA B*4403	1:177-185	9	NATETRIVV	1.258391	0.095723	-4.621482	1.354114	-3.267368	41829.4004
HLA B*4002	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.601011	1.333568	-3.267442	39903.462019	
HLA A*6901	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.375486	1.108038	-3.267448	23740.281308	
HLA B*5701	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.393032	1.125530	-3.267502	24719.052209	
HLA B*5401	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.357263	1.089590	-3.267674	22764.769385	
HLA A*6802	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.401232	1.133400	-3.267831	25190.1943
HLA B*0702	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.419849	1.151985	-3.267864	26293.526428	
HLA A*2902	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.283663	1.015721	-3.267942	19216.0131
HLA B*4001	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.148580	0.880633	-3.267947	14079.254121	
HLA A*8001	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.436709	1.168653	-3.268056	27334.3493
HLA A*2403	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.415669	1.147510	-3.268159	26041.6862
HLA B*5101	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.324439	1.056254	-3.268185	21107.5875
HLA A*0201	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.372389	1.104113	-3.268277	23571.609599	
HLA A*6801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.282677	1.014245	-3.268431	19172.4010
HLA B*1517	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.394145	1.125530	-3.268616	24782.520304	
HLA B*3501	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.149322	0.880566	-3.268756	14103.343542	
HLA B*1517	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.473668	1.204727	-3.268942	29762.4370
HLA A*2403	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.437815	1.168653	-3.269163	27404.0876
HLA A*0219	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.261195	0.991777	-3.269418	18247.1550
HLA B*1503	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.231524	0.962074	-3.269450	17042.115988	
HLA B*4402	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.389430	1.119963	-3.269467	24514.8959
HLA A*8001	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.424621	1.154646	-3.269975	26584.0191
HLA B*1501	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.282411	1.012095	-3.270316	19160.6841
HLA B*1503	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.307036	1.036697	-3.270339	20278.5064
HLA B*5701	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.403922	1.133400	-3.270521	25346.7147
HLA A*0206	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.374645	1.104113	-3.270532	23694.347044	
HLA A*2601	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.378580	1.108038	-3.270542	23910.030633	
HLA A*0211	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-3.587490	0.316807	-3.270683	3868.029133	
HLA A*0201	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.382802	1.112050	-3.270752	24143.6072
HLA B*3801	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.493613	1.222842	-3.270772	31161.134991	
HLA B*4801	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.396366	1.125530	-3.270836	24909.541516	
HLA B*1502	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.456555	1.185494	-3.271060	28612.436430	
HLA A*2301	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.457027	1.185494	-3.271533	28643.566164	
HLA B*1501	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.383596	1.112050	-3.271546	24187.7952
HLA A*0219	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.426275	1.154646	-3.271629	26685.4590
HLA B*1503	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.306075	1.034236	-3.271839	20233.686900	
HLA A*6901	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.182008	0.910145	-3.271864	15205.7596
HLA A*2902	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.245642	0.973692	-3.271950	17605.2246
HLA A*0206	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.380984	1.108664	-3.272320	24042.7231
HLA A*3001	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.177784	0.905427	-3.272357	15058.5704
HLA B*4403	1:57-65 9	NAGYLRHII	1.129740	0.203828	-4.605926	1.333568	-3.272358	40357.634172	
HLA B*5801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.305067	1.032480	-3.272587	20186.7821
HLA B*1503	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.287556	1.014245	-3.273311	19389.0434
HLA B*2705	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.442134	1.168653	-3.273481	27677.9360
HLA B*4402	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.442211	1.168653	-3.273558	27682.8777
HLA A*0301	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.363353	1.089590	-3.273763	23086.235431	
HLA A*0212	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.421348	1.147510	-3.273838	26384.4355
HLA A*0203	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.363724	1.089590	-3.274135	23105.977115	
HLA B*1501	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.382969	1.108664	-3.274305	24152.8826
HLA B*0702	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.407897	1.133400	-3.274497	25579.7918
HLA A*2601	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.387008	1.112498	-3.274510	24378.5423
HLA A*0219	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.037369	0.762047	-3.275322	10898.5601
HLA A*6802	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.430128	1.154646	-3.275482	26923.2716
HLA B*1509	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.470309	1.194587	-3.275722	29533.078923	
HLA A*0216	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.312799	1.036697	-3.276103	20549.4049
HLA B*1801	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.365919	1.089590	-3.276329	23223.023297	
HLA A*0206	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-3.636298	0.359849	-3.276449	4328.1064
HLA B*0702	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.317740	1.041264	-3.276476	20784.5304
HLA A*2902	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.406971	1.130392	-3.276580	25525.326697	
HLA A*2501	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.422034	1.145357	-3.276677	26426.1476
HLA B*4801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.424308	1.147510	-3.276798	26564.8983
HLA B*0802	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.407227	1.130392	-3.276836	25540.382857	
HLA A*0206	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.313732	1.036697	-3.277035	20593.5869
HLA A*2301	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.389585	1.112498	-3.277088	24523.6506
HLA A*0212	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.313819	1.036697	-3.277122	20597.7094
HLA A*2403	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.389867	1.112498	-3.277369	24539.5762
HLA A*2301	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.381700	1.104113	-3.277588	24082.426784	
HLA A*0101	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.385666	1.108038	-3.277628	24303.352124	
HLA B*4601	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.408635	1.130392	-3.278243	25623.281315	
HLA A*6901	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.161525	0.883157	-3.278368	14505.2530
HLA A*1101	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.236166	0.957621	-3.278545	17225.2724
HLA B*3901	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.382802	1.104113	-3.278689	24143.607215	
HLA A*0216	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.184151	0.905427	-3.278724	15280.9674
HLA B*5401	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.501834	1.222842	-3.278992	31756.608552	
HLA B*4001	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.409401	1.130392	-3.279009	25668.511018	
HLA A*1101	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.431079	1.151985	-3.279094	26982.325365	
HLA B*4601	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.387372	1.108038	-3.279334	24398.993168	
HLA A*8001	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.404993	1.125530	-3.279463	25409.320014	
HLA A*0206	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.434277	1.154646	-3.279631	27181.7256
HLA A*8001	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.399704	1.119963	-3.279741	25101.7703
HLA B*3901	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.294161	1.014245	-3.279916	19686.1498
HLA B*4001	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.388138	1.108038	-3.280100	24442.061782	
HLA B*4001	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.389183	1.108664	-3.280519	24500.9745
HLA B*0802	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.449189	1.168653	-3.280536	28131.2613
HLA A*0101	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.392609	1.112050	-3.280559	24694.9930
HLA B*0801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.400567	1.119963	-3.280604	25151.6576
HLA B*0702	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.393203	1.112498	-3.280706	24728.8162
HLA A*1101	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.324986	1.044178	-3.280808	21134.2105
HLA A*2501	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.281647	1.000751	-3.280896	19127.0251
HLA B*5701	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.393521	1.112498	-3.281023	24746.8831
HLA B*1501	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.208148	0.927121		
HLA A*8001	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.356103	1.074983		

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HLA A*2601	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.370719	1.089590	-3.281129	23481.117173		
HLA A*3002	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.356321	1.074983	-3.281338	22715.437	
HLA A*0101	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.313617	1.031880	-3.281737	20588.1285	
HLA B*5701	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.361831	1.080003	-3.281827	23005.4458	
HLA B*1503	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.429404	1.147510	-3.281894	26878.4482	
HLA B*5701	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.412335	1.130392	-3.281944	25842.539190		
HLA A*3301	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.631018	1.349023	-3.281995	42758.0803	
HLA B*1509	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.126119	0.843953	-3.282166	13369.6048	
HLA A*2902	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.434500	1.152145	-3.282356	27195.6985	
HLA A*0211	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.372147	1.089590	-3.282557	23558.478719		
HLA B*1509	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.505913	1.222842	-3.283071	32056.257772		
HLA A*2501	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.478135	1.194587	-3.283548	30070.099180		
HLA A*0201	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.413977	1.130392	-3.283586	25940.448081		
HLA B*0802	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.431516	1.147510	-3.284007	27009.4897	
HLA A*8001	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.431711	1.147510	-3.284202	27021.6202	
HLA B*4402	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.392999	1.108664	-3.284335	24717.1800	
HLA A*0212	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.165402	0.880566	-3.284836	14635.311159		
HLA A*0202	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.430541	1.145357	-3.285184	26948.9186	
HLA B*0803	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.317139	1.031880	-3.285258	20755.7652	
HLA A*6801	1:114-122	9	SRVVVPPGM	1.131267	0.217756	-4.634284	1.349023	-3.285261	43080.8222	
HLA A*1101	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.470804	1.185494	-3.285310	29566.809785		
HLA B*1501	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.301132	1.015721	-3.285411	20004.6846	
HLA A*0203	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.397804	1.112050	-3.285754	24992.1500	
HLA A*2902	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.365787	1.080003	-3.285784	23215.9888	
HLA B*1501	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.394059	1.108038	-3.286020	24777.560185		
HLA B*1517	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.438022	1.151985	-3.286037	27417.137058		
HLA B*1801	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.438278	1.151985	-3.286293	27433.309106		
HLA A*6901	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.318215	1.031880	-3.286335	20807.2561	
HLA A*2402	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.327613	1.041264	-3.286349	21262.4230	
HLA A*2301	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.491092	1.204727	-3.286365	30980.7744	
HLA A*6802	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.376120	1.089590	-3.286530	23774.983365		
HLA B*4801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.406685	1.119963	-3.286722	25508.4853	
HLA A*0206	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.039498	0.752698	-3.286800	10952.1090	
HLA B*5801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.367277	1.080003	-3.287273	23295.7533	
HLA B*3901	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.413848	1.126312	-3.287536	25932.7308	
HLA A*0219	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-3.907297	0.619672	-3.287625	8077.871419		
HLA B*0802	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.442392	1.154646	-3.287747	27694.4117	
HLA A*0219	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.421282	1.133400	-3.287882	26380.4392	
HLA A*0212	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-3.907696	0.619672	-3.288024	8085.303903		
HLA A*3101	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.400191	1.112050	-3.288141	25129.8962	
HLA B*3901	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.413674	1.125530	-3.288145	25922.351188		
HLA A*0201	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.396272	1.108038	-3.288234	24904.151784		
HLA B*1501	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.226037	0.937566	-3.288472	16828.1924	
HLA B*0801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.316030	1.027504	-3.288526	20702.8336	
HLA A*3101	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.250630	0.962074	-3.288556	17808.589728		
HLA A*0211	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-3.992005	0.703256	-3.288749	9817.598522		
HLA B*0801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.297725	1.008953	-3.288772	19848.3749	
HLA A*0206	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.316354	1.027504	-3.288850	20718.2954	
HLA B*5801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.355175	1.066259	-3.288915	22655.5475	
HLA A*0219	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.397592	1.108664	-3.288928	24979.9845	
HLA A*2902	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.434639	1.145357	-3.289282	27204.3807	
HLA B*3801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.434808	1.145357	-3.289451	27214.9792	
HLA B*7301	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.216625	0.927116	-3.289510	16467.415074		
HLA B*4001	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.364671	1.074983	-3.289688	23156.4073	
HLA A*3101	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.322204	1.032480	-3.289724	20999.2720	
HLA A*0216	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.135860	0.846009	-3.289850	13672.8653	
HLA A*8001	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.416219	1.126312	-3.289906	26074.6736	
HLA B*4601	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.398581	1.108664	-3.289917	25036.9428	
HLA A*2601	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.394336	1.104113	-3.290223	24793.382410		
HLA B*4601	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.306138	1.015721	-3.290418	20236.6425	
HLA A*0206	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.271237	0.980470	-3.290767	18673.9788	
HLA B*0801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.323525	1.032480	-3.291045	21063.2145	
HLA B*3801	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.485829	1.194587	-3.291242	30607.610348		
HLA A*2403	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.411292	1.119963	-3.291329	25780.5401	
HLA B*4001	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.357714	1.066259	-3.291455	22788.4274	
HLA B*1501	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.349416	1.057871	-3.291545	22357.1260	
HLA B*4403	1:233-241	9	TTLADGTEV	1.178752	0.144786	-4.615145	1.323538	-3.291607	41223.5205	
HLA B*1503	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-3.860068	0.568388	-3.291679	7245.487115		
HLA A*3001	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.272412	0.980470	-3.291942	18724.5592	
HLA B*1509	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.439928	1.147510	-3.292418	27537.6918	
HLA B*0801	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.400851	1.108038	-3.292813	25168.127238		
HLA B*1501	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.327192	1.034236	-3.292956	21241.843095		
HLA A*2403	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.423404	1.130392	-3.293012	26509.626408		
HLA B*1517	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-3.985145	0.692096	-3.293049	9663.729656		
HLA B*5801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.349414	1.056254	-3.293160	22357.0050	
HLA B*3501	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.447834	1.154646	-3.293188	28043.5863	
HLA A*0203	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.346012	1.052696	-3.293316	22182.5552	
HLA A*6901	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.352282	1.058921	-3.293362	22505.1725	
HLA A*0301	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.309223	1.015721	-3.293502	20380.8985	
HLA A*0219	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.441337	1.147510	-3.293827	27627.2225	
HLA B*5701	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.306040	1.012095	-3.293944	20232.0450	
HLA B*4402	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.042435	0.748410	-3.294025	11026.4221	
HLA B*4601	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.406332	1.112050	-3.294282	25487.7940	
HLA B*1801	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.420034	1.125530	-3.294505	26304.766189		
HLA A*0216	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.403198	1.108664	-3.294534	25304.5160	
HLA A*0250	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.480036	1.185494	-3.294541	30201.992397		
HLA B*1509	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.360813	1.066259	-3.294554	22951.6190	
HLA A*2403	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.369708	1.074983	-3.294725	23426.5576	
HLA B*1503	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.322350	1.027504	-3.294846	21006.3166	
HLA A*8001	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.403560	1.108664	-3.294896	25325.6066	
HLA B*5801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.322517	1.027504	-3.295012	21014.3867	
HLA B*2705	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.425410	1.130392	-3.295019	26632.385442		
HLA B*4601	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.399220	1.104113	-3.295108	25073.811597		
HLA A*3002	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.447291	1.152145	-3.295146	28008.5626	
HLA B*7301	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-3.402402	0.107209	-3.295193	2525.81772	
HLA B*2705	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.443062	1.147510	-3.295552	27737.1444	
HLA A*3301	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.630844	1.335227	-3.295618	42740.9663	
HLA B*3901	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.429056	1.133400	-3.295656	26856.9362	
HLA A*2601	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.310175	1.014245	-3.295930	20425.6025	
HLA A*6802	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.400167	1.104113	-3.296055	25128.536787		
HLA A*0216	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.450806	1.154646	-3.296160	28236.1610	
HLA A*2403	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.404302	1.108038	-3.296264	25368.938424		
HLA B*1801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.429853	1.133400	-3.296453	26906.2357	
HLA A*0101	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.354343	1.057871	-3.296472	22612.2014	
HLA B*1503	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.329163	1.032480	-3.296683	21338.4767	
HLA B*1517	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.465469	1.168653	-3.296816	29205.7784	
HLA B*0802	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.416870	1.119963	-3.296907	26113.7769	
HLA A*0201	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.386655	1.089590	-3.297066	24358.767630		
HLA A*6901	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.100265	0.803085	-3.297180	12596.933542		
HLA A*0216	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.444704	1.147510	-3.297194	27842.2313	
HLA B*0803	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.430901	1.133400	-3.297501	26971.2338	
HLA A*0202	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.406203	1.108664	-3.297539	25480.2114	
HLA B*1517	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.183047	0.885414	-3.297632	15242.1626	
HLA B*1801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.046274	0.748410	-3.297864	11124.3251	
HLA A*1101	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.452565	1.154646	-3.297920	28350.8063	
HLA A*0301	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.330406	1.032480			
HLA A*1101	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.443503	1.145357			

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HLA B*4402	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.357146	1.058921	-3.298225	22758.6124
HLA A*2501	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.428706	1.130392	-3.298315	26835.296311	
HLA B*1801	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.492904	1.194587	-3.298317	31110.265915	
HLA A*8001	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.429141	1.130392	-3.298750	26862.167311	
HLA B*3501	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.184578	0.885414	-3.299164	15296.0204
HLA A*3001	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.226395	0.927121	-3.299273	16842.0359
HLA B*0801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.291083	0.991777	-3.299306	19547.1282
HLA A*2902	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.447105	1.147510	-3.299595	27996.5948
HLA B*3801	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.537643	1.238012	-3.299630	34485.983547	
HLA A*0219	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.411832	1.112050	-3.299782	25812.6381
HLA B*0702	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.352529	1.052696	-3.299833	22517.9599
HLA B*5801	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.261916	0.962074	-3.299843	18277.485782	
HLA B*1801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.447483	1.147510	-3.299974	28020.9902
HLA B*5701	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.412366	1.112050	-3.300316	25844.3567
HLA B*4801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.366656	1.066259	-3.300397	23262.5058
HLA A*0219	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.366781	1.066259	-3.300522	23269.1767
HLA B*4601	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.390229	1.089590	-3.300639	24560.029220	
HLA A*0212	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.375707	1.074983	-3.300723	23752.3570
HLA B*5701	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.408900	1.108038	-3.300862	25638.950063	
HLA A*0301	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.367171	1.066259	-3.300912	23290.0828
HLA B*4501	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.453071	1.152145	-3.300926	28383.8010
HLA A*3001	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.291177	0.990022	-3.301155	19551.3585
HLA B*2705	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.357437	1.056254	-3.301184	22773.8846
HLA A*3201	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.328787	1.027504	-3.301283	21320.0145
HLA A*0203	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.405501	1.104113	-3.301388	25439.029075	
HLA B*4002	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.574779	1.273350	-3.301429	37564.5833
HLA B*4402	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.426970	1.125530	-3.301441	26728.225435	
HLA B*7301	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.539499	1.238012	-3.301486	34633.685572	
HLA B*1801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.360475	1.058921	-3.301554	22933.7461
HLA B*7301	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.609845	1.308218	-3.301627	40723.457212	
HLA A*2501	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.405952	1.104113	-3.301839	25465.466290	
HLA B*4403	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.637134	1.335227	-3.301907	43364.4565
HLA A*0201	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.368210	1.066259	-3.301950	23345.8400
HLA A*3201	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.316516	1.014245	-3.302271	20726.0306
HLA B*3801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.507015	1.204727	-3.302288	32137.6953
HLA B*5101	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.414447	1.112050	-3.302397	25968.5302
HLA A*0216	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.377598	1.074983	-3.302615	23856.0231
HLA A*2403	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.346857	1.044178	-3.302680	22225.7991
HLA A*8001	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.361626	1.058921	-3.302706	22994.6206
HLA A*0203	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.361654	1.058921	-3.302734	22996.1134
HLA B*3901	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.488287	1.185494	-3.302792	30781.301956	
HLA B*5801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.360825	1.057871	-3.302954	22952.2398
HLA B*5801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.347212	1.044178	-3.303034	22243.9627
HLA A*2301	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.448435	1.145357	-3.303078	28082.4517
HLA A*1101	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.208623	0.905427	-3.303196	16166.7635
HLA B*1801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.457925	1.154646	-3.303279	28702.8215
HLA B*4403	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.876631	0.573275	-3.303356	7527.16537
HLA B*7301	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.451125	1.147510	-3.303615	28256.9433
HLA B*0801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.361619	1.057871	-3.303749	22994.2474
HLA B*4002	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.639072	1.335227	-3.303845	43558.4315
HLA B*5301	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.577539	1.273350	-3.304189	37804.1276
HLA A*2902	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.336299	1.031880	-3.304418	21691.9602
HLA A*3002	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.424440	1.119963	-3.304477	26572.9475
HLA B*5101	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.473154	1.168653	-3.304501	29727.1963
HLA A*1101	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.337192	1.032480	-3.304712	21736.5995
HLA B*5801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.357437	1.052696	-3.304741	22773.8846
HLA A*3101	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.414177	1.108664	-3.305513	25952.3792
HLA B*5401	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.380796	1.074983	-3.305812	24032.3195
HLA A*2501	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.460547	1.154646	-3.305901	28876.6371
HLA B*0803	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.473471	1.167504	-3.305967	29748.9151
HLA B*1501	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.342945	1.036697	-3.306249	22026.5000
HLA B*5701	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.414992	1.108664	-3.306328	26001.1436
HLA B*0702	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.268587	0.962074	-3.306513	18560.370558	
HLA A*0216	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.418740	1.112050	-3.306690	26226.4724
HLA A*8001	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.386735	1.080003	-3.306732	24363.2485
HLA B*0802	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.419261	1.112498	-3.306764	26257.9891
HLA B*5401	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.459104	1.151985	-3.307119	28780.877567	
HLA A*0101	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.387186	1.080003	-3.307183	24388.5677
HLA A*3002	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.474883	1.167504	-3.307379	29845.7964
HLA A*0212	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.419534	1.112050	-3.307484	26274.4724
HLA A*6901	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.319587	1.012095	-3.307492	20873.0980
HLA B*4002	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.641683	1.334180	-3.307503	43821.0229
HLA A*0203	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.344235	1.036697	-3.307539	22092.0165
HLA B*1501	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.316594	1.008953	-3.307641	20729.7311
HLA B*1517	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.245219	0.937566	-3.307653	17588.0894
HLA B*4001	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.365665	1.057871	-3.307794	23209.4587
HLA A*0301	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.364194	1.056254	-3.307941	23130.9907
HLA A*3002	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.462591	1.154646	-3.307945	29012.8683
HLA A*6901	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.213463	0.905427	-3.308036	16347.9396
HLA A*6901	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.366090	1.057871	-3.308220	23232.1963
HLA A*2902	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.463162	1.154646	-3.308516	29051.0338
HLA A*0212	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.412716	1.104113	-3.308603	25865.197572	
HLA B*1503	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.145027	0.836190	-3.308837	13964.559037	
HLA A*0219	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.388904	1.080003	-3.308900	24485.2064
HLA A*0301	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.366887	1.057871	-3.309016	23274.8422
HLA B*5801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.350318	1.041264	-3.309054	22403.6189
HLA B*5801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.324850	1.015721	-3.309129	21127.5802
HLA A*0101	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.361845	1.052696	-3.309149	23006.1925
HLA A*0202	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.155478	0.846009	-3.309469	14304.6664
HLA B*4601	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.389623	1.080003	-3.309619	24525.7734
HLA A*0202	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.071737	0.762047	-3.309690	11796.0713
HLA A*6802	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.418004	1.108038	-3.309966	26182.100819	
HLA A*0212	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.390081	1.080003	-3.310077	24551.6600
HLA A*3002	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.366476	1.056254	-3.310222	23252.8176
HLA A*3301	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.583660	1.273350	-3.310310	38340.6640
HLA A*0211	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.440703	1.130392	-3.310311	27586.897768	
HLA B*1503	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.237501	0.927121	-3.310379	17278.2839
HLA B*5401	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.479260	1.168653	-3.310607	30148.1219
HLA A*2902	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.311460	1.000751	-3.310709	20486.1356
HLA B*0803	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.322853	1.012095	-3.310757	21030.6500
HLA B*4801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.422812	1.112050	-3.310761	26473.5106
HLA A*0101	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.352212	1.041264	-3.310948	22501.5203
HLA A*0212	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.419666	1.108664	-3.311002	26282.4336
HLA A*0212	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.441504	1.130392	-3.311113	27637.836281	
HLA A*0211	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.046081	0.734934	-3.311147	11119.391335	
HLA A*2601	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.377506	1.066259	-3.311247	23850.9904
HLA B*1517	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.465962	1.154646	-3.311317	29238.9773
HLA B*3901	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.269047	0.957621	-3.311426	18580.0612
HLA A*0202	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.323590	1.012095	-3.311495	21066.4053
HLA B*4601	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.325822	1.014245	-3.311577	21174.9525
HLA B*6801	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-3.949273	0.637604	-3.311668	8897.59912
HLA A*2501	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.423737	1.112050	-3.311687	26529.9990
HLA A*8001	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.353116	1.041264	-3.311852	22548.4354
HLA B*4501	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.292352	0.980281	-3.312070	19604.315513	
HLA B*0702	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.416259	1.104113	-3.3121[illegible]	26077.071844	
HLA B*2705	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.192820	0.880633	-3.3121[illegible]		
HLA B*1501	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.364979	1.052696		

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HLA A*0206	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.321307	1.008953	-3.312354	20955.9202
HLA B*4601	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.378735	1.066259	-3.312476	23918.5692
HLA A*0201	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.392595	1.080003	-3.312591	24694.1914
HLA A*0201	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.356770	1.044178	-3.312592	22738.9215
HLA B*4801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.421308	1.108664	-3.312644	26382.0091
HLA A*3101	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.185368	0.872645	-3.312723	15323.8497
HLA B*4402	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.417116	1.104113	-3.313004	26128.614751
HLA A*0301	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.345039	1.031880	-3.313159	22132.9286
HLA A*2403	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.287028	0.973692	-3.313336	19365.4570
HLA A*2601	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.393375	1.080003	-3.313371	24738.5841
HLA B*7301	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.066240	0.752698	-3.313542	11647.6844
HLA B*4002	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.621789	1.308218	-3.313572	41859.055234
HLA A*3301	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.251161	0.937566	-3.313595	17830.3764
HLA B*4001	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.354916	1.041264	-3.313652	22642.0695
HLA B*4601	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.315022	1.000751	-3.314270	20654.8413
HLA B*1801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.434832	1.119963	-3.314869	27216.4515
HLA A*3201	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.306698	0.991777	-3.314921	20262.7151
HLA B*0801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.329168	1.014245	-3.314923	21338.7076
HLA B*1801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.356281	1.041264	-3.315017	22713.3488
HLA A*3002	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.500648	1.185494	-3.315153	31669.968092
HLA A*0301	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.367895	1.052696	-3.315199	23328.9221
HLA A*0301	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.288912	0.973692	-3.315220	19449.6610
HLA A*0216	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.118426	0.803085	-3.315342	13134.887494
HLA B*5401	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.520167	1.204727	-3.315440	33125.8588
HLA A*3001	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.273260	0.957621	-3.315639	18761.1635
HLA A*3101	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.356965	1.041264	-3.315701	22749.1340
HLA B*5701	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.381968	1.066259	-3.315709	24097.2836
HLA B*5301	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.348370	1.032480	-3.315890	22303.3682
HLA B*0802	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.441445	1.125530	-3.315916	27634.098593
HLA A*0202	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.520698	1.204727	-3.315971	33166.3844
HLA B*2705	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.253583	0.937566	-3.316017	17930.1049
HLA A*3001	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-3.984769	0.668648	-3.316121	9655.368522
HLA A*3101	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.405738	1.089590	-3.316148	25452.932728
HLA B*4501	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.650498	1.334180	-3.316318	44719.5865
HLA A*0219	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.446757	1.130392	-3.316366	27974.187942
HLA B*1801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.461818	1.145357	-3.316461	28961.2756
HLA B*3501	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.446967	1.130392	-3.316575	27987.660201
HLA B*0702	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.424717	1.108038	-3.316679	26589.916255
HLA B*1503	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-3.580620	0.263887	-3.316733	3807.32405
HLA B*5701	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.406337	1.089590	-3.316747	25488.069833
HLA A*2601	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.353633	1.036697	-3.316937	22575.2880
HLA B*4801	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.425060	1.108038	-3.317022	26610.926432
HLA A*8001	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.373289	1.056254	-3.317036	23620.5003
HLA B*0801	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.279437	0.962074	-3.317363	19029.902554
HLA B*1509	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.332265	1.014245	-3.318020	21491.4013
HLA B*5401	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.233091	0.915034	-3.318056	17103.7217
HLA A*0219	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.422191	1.104113	-3.318079	26435.727904
HLA B*3801	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.451588	1.133400	-3.318188	28287.0741
HLA B*4402	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.448625	1.130392	-3.318234	28094.760157
HLA A*2501	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.465770	1.147510	-3.318260	29226.0094
HLA A*3002	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.486920	1.168653	-3.318267	30684.5377
HLA B*0702	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.426944	1.108664	-3.318280	26726.6349
HLA A*0211	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.384562	1.066259	-3.318303	24241.6357
HLA B*5101	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.465864	1.147510	-3.318354	29232.3345
HLA A*3201	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.355102	1.036697	-3.318405	22651.7483
HLA A*0212	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.292119	0.973692	-3.318427	19593.8186
HLA A*6901	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.398701	1.080003	-3.318698	25043.8516
HLA B*0801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.362895	1.044178	-3.318717	23061.8939
HLA A*6802	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.449161	1.130392	-3.318769	28129.435152
HLA A*3201	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.487455	1.168653	-3.318802	30722.4090
HLA A*0301	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.333289	1.014245	-3.319044	21542.1532
HLA B*1503	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.192614	0.873495	-3.319119	15581.6589
HLA B*1503	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.309411	0.990022	-3.319389	20389.7215
HLA A*0101	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.378350	1.058921	-3.319429	23897.3576
HLA B*4001	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.378463	1.058921	-3.319542	23903.5639
HLA A*0101	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.352146	1.032480	-3.319666	22498.1121
HLA A*0201	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.229879	0.910145	-3.319734	16977.7008
HLA B*4501	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.655216	1.335227	-3.319989	45208.0261
HLA B*1509	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.424496	1.104113	-3.320383	26576.397933
HLA A*8001	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.278156	0.957621	-3.320535	18973.8776
HLA A*0216	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.425060	1.104113	-3.320947	26610.926432
HLA B*5801	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.357724	1.036697	-3.321027	22788.9205
HLA B*5801	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.355311	1.034236	-3.321074	22662.657381
HLA B*1509	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.488724	1.167504	-3.321220	30812.2909
HLA A*0212	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.379471	1.057871	-3.321600	23959.1048
HLA A*2601	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.396702	1.074983	-3.321718	24928.8193
HLA A*1101	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.473934	1.152145	-3.321789	29780.6368
HLA B*2705	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.167986	0.846009	-3.321977	14722.6637
HLA A*1101	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.489495	1.167504	-3.321990	30867.0141
HLA B*1501	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.284131	0.962074	-3.322057	19236.711663
HLA B*0803	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.378411	1.056254	-3.322157	23900.7192
HLA A*0202	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.202876	0.880633	-3.322243	15954.244602
HLA B*3901	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.469804	1.147510	-3.322294	29498.7481
HLA A*2402	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.381216	1.058921	-3.322296	24055.6033
HLA A*0101	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.337029	1.014245	-3.322784	21728.4871
HLA A*0206	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.249948	0.927121	-3.322827	17780.6723
HLA B*4601	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.397902	1.074983	-3.322919	24997.8292
HLA A*2602	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.475172	1.152145	-3.323028	29865.6629
HLA B*1801	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.453465	1.130392	-3.323074	28409.609747
HLA B*1502	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.491752	1.168653	-3.323100	31027.9066
HLA A*0301	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.364493	1.041264	-3.323229	23146.8885
HLA A*2601	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.356147	1.032480	-3.323667	22706.3459
HLA A*2403	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.390175	1.066259	-3.323915	24556.9734
HLA A*0216	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.356072	1.031880	-3.324192	22702.4154
HLA B*4501	1:70-78	9	FSVLEHASV	1.102668	0.135344	-4.562268	1.238012	-3.324255	36497.874119
HLA A*2601	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.383392	1.058921	-3.324471	24176.4136
HLA A*3101	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.234644	0.910145	-3.324499	17164.9930
HLA A*2601	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.325327	1.000751	-3.324575	21150.7954
HLA A*0212	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.369006	1.044178	-3.324828	23388.6944
HLA A*2902	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.433497	1.108664	-3.324833	27132.9487
HLA A*3101	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.339207	1.014245	-3.324962	21837.7285
HLA B*4001	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.361793	1.036697	-3.325097	23003.4546
HLA A*2403	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.437256	1.112050	-3.325206	27368.8261
HLA B*3901	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.493909	1.168653	-3.325257	31182.3830
HLA A*3101	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.299020	0.973692	-3.325328	19907.6282
HLA A*6901	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.317167	0.991777	-3.325390	20757.1127
HLA A*3201	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.445604	1.119963	-3.325641	27899.9799
HLA B*2705	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.362458	1.036697	-3.325761	23038.6998
HLA A*1101	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.473316	1.147510	-3.325806	29738.2951
HLA B*5801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.357717	1.031880	-3.325836	22788.5506
HLA A*0250	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.459304	1.133400	-3.325904	28794.1152
HLA B*5101	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.435308	1.108664	-3.326644	27246.3573
HLA B*1509	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.495902	1.168653	-3.327249	31325.7635
HLA A*0101	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.364150	1.036697	-3.327453	23128.6133
HLA A*0250	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.285129	0.957621	-3.327508	19280.9916
HLA B*4501	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.402601	1.074983		
HLA A*2902	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.417241	1.089590	-3.3276	

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HLA B*0702	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.328513	1.000751	-3.327761	21306.5241
HLA B*1502	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.386749	1.058921	-3.327829	24364.0393
HLA A*6901	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.355339	1.027504	-3.327835	22664.1286
HLA A*2602	1:74-82	9	EHASVSFYI	0.978340	0.173645	-4.479826	1.151985	-3.327841	30187.454237
HLA A*0101	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.372516	1.044178	-3.328338	23578.4966
HLA A*0201	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.387276	1.058921	-3.328355	24393.5819
HLA B*1502	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.551225	1.222842	-3.328383	35581.560373
HLA A*1101	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.440914	1.112498	-3.328417	27600.3328
HLA A*2402	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.462067	1.133400	-3.328667	28977.8882
HLA A*3101	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.384957	1.056254	-3.328703	24263.6780
HLA A*2402	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.448769	1.119963	-3.328806	28104.0330
HLA A*0250	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.320595	0.991777	-3.328818	20921.5975
HLA A*6901	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.319190	0.990022	-3.329168	20854.0231
HLA A*0301	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.363605	1.034236	-3.329368	23099.602955
HLA B*1503	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.437407	1.108038	-3.329368	27378.303783
HLA A*2403	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.419076	1.089590	-3.329486	26246.769424
HLA B*0803	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.433669	1.104113	-3.329556	27143.666291
HLA B*1509	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.382311	1.052696	-3.329615	24116.3242
HLA B*5801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.344090	1.014245	-3.329844	22084.6078
HLA A*6901	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.374076	1.044178	-3.329898	23663.3468
HLA A*6801	1:120-128	9	PGMEDDADL	1.278233	0.056994	-4.665130	1.335227	-3.329904	46251.9845
HLA A*2402	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.374238	1.044178	-3.330061	23672.1816
HLA B*1501	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.114493	0.784286	-3.330207	13016.472924
HLA B*3901	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.065859	0.735649	-3.330210	11637.4808
HLA B*1509	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.287888	0.957621	-3.330267	19403.8389
HLA B*1517	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.442794	1.112498	-3.330296	27720.0434
HLA A*3001	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.035739	0.705319	-3.330420	10857.718605
HLA B*1509	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.456160	1.125530	-3.330631	28586.443505
HLA B*1501	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.396953	1.066259	-3.330694	24943.2537
HLA A*0212	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.397005	1.066259	-3.330745	24946.2226
HLA B*4402	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.133877	0.803085	-3.330792	13610.578057
HLA A*0203	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.311646	0.980470	-3.331176	20494.8929
HLA A*3101	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.311918	0.980470	-3.331449	20507.7585
HLA A*3002	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.289081	0.957621	-3.331460	19457.2384
HLA A*3101	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.365717	1.034236	-3.331480	23212.221288
HLA B*0803	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.457025	1.125530	-3.331495	28643.411206
HLA B*0803	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.444016	1.112498	-3.331518	27798.1336
HLA A*0212	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.439603	1.108038	-3.331565	27517.140828
HLA B*1801	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.435922	1.104113	-3.331809	27284.855838
HLA A*2403	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.440503	1.108664	-3.331839	27574.2151
HLA B*4601	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.390830	1.058921	-3.331910	24594.0667
HLA A*1101	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.363905	1.031880	-3.332025	23115.6041
HLA A*2601	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.390128	1.057871	-3.332257	24554.3166
HLA A*0203	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.440475	1.108038	-3.332437	27572.425086
HLA A*8001	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.444558	1.112050	-3.332508	27832.8943
HLA A*0203	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.247563	0.915034	-3.332529	17683.3055
HLA B*4403	1:205-213	9	DVEIRRLAI	1.175755	0.158425	-4.666761	1.334180	-3.332581	46425.9623
HLA A*6901	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.385380	1.052696	-3.332684	24287.3170
HLA A*0219	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.146930	0.814245	-3.332685	14025.8861
HLA A*3002	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.145633	0.812772	-3.332862	13984.0636
HLA B*0702	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.452899	1.119963	-3.332936	28372.5939
HLA B*5801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.324979	0.991777	-3.333202	21133.8675
HLA B*1517	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.325014	0.991777	-3.333237	21135.5826
HLA B*1502	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.206805	0.873495	-3.333310	16099.2107
HLA A*3001	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.118027	0.784286	-3.333741	13122.813138
HLA B*1517	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.441800	1.108038	-3.333762	27656.681925
HLA B*3501	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.442434	1.108664	-3.333770	27697.1087
HLA B*4002	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.528397	1.194587	-3.333810	33759.607845
HLA A*0201	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.391822	1.057871	-3.333951	24650.2784
HLA B*3801	1:47-55	9	WSKPNPKTA	1.389094	-0.203600	-4.519519	1.185494	-3.334024	33076.434581
HLA A*1101	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.502858	1.168653	-3.334206	31831.6016
HLA A*3301	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-3.624377	0.290041	-3.334336	4210.9167
HLA B*1502	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.479829	1.145357	-3.334472	30187.6175
HLA A*2902	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.446537	1.112050	-3.334487	27959.9658
HLA B*2705	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.454523	1.119963	-3.334560	28478.8557
HLA B*5401	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.460248	1.125530	-3.334719	28856.804102
HLA B*0801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.217913	0.883157	-3.334756	16516.3071
HLA A*1101	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.460415	1.125530	-3.334885	28867.890191
HLA A*6802	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.250507	0.915034	-3.335473	17803.5806
HLA A*3001	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.262934	0.927116	-3.335818	18320.350649
HLA B*4402	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.443983	1.108038	-3.335945	27796.028387
HLA B*1503	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.392405	1.056254	-3.336151	24683.3727
HLA A*0301	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.345149	1.008953	-3.336197	22138.5570
HLA A*1101	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.444420	1.108038	-3.336382	27824.011922
HLA A*2501	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.456454	1.119963	-3.336491	28605.7812
HLA B*4001	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.416881	1.080003	-3.336878	26114.4832
HLA B*1501	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.378192	1.041264	-3.336928	23888.6973
HLA B*4002	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.183004	0.846009	-3.336995	15240.6785
HLA B*7301	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.505734	1.168653	-3.337081	32043.0805
HLA B*1502	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.541820	1.204727	-3.337093	34819.2972
HLA B*4601	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.390036	1.052696	-3.337341	24549.1365
HLA B*1502	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.338115	1.000751	-3.337364	21782.8626
HLA A*0219	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.317872	0.980470	-3.337402	20790.8281
HLA A*2603	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.467814	1.130392	-3.337422	29363.888947
HLA B*5101	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.470924	1.133400	-3.337524	29574.9685
HLA A*3002	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.463848	1.126312	-3.337535	29096.9616
HLA A*2501	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.351808	1.014245	-3.337563	22480.5923
HLA A*3101	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.403875	1.066259	-3.337615	25343.9724
HLA A*3001	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-3.957604	0.619672	-3.337932	9069.933624
HLA A*6801	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.468704	1.130392	-3.338313	29424.156901
HLA A*0211	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.413336	1.074983	-3.338353	25902.1649
HLA A*2402	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.318837	0.980470	-3.338368	20837.1072
HLA A*0216	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.152672	0.814245	-3.338427	14212.5649
HLA A*2601	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.382873	1.044178	-3.338695	24147.5259
HLA B*3501	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.312677	0.973692	-3.338985	20543.6249
HLA B*1517	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.428591	1.089590	-3.339002	26828.183630
HLA B*2705	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.451095	1.112050	-3.339045	28254.9561
HLA A*0219	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.429047	1.089590	-3.339457	26856.355086
HLA B*0803	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.487162	1.147510	-3.339652	30701.6404
HLA B*1509	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.451748	1.112050	-3.339698	28297.4821
HLA B*5801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.351866	1.012095	-3.339771	22483.6330
HLA A*2601	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.392506	1.052696	-3.339810	24689.1154
HLA B*5401	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.406461	1.066259	-3.340202	25495.3785
HLA B*4402	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.406591	1.066259	-3.340331	25502.9660
HLA B*4801	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.430128	1.089590	-3.340538	26923.271670
HLA B*4001	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.396941	1.056254	-3.340688	24942.5790
HLA A*8001	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.407093	1.066259	-3.340834	25532.5083
HLA B*0702	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.355348	1.014245	-3.341103	22664.6191
HLA A*6802	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.421148	1.080003	-3.341145	26372.3057
HLA A*2403	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.399124	1.057871	-3.341253	25068.2507
HLA A*0201	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.393986	1.052696	-3.341290	24773.4051
HLA B*0802	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.467821	1.126312	-3.341508	29364.3655
HLA A*0203	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.268699	0.927121	-3.341578	18565.1908
HLA A*4403	1:4-12	9	TAPLRVQLI	1.142542	0.165676	-4.650122	1.308218	-3.341904	44680.894774
HLA B*5701	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.399895	1.057871	-3.342024	25112.7726
HLA A*0212	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.227555	0.885414		
HLA B*1502	1:59-67	9	GYLRHIIDV	0.947497	0.247090	-4.536766	1.194587	-3.3421	

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HLA A*8001	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.431803	1.089590	-3.342213	27027.322030	
HLA A*0211	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.188253	0.846009	-3.342244	15425.9902
HLA B*4402	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.343063	1.000751	-3.342312	22032.4588
HLA A*0201	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.351345	1.008953	-3.342392	22456.6464
HLA B*5301	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.446508	1.104113	-3.342396	27958.150792	
HLA B*3901	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.451083	1.108664	-3.342419	28254.1918
HLA B*0702	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.408726	1.066259	-3.342467	25628.6880
HLA A*8001	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.304581	0.962074	-3.342507	20164.188696	
HLA A*3002	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.450550	1.108038	-3.342511	28219.515761	
HLA A*1101	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.451189	1.108664	-3.342525	28261.0710
HLA B*4501	1:4-12 9	TAPLRVQLI	1.142542	0.165676	-4.650921	1.308218	-3.342703	44763.154757	
HLA A*3101	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.358426	1.015721	-3.342705	22825.8127
HLA B*4801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.383972	1.041264	-3.342708	24208.7408
HLA A*2402	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.399051	1.056254	-3.342798	25064.0469
HLA B*4601	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.400691	1.057871	-3.342820	25158.8702
HLA A*2601	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.046321	0.703401	-3.342919	11125.528805	
HLA B*4002	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.455035	1.112050	-3.342985	28512.4622
HLA B*4501	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.455528	1.112498	-3.343031	28544.8730
HLA B*3901	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.455220	1.112050	-3.343170	28524.6505
HLA B*4501	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-3.898477	0.555227	-3.343250	7915.47477
HLA A*0201	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.323738	0.980470	-3.343269	21073.5864
HLA A*0202	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-3.903270	0.559811	-3.343459	8003.31515
HLA B*4402	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.401474	1.057871	-3.343603	25204.2346
HLA B*5101	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.469181	1.125530	-3.343651	29456.488481	
HLA A*0211	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.499081	1.154646	-3.344435	31555.8962
HLA B*0803	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.381263	1.036697	-3.344567	24058.2062
HLA B*2705	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-3.288612	-0.055989	-3.344600	1943.621745	
HLA B*3501	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.456719	1.112050	-3.344669	28623.2737
HLA B*4801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.403677	1.058921	-3.344757	25332.4580
HLA B*5701	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.403708	1.058921	-3.344787	25334.2396
HLA A*3002	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.470342	1.125530	-3.344812	29535.315797	
HLA B*4402	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.434451	1.089590	-3.344861	27192.609490	
HLA B*5701	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.397820	1.052696	-3.345124	24993.0964
HLA B*4801	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.381898	1.036697	-3.345201	24093.3730
HLA A*1101	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.465175	1.119963	-3.345212	29186.0351
HLA B*2705	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.453348	1.108038	-3.345310	28401.926144	
HLA B*0803	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.472007	1.126312	-3.345695	29648.8193
HLA B*4801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.403689	1.057871	-3.345818	25333.1432
HLA B*5401	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.403804	1.057871	-3.345934	25339.8595
HLA A*6802	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.382631	1.036697	-3.345934	24134.0742
HLA B*4402	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.420923	1.074983	-3.345939	26358.6128
HLA A*3002	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.319733	0.973692	-3.346041	20880.1003
HLA B*5701	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.390271	1.044178	-3.346093	24562.4209
HLA A*0219	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.421693	1.074983	-3.346710	26405.4262
HLA A*2403	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.361074	1.014245	-3.346829	22965.4055
HLA A*2601	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.379048	1.031880	-3.347167	23935.7852
HLA A*6901	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.323527	0.976308	-3.347219	21063.328450	
HLA A*2301	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.514883	1.167504	-3.347379	32725.2637
HLA A*0301	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.359697	1.012095	-3.347602	22892.7160
HLA B*4801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.339590	0.991777	-3.347814	21856.9937
HLA A*0216	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.455925	1.108038	-3.347887	28570.982739	
HLA A*0250	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.493425	1.145357	-3.348068	31147.6516
HLA B*7301	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.533592	1.185494	-3.348098	34165.840140	
HLA A*3002	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.553126	1.204727	-3.348399	35737.6279
HLA A*6802	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.406330	1.057871	-3.348459	25487.6561
HLA B*0802	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.460551	1.112050	-3.348501	28876.9495
HLA A*2902	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.324934	0.976308	-3.348627	21131.695375	
HLA B*4001	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-3.973646	0.625007	-3.348639	9411.23011
HLA B*5301	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.424007	1.074983	-3.349024	26546.5094
HLA B*4601	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.390313	1.041264	-3.349049	24564.8128
HLA B*4402	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.393300	1.044178	-3.349122	24734.3018
HLA A*2402	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.494713	1.145357	-3.349356	31240.1295
HLA B*0802	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.405665	1.056254	-3.349411	25448.6644
HLA A*0201	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.386178	1.036697	-3.349482	24332.0313
HLA B*0702	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.407418	1.057871	-3.349547	25551.5771
HLA A*0216	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.272820	0.923260	-3.349561	18742.1933
HLA A*0219	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.457753	1.108038	-3.349715	28691.488389	
HLA A*0250	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.501733	1.151985	-3.349748	31749.222023	
HLA B*0702	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.381940	1.031880	-3.350060	24095.7193
HLA A*3001	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.230983	0.880633	-3.350350	17020.924104	
HLA A*3301	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.544968	1.194587	-3.350381	35072.628163	
HLA B*4601	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.382948	1.032480	-3.350468	24151.7066
HLA A*0211	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.454602	1.104113	-3.350490	28484.094553	
HLA A*0201	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.231239	0.880566	-3.350673	17030.963927	
HLA A*2402	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.555435	1.204727	-3.350708	35928.1840
HLA B*4402	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.403464	1.052696	-3.350768	25319.9899
HLA B*2705	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.378310	1.027504	-3.350806	23895.1599
HLA A*3101	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.103512	0.752698	-3.350814	12691.4670
HLA B*4801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.407068	1.056254	-3.350814	25530.9889
HLA A*0202	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-3.710791	0.359849	-3.350942	5137.95988
HLA B*5401	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.545612	1.194587	-3.351025	35124.655207	
HLA A*2402	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.518565	1.167504	-3.351060	33003.8647
HLA A*3101	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.308690	0.957621	-3.351069	20355.8856
HLA B*4001	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.313210	0.962074	-3.351137	20568.868957	
HLA B*1503	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.463359	1.112050	-3.351309	29064.2385
HLA B*2705	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.383251	1.031880	-3.351371	24168.5674
HLA B*1801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.464212	1.112498	-3.351714	29121.3706
HLA B*5701	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.384336	1.032480	-3.351856	24229.0491
HLA B*0702	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.463920	1.112050	-3.351870	29101.8418
HLA B*4402	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.007883	0.655774	-3.352109	10183.1722
HLA B*5101	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.352910	1.000751	-3.352158	22537.7034
HLA A*0216	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.418420	1.066259	-3.352161	26207.1835
HLA B*1502	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.314284	0.962074	-3.352210	20619.784683	
HLA B*5401	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.464717	1.112498	-3.352219	29155.2622
HLA B*7301	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.384708	1.032480	-3.352228	24249.7680
HLA B*1509	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.225074	0.872645	-3.352429	16790.9075
HLA A*0202	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.328813	0.976308	-3.352506	21321.283323	
HLA A*3101	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.410543	1.057871	-3.352672	25736.0876
HLA B*0802	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.353849	1.000751	-3.353098	22586.5268
HLA A*1101	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.354026	1.000751	-3.353274	22595.6929
HLA A*3001	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.226864	0.873495	-3.353370	16860.2685
HLA A*0203	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.411344	1.057871	-3.353473	25783.6086
HLA A*2301	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.522235	1.168653	-3.353582	33283.9372
HLA B*3901	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.412568	1.058921	-3.353647	25856.3836
HLA A*0216	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.443276	1.089590	-3.353686	27750.802816	
HLA A*0212	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.334236	0.980470	-3.353766	21589.1703
HLA B*3901	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.334224	0.980281	-3.353943	21588.586355	
HLA B*5801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.363177	1.008953	-3.354224	23076.8702
HLA B*4001	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.354991	1.000751	-3.354240	22645.9895
HLA A*2601	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.370019	1.015721	-3.354298	23443.2926
HLA A*0202	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.501846	1.147510	-3.354336	31757.4675
HLA A*3002	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.368628	1.014245	-3.354383	23368.3319
HLA A*0211	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.466524	1.112050	-3.354474	29276.8067
HLA A*0216	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.398664	1.044178	-3.354486	25041.6839
HLA B*3801	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.458636	1.104113	-3.354524	28749.909669	
HLA B*4501	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.549289	1.194587	-3.3547		
HLA A*2403	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.396208	1.041264		

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HLA A*2601	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.396274	1.041264	-3.355010	24904.2865
HLA B*5701	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.411461	1.056254	-3.355208	25790.5839
HLA B*4001	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.387142	1.031880	-3.355261	24386.0610
HLA B*3501	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.413143	1.057871	-3.355273	25890.6769
HLA A*6802	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.414217	1.058921	-3.355297	25954.7661
HLA B*2705	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.435405	1.080003	-3.355401	27252.4013
HLA A*0203	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.236037	0.880633	-3.355404	17220.147910
HLA B*1517	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.467600	1.112050	-3.355550	29349.4366
HLA A*0219	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.335913	0.980281	-3.355632	21672.723230
HLA B*3901	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.475687	1.119963	-3.355724	29901.0677
HLA B*3801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.468509	1.112498	-3.356011	29410.9478
HLA A*3101	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.261468	0.905427	-3.356041	18258.6096
HLA A*2602	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.524767	1.168653	-3.356115	33478.6115
HLA A*6901	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.365167	1.008953	-3.356214	23182.8552
HLA A*6901	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.390466	1.034236	-3.356230	24573.452458
HLA B*0803	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.468302	1.112050	-3.356252	29396.9494
HLA B*4001	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.372020	1.015721	-3.356300	23551.5974
HLA A*2601	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.384031	1.027504	-3.356527	24212.0151
HLA A*2403	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.384111	1.027504	-3.356607	24216.4690
HLA A*0216	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.266839	0.910145	-3.356694	18485.8159
HLA B*5101	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.511467	1.154646	-3.356821	32468.8572
HLA B*5701	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.398100	1.041264	-3.356836	25009.1916
HLA A*1101	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.468977	1.112050	-3.356926	29442.6277
HLA B*4403	1:218-226	9	QLAAVAPAV	1.059036	0.214314	-4.630356	1.273350	-3.357006	42692.8988
HLA A*0301	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.357811	1.000751	-3.357059	22793.4825
HLA B*1509	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.487617	1.130392	-3.357226	30733.879346
HLA B*3901	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.230008	0.872645	-3.357363	16982.7532
HLA A*0212	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.416332	1.058921	-3.357411	26081.4459
HLA A*0101	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.385025	1.027504	-3.357521	24267.4850
HLA B*3501	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.358452	1.000751	-3.357701	22827.1711
HLA A*0206	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.423965	1.066259	-3.357706	26543.9245
HLA B*5101	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.488372	1.130392	-3.357980	30787.297383
HLA B*0801	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.268175	0.910145	-3.358031	18542.8072
HLA B*3901	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.488689	1.130392	-3.358297	30809.790638
HLA B*0702	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.350104	0.991777	-3.358328	22392.5923
HLA B*0803	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.424947	1.066259	-3.358688	26604.0171
HLA B*4501	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.107139	0.748410	-3.358730	12797.9211
HLA A*2601	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.393100	1.034236	-3.358864	24722.930605
HLA A*0212	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.286210	0.927116	-3.359095	19329.033095
HLA B*1517	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.403346	1.044178	-3.359168	25313.1419
HLA B*4402	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.400733	1.041264	-3.359469	25161.3203
HLA A*6801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.245151	0.885414	-3.359736	17585.3302
HLA B*1517	1:6-14	9	PLRVQLIAK	1.039672	0.090720	-4.490157	1.130392	-3.359766	30914.140421
HLA B*5101	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.449417	1.089590	-3.359827	28146.027350
HLA A*8001	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.374182	1.014245	-3.359937	23669.1082
HLA A*6801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-3.558704	0.198739	-3.359964	3619.96062
HLA B*4801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.440080	1.080003	-3.360077	27547.3769
HLA A*0211	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.369065	1.008953	-3.360112	23391.8579
HLA A*0206	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.372312	1.012095	-3.360216	23567.4018
HLA A*0219	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.418091	1.057871	-3.360221	26187.3421
HLA B*4601	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.397291	1.036697	-3.360595	24962.6927
HLA B*5701	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.388121	1.027504	-3.360617	24441.1361
HLA B*2705	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.469496	1.108664	-3.360832	29477.8499
HLA B*4001	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.393643	1.032480	-3.361163	24753.8457
HLA B*0702	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.420300	1.058921	-3.361379	26320.8516
HLA B*0803	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.362188	1.000751	-3.361436	23024.3710
HLA A*3101	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.414149	1.052696	-3.361453	25950.6945
HLA A*2501	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.474091	1.112498	-3.361594	29791.4332
HLA A*2501	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.451207	1.089590	-3.361618	28262.294199
HLA A*2602	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.197975	0.836190	-3.361785	15775.212583
HLA B*0702	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.405975	1.044178	-3.361797	25466.8439
HLA A*2501	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.323886	0.962074	-3.361813	21080.770059
HLA B*0802	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.398516	1.036697	-3.361819	25033.1506
HLA A*6801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.481997	1.119963	-3.362034	30338.7311
HLA B*5101	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.394834	1.032480	-3.362354	24821.8341
HLA B*4402	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.208416	0.846009	-3.362407	16159.0688
HLA A*3101	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.175331	0.812772	-3.362559	14973.7605
HLA A*0219	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.336320	0.973692	-3.362628	21693.0164
HLA A*0219	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.406915	1.044178	-3.362737	25522.0127
HLA B*3801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.530268	1.167504	-3.362763	33905.2993
HLA A*0201	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.397028	1.034236	-3.362792	24947.572234
HLA B*5701	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.354637	0.991777	-3.362860	22627.4977
HLA A*8001	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.395402	1.032480	-3.362922	24854.3520
HLA B*4001	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.354886	0.991777	-3.363109	22640.4771
HLA A*2602	1:1-9	9	VAETAPLRV	1.127505	0.095337	-4.585964	1.222842	-3.363123	38544.682682
HLA A*2403	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.363936	1.000751	-3.363184	23117.2299
HLA B*0702	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.372173	1.008953	-3.363220	23559.8806
HLA A*1101	1:64-72	9	IIDVGHFSV	0.847576	0.114498	-4.325334	0.962074	-3.363260	21151.138737
HLA A*0250	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.438262	1.074983	-3.363278	27432.2702
HLA B*1801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.429590	1.066259	-3.363330	26889.9380
HLA A*6802	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.375488	1.012095	-3.363393	23740.4097
HLA A*6801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.337206	0.973692	-3.363514	21737.3051
HLA B*4601	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.397858	1.034236	-3.363621	24995.259905
HLA A*2902	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.203934	0.839978	-3.363956	15993.131729
HLA A*0203	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.344369	0.980281	-3.364088	22098.830020
HLA B*4801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.416910	1.052696	-3.364214	26116.1786
HLA A*0211	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.512083	1.147510	-3.364573	32514.9109
HLA A*0203	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.210620	0.846009	-3.364611	16241.2760
HLA B*4601	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.408825	1.044178	-3.364647	25634.5119
HLA A*2501	1:88-96	9	SCTHELIRH	1.266403	-0.158365	-4.472769	1.108038	-3.364730	29700.833473
HLA B*4601	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.345217	0.980470	-3.364748	22142.0305
HLA A*2403	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.444791	1.080003	-3.364788	27847.8050
HLA A*2603	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.002446	0.637604	-3.364842	10056.4889
HLA B*5801	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.345133	0.980281	-3.364851	22137.718669
HLA A*0201	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.376978	1.012095	-3.364882	23821.9760
HLA A*2501	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.491264	1.126312	-3.364951	30993.0118
HLA A*0206	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.355092	0.990022	-3.365070	22651.2582
HLA A*8001	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.380803	1.015721	-3.365082	24032.7099
HLA B*4501	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.374064	1.008953	-3.365112	23662.7067
HLA B*3501	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.270565	0.905427	-3.365138	18645.1082
HLA A*0211	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.474068	1.108664	-3.365404	29789.8219
HLA B*5801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.355482	0.990022	-3.365460	22671.6091
HLA A*6901	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.346150	0.980470	-3.365681	22189.6366
HLA A*8001	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.409946	1.044178	-3.365768	25700.7476
HLA B*1502	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.533421	1.167504	-3.365916	34152.3499
HLA B*4001	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.418789	1.052696	-3.366094	26229.4521
HLA A*6802	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.169232	0.803085	-3.366147	14764.937771
HLA A*0101	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.323797	0.957621	-3.366176	21076.4368
HLA A*0219	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.419050	1.052696	-3.366354	26245.2079
HLA A*3002	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.304186	0.937566	-3.366620	20145.8705
HLA B*0801	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.289922	0.923260	-3.366663	19494.9585
HLA A*3101	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.378958	1.012095	-3.366863	23930.8651
HLA A*6801	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-3.986611	0.619672	-3.366938	9696.407318
HLA B*5801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.347442	0.980470	-3.366973	22255.7588
HLA A*6802	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.324948	0.957621	-3.367327	21132.3813
HLA A*0101	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.401718	1.034236	-3.3674	
HLA A*6801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.536181	1.168653		

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HLA B*1503	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.457145	1.089590	-3.367555	28651.315138		
HLA A*0201	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.294711	0.927116	-3.367595	19711.086618		
HLA A*2402	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.480226	1.112498	-3.367728	30215.2298	
HLA B*2705	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.457387	1.089590	-3.367797	28667.284632		
HLA A*2902	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.404511	1.036697	-3.367815	25381.1560	
HLA B*1502	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.519881	1.151985	-3.367895	33104.002799		
HLA A*6802	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.348594	0.980470	-3.368124	22314.8337	
HLA B*0802	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.476194	1.108038	-3.368156	29936.028658		
HLA B*4402	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.448172	1.080003	-3.368168	28065.4414	
HLA A*0250	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.377784	1.008953	-3.368831	23866.2209	
HLA B*4001	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.383159	1.014245	-3.368914	24163.4687	
HLA B*3901	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.477449	1.108038	-3.369411	30022.635315		
HLA A*2403	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.406149	1.036697	-3.369452	25477.0412	
HLA B*1801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.427355	1.057871	-3.369485	26751.9498	
HLA B*7301	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.413693	1.044178	-3.369515	25923.4731	
HLA A*3201	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.428453	1.058921	-3.369532	26819.6218	
HLA B*0702	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.343272	0.973692	-3.369580	22043.0696	
HLA B*4002	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.118065	0.748410	-3.369655	13123.9490	
HLA A*2602	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.370439	1.000751	-3.369688	23466.0054	
HLA B*0801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.182036	0.812136	-3.369900	15206.746778		
HLA A*1101	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.411240	1.041264	-3.369976	25777.4719	
HLA B*1503	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.173146	0.803085	-3.370061	14898.613812		
HLA A*0202	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.474176	1.104113	-3.370063	29797.235838		
HLA B*1517	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.436486	1.066259	-3.370226	27320.3047	
HLA A*2501	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.478910	1.108664	-3.370246	30123.8301	
HLA B*3801	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.242893	0.872645	-3.370248	17494.1431	
HLA B*0802	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.479232	1.108664	-3.370568	30146.1648	
HLA B*1503	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.402470	1.031880	-3.370589	25262.1143	
HLA A*0301	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.332800	0.962074	-3.370727	21517.926377		
HLA B*2705	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.297878	0.927116	-3.370762	19855.355724		
HLA A*3201	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.556448	1.185494	-3.370953	36012.054159		
HLA B*0801	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.405249	1.034236	-3.371013	25424.307747		
HLA A*3201	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.575897	1.204727	-3.371170	37661.4408	
HLA B*2705	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.430180	1.058921	-3.371259	26926.4762	
HLA A*1101	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.380291	1.008953	-3.371338	24004.3835	
HLA A*8001	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.408205	1.036697	-3.371508	25597.9265	
HLA B*4601	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.404387	1.031880	-3.372507	25373.8796	
HLA B*2705	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.125353	0.752698	-3.372655	13346.0466	
HLA A*0101	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.384853	1.012095	-3.372758	24257.9031	
HLA B*1503	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-3.671700	0.298936	-3.372764	4695.696054		
HLA B*0702	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.409732	1.036697	-3.373035	25688.0982	
HLA A*2403	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.310678	0.937566	-3.373112	20449.2632	
HLA B*1801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.499459	1.126312	-3.373146	31583.3931	
HLA A*1101	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.388963	1.015721	-3.373242	24488.5181	
HLA B*0802	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.432165	1.058921	-3.373244	27049.8484	
HLA B*4403	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.567909	1.194587	-3.373322	36975.042551		
HLA A*2501	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.405865	1.032480	-3.373385	25460.3694	
HLA A*3201	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.518757	1.145357	-3.373401	33018.5088	
HLA A*2403	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.426098	1.052696	-3.373403	26674.6338	
HLA A*2601	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.385647	1.012095	-3.373552	24302.3003	
HLA A*6802	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.365717	0.991777	-3.373940	23212.2212	
HLA A*8001	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.426641	1.052696	-3.373946	26707.9895	
HLA A*2301	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.528729	1.154646	-3.374083	33785.3693	
HLA B*4001	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.401629	1.027504	-3.374124	25213.2355	
HLA A*0201	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.188465	0.814245	-3.374219	15433.5028	
HLA B*5801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.350610	0.976308	-3.374302	22418.652930		
HLA B*5401	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.301472	0.927121	-3.374351	20020.3831	
HLA A*2902	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.418538	1.044178	-3.374360	26214.2733	
HLA B*1517	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.433297	1.058921	-3.374377	27120.4748	
HLA B*5701	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.390346	1.015721	-3.374625	24566.6734	
HLA B*3901	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.449640	1.074983	-3.374657	28160.4964	
HLA A*6802	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.418930	1.044178	-3.374752	26237.9673	
HLA A*0212	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.364869	0.990022	-3.374847	23166.9327	
HLA B*3501	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.441471	1.066259	-3.375212	27635.7431	
HLA B*5101	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.337704	0.962074	-3.375630	21762.249869		
HLA B*2705	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.164993	0.789295	-3.375699	14621.541120		
HLA A*2403	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.407606	1.031880	-3.375725	25562.6380	
HLA A*2501	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.455747	1.080003	-3.375743	28559.2381	
HLA A*2301	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.434876	1.058921	-3.375956	27219.2492	
HLA A*6801	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.501510	1.125530	-3.375980	31732.909037		
HLA B*5101	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.388330	1.012095	-3.376235	24452.9069	
HLA A*0101	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.392007	1.015721	-3.376287	24660.8158	
HLA B*0702	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.410716	1.034236	-3.376480	25746.392658		
HLA B*1509	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.434615	1.057871	-3.376745	27202.9090	
HLA B*4601	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.385713	1.008953	-3.376760	24305.9818	
HLA B*4801	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.411005	1.034236	-3.376769	25763.530430		
HLA B*0802	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.466387	1.089590	-3.376798	29267.621876		
HLA A*0212	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.282244	0.905427	-3.376817	19153.3259	
HLA A*1101	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.404401	1.027504	-3.376897	25374.7032	
HLA B*1502	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.456912	1.080003	-3.376909	28635.9742	
HLA B*5101	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.481067	1.104113	-3.376954	30273.805599		
HLA B*0801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.309546	-0.067515	-3.377061	2039.60308	
HLA B*1501	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.304191	0.927116	-3.377075	20146.088544		
HLA A*2301	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.507527	1.130392	-3.377135	32175.619535		
HLA B*4402	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.409170	1.031880	-3.377290	25654.9059	
HLA A*0216	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.262847	0.885414	-3.377432	18316.6839	
HLA B*5301	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.545149	1.167504	-3.377645	35087.2411	
HLA B*4001	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.351338	0.973692	-3.377646	22456.2820	
HLA B*3801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.489734	1.112050	-3.377684	30884.0515	
HLA A*6901	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.301054	0.923260	-3.377795	20001.1135	
HLA B*1502	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.508286	1.130392	-3.377894	32231.892176		
HLA A*3101	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.046635	0.668648	-3.377988	11133.596905		
HLA B*4601	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.405545	1.027504	-3.378041	25441.6440	
HLA A*2403	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.387071	1.008953	-3.378118	24382.1035	
HLA A*3001	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.163400	0.785066	-3.378334	14568.008934		
HLA A*0301	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.368376	0.990022	-3.378354	23354.8089	
HLA B*5401	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.533211	1.154646	-3.378566	34135.9102	
HLA B*5301	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.504912	1.126312	-3.378599	31982.4659	
HLA A*8001	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.379412	1.000751	-3.378660	23955.8646	
HLA B*4002	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.601591	1.222842	-3.378749	39956.818366		
HLA B*3501	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.275085	0.896310	-3.378776	18840.191732		
HLA A*2402	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.406396	1.027504	-3.378891	25491.5172	
HLA A*0212	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.431676	1.052696	-3.378980	27019.4275	
HLA B*5301	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.583763	1.204727	-3.379036	38349.7915	
HLA A*2601	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.388044	1.008953	-3.379091	24436.7732	
HLA A*3301	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.341212	0.962074	-3.379138	21938.734559		
HLA A*0212	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.388143	1.008953	-3.379190	24442.3262	
HLA A*0250	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.533977	1.154646	-3.379332	34196.1662	
HLA A*0101	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.359775	0.980281	-3.379493	22896.803370		
HLA B*4601	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.391653	1.012095	-3.379557	24640.6787	
HLA A*2501	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.454609	1.074983	-3.379626	28484.5568	
HLA B*0702	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.407270	1.027504	-3.379765	25542.8700	
HLA A*3002	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.290040	0.910145	-3.379895	19500.2325	
HLA B*1801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.412551	1.032480	-3.380071	25855.4044	
HLA A*3101	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.360397	0.980281	-3.380116	22929.652240		
HLA B*1501	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.252892	0.872645			
HLA A*0203	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.115189	0.734934	-3.3802			

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HLA A*0301	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.360569	0.980281	-3.380288	22938.709450
HLA B*1503	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.360759	0.980470	-3.380290	22948.7634
HLA B*4002	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.566020	1.185494	-3.380525	36814.566974
HLA B*0803	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.338237	0.957621	-3.380616	21788.9913
HLA A*3002	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.421914	1.041264	-3.380650	26418.8575
HLA A*2403	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.372735	0.991777	-3.380958	23590.3624
HLA B*5701	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.415225	1.034236	-3.380989	26015.073073
HLA B*5101	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.456106	1.074983	-3.381123	28582.8867
HLA A*1101	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.440214	1.058921	-3.381294	27555.8728
HLA B*5801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.339231	0.957621	-3.381610	21838.9095
HLA B*2705	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.414118	1.032480	-3.381638	25948.8695
HLA A*3201	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.456679	1.074983	-3.381696	28620.6414
HLA B*5401	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.084960	0.703256	-3.381704	12160.748109
HLA A*0219	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.409246	1.027504	-3.381741	25659.3476
HLA A*0202	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.471436	1.089590	-3.381847	29609.868509
HLA A*2301	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.534154	1.152145	-3.382009	34210.0438
HLA B*3501	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.426225	1.044178	-3.382048	26682.4275
HLA B*1502	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.471758	1.089590	-3.382169	29631.822140
HLA B*0801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.398003	1.015721	-3.382282	25003.6450
HLA A*6802	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.409852	1.027504	-3.382348	25695.1867
HLA A*0301	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.362829	0.980470	-3.382360	23058.4008
HLA B*0803	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.426667	1.044178	-3.382489	26709.5789
HLA A*2402	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.344663	0.962074	-3.382589	22113.779102
HLA B*5401	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.278931	0.896310	-3.382622	19007.781244
HLA B*4402	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.439011	1.056254	-3.382758	27479.6524
HLA A*0250	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.268197	0.885414	-3.382782	18543.7100
HLA A*0101	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.374591	0.991777	-3.382814	23691.3990
HLA B*4002	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.298042	0.915034	-3.383008	19862.8762
HLA A*6901	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.320581	0.937566	-3.383015	20920.9184
HLA A*2603	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.568545	1.185494	-3.383051	37029.290676
HLA B*4402	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.395278	1.012095	-3.383183	24847.2267
HLA A*0201	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.145234	0.762047	-3.383187	13971.2087
HLA A*8001	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.363854	0.980281	-3.383572	23112.853180
HLA B*5301	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.578293	1.194587	-3.383706	37869.834414
HLA B*0702	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.198252	0.814245	-3.384007	15785.2861
HLA A*3101	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.195922	0.811904	-3.384017	15700.7996
HLA B*4402	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.311267	0.927116	-3.384152	20477.049834
HLA B*0803	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.425793	1.041264	-3.384529	26655.8805
HLA B*1501	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.365118	0.980470	-3.384648	23180.2216
HLA A*6802	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.294908	0.910145	-3.384763	19720.0459
HLA A*0203	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.308159	0.923260	-3.384900	20331.0130
HLA B*4601	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.375037	0.990022	-3.385015	23715.7634
HLA B*4001	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.394026	1.008953	-3.385073	24775.6836
HLA A*2403	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.365766	0.980281	-3.385485	23214.858524
HLA B*0803	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.494288	1.108664	-3.385624	31209.5545
HLA A*2601	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.221921	0.836190	-3.385731	16669.446193
HLA B*4001	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.398116	1.012095	-3.386021	25010.1387
HLA A*1101	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.452286	1.066259	-3.386026	28332.5606
HLA B*5701	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.422725	1.036697	-3.386028	26468.2121
HLA A*0101	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.323605	0.937566	-3.386039	21067.0891
HLA A*0219	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.445024	1.058921	-3.386103	27862.7237
HLA B*4402	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.377892	0.991777	-3.386115	23872.1609
HLA B*1517	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.494788	1.108664	-3.386124	31245.5382
HLA A*0211	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.148288	0.762047	-3.386241	14069.8125
HLA A*0203	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.420643	1.034236	-3.386407	26341.649243
HLA B*4403	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.134835	0.748410	-3.386425	13640.6529
HLA B*7301	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.581024	1.194587	-3.386436	38108.645050
HLA B*0802	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.461444	1.074983	-3.386461	28936.3746
HLA A*0201	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.376597	0.990022	-3.386575	23801.1075
HLA B*3801	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.516977	1.130392	-3.386585	32883.387222
HLA B*3801	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.555308	1.168653	-3.386656	35917.6897
HLA B*4001	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.376764	0.990022	-3.386742	23810.2513
HLA A*2301	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.534356	1.147510	-3.386846	34225.9638
HLA B*5701	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.418813	1.031880	-3.386932	26230.8711
HLA A*0219	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.377229	0.990022	-3.387207	23835.7695
HLA A*2602	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.592003	1.204727	-3.387276	39084.3281
HLA A*2902	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.200428	0.812772	-3.387656	15864.5618
HLA B*4402	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.361530	0.973692	-3.387838	22989.5208
HLA B*5701	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.361676	0.973692	-3.387984	22997.2331
HLA A*6901	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.345889	0.957621	-3.388268	22176.3158
HLA B*3801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.378655	0.990022	-3.388633	23914.1702
HLA A*2403	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.421141	1.032480	-3.388661	26371.8777
HLA A*2601	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.026773	0.638108	-3.388665	10635.8682
HLA B*5301	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.536191	1.147510	-3.388681	34370.8786
HLA B*3901	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.445118	1.056254	-3.388864	27868.7537
HLA A*3002	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.534353	1.145357	-3.388996	34225.7786
HLA A*0301	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.299428	0.910145	-3.389284	19926.3765
HLA B*2705	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.398335	1.008953	-3.389382	25022.7249
HLA A*0219	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.421273	1.031880	-3.389392	26379.8683
HLA A*6801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.464463	1.074983	-3.389480	29138.2327
HLA A*2301	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.369979	0.980470	-3.389509	23441.1367
HLA A*0201	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.369852	0.980281	-3.389570	23434.289769
HLA A*6802	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.442719	1.052696	-3.390023	27715.2450
HLA B*4402	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.422548	1.032480	-3.390068	26457.4750
HLA B*0803	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.510069	1.119963	-3.390106	32364.5118
HLA A*0301	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.366490	0.976308	-3.390182	23253.572430
HLA B*4403	1:70-78 9	FSVLEHASV	1.102668	0.135344	-4.628196	1.238012	-3.390184	42481.169825
HLA B*1509	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.510431	1.119963	-3.390468	32391.4866
HLA B*0802	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.431855	1.041264	-3.390591	27030.5389
HLA B*3501	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.427384	1.036697	-3.390687	26753.6865
HLA A*1101	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.404995	1.014245	-3.390750	25409.4574
HLA A*6801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.432054	1.041264	-3.390790	27042.9715
HLA B*3501	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.352975	0.962074	-3.390902	22541.117610
HLA B*5301	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.503093	1.112050	-3.391043	31848.8268
HLA A*2403	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.425340	1.034236	-3.391103	26628.063445
HLA B*1502	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.503613	1.112498	-3.391115	31886.9276
HLA A*8001	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.448989	1.057871	-3.391119	28118.3284
HLA A*0202	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.521530	1.130392	-3.391138	33229.962296
HLA B*5101	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.432740	1.041264	-3.391476	27085.7247
HLA A*2601	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.231455	0.839978	-3.391478	17039.442514
HLA B*5101	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.457880	1.066259	-3.391621	28699.8713
HLA A*0101	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.381672	0.990022	-3.391650	24080.8634
HLA A*2601	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.381674	0.990022	-3.391652	24080.9937
HLA A*0216	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.400820	1.008953	-3.391868	25166.3572
HLA A*2602	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.297457	0.905427	-3.392030	19836.1376
HLA B*4801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.420032	1.027504	-3.392528	26304.6238
HLA B*5101	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.445294	1.052696	-3.392598	27880.0635
HLA B*1801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.501559	1.108664	-3.392895	31736.5143
HLA B*3801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.501625	1.108664	-3.392961	31741.3220
HLA A*8001	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.384832	0.991777	-3.393055	24256.7220
HLA B*1501	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.316587	0.923260	-3.393327	20729.3947
HLA A*8001	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.425222	1.031880	-3.393342	26620.8616
HLA B*5401	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.446090	1.052696	-3.393395	27931.2411
HLA B*7301	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.616303	1.222842	-3.393462	41333.613534
HLA B*4402	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.430607	1.036697	-3.393911	26953.0016
HLA B*5301	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.506636	1.112498		
HLA A*0216	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.446849	1.052696		

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HLA B*1502	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.520903	1.126312	-3.394590	33181.9982
HLA B*3901	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.275271	0.880633	-3.394638	18848.245397	
HLA A*6901	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.234862	0.839978	-3.394884	17173.631305	
HLA B*0803	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.454053	1.058921	-3.395132	28448.0589
HLA B*2705	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.375472	0.980281	-3.395190	23739.510727	
HLA B*1509	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.275875	0.880566	-3.395309	18874.469121	
HLA B*3501	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.407469	1.012095	-3.395374	25554.6183
HLA A*3301	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.618848	1.222842	-3.396006	41576.494267	
HLA A*0202	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.405014	1.008953	-3.396061	25410.5571
HLA B*1509	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.476455	1.080003	-3.396452	29954.0105
HLA B*4801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.397348	1.000751	-3.396596	24965.9340
HLA B*5301	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.582182	1.185494	-3.396687	38210.419338	
HLA A*2603	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.601457	1.204727	-3.396730	39944.4990
HLA B*1801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.508843	1.112050	-3.396793	32273.2445
HLA B*1503	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.405839	1.008953	-3.396886	25458.8544
HLA B*0803	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.449650	1.052696	-3.396954	28161.1058
HLA B*1502	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.551606	1.154646	-3.396960	35612.7577
HLA B*4501	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.530517	1.133400	-3.397116	33924.7478
HLA A*1101	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.455216	1.057871	-3.397345	28524.3419
HLA B*1503	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.066075	0.668648	-3.397428	11643.274392	
HLA B*7301	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.565106	1.167504	-3.397601	36737.1741
HLA B*1801	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.434618	1.036697	-3.397921	27203.0562
HLA A*3301	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.602672	1.204727	-3.397945	40056.3766
HLA B*1501	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.388018	0.990022	-3.397996	24435.3190
HLA B*3501	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.478271	1.080003	-3.398268	30079.5358
HLA B*4403	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.524584	1.126312	-3.398272	33464.4875
HLA B*0802	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.464555	1.066259	-3.398295	29144.3810
HLA A*0202	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.553069	1.154646	-3.398424	35732.9881
HLA B*1517	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.440172	1.041264	-3.398908	27553.1896
HLA A*2301	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.440198	1.041264	-3.398934	27554.8293
HLA B*7301	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.524558	1.125530	-3.399029	33462.496185	
HLA A*0202	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.511192	1.112050	-3.399142	32448.3123
HLA B*5101	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.507198	1.108038	-3.399160	32151.259446	
HLA B*4801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.431702	1.032480	-3.399222	27021.0355
HLA B*1501	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.314284	0.915034	-3.399250	20619.7846
HLA B*4801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.431345	1.031880	-3.399465	26998.8251
HLA A*0301	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.211457	0.811904	-3.399552	16272.5856
HLA A*2602	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.585199	1.185494	-3.399704	38476.764269	
HLA A*2902	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.457683	1.057871	-3.399812	28686.8322
HLA A*0212	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.434160	1.034236	-3.399923	27174.374091	
HLA A*2602	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.434185	1.034236	-3.399949	27175.991253	
HLA B*3801	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.547461	1.147510	-3.399951	35274.5201
HLA B*4501	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.068702	0.668648	-3.400054	11713.909290	
HLA A*8001	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.434373	1.034236	-3.400137	27187.755326	
HLA A*0216	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.357982	0.957621	-3.400361	22802.4859
HLA B*1801	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.362634	0.962074	-3.400560	23048.049490	
HLA B*7301	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.552940	1.152145	-3.400796	35722.3575
HLA B*4402	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.416689	1.015721	-3.400968	26102.9011
HLA B*4002	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.553140	1.152145	-3.400995	35738.7879
HLA B*4601	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.297361	0.896310	-3.401051	19831.738421	
HLA A*1101	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.213327	0.811904	-3.401422	16342.8108
HLA A*0201	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.377774	0.976308	-3.401467	23865.704511	
HLA A*2601	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.375213	0.973692	-3.401522	23725.3878
HLA A*2402	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.532084	1.130392	-3.401692	34047.382921	
HLA A*2603	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.513941	1.112050	-3.401891	32654.3476
HLA A*3301	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.282500	0.880566	-3.401934	19164.623550	
HLA B*0802	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.411076	1.008953	-3.402123	25767.7121
HLA A*3001	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.282944	0.880566	-3.402378	19184.228806	
HLA B*5701	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.416708	1.014245	-3.402462	26104.0309
HLA B*5401	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.138280	0.735649	-3.402631	13749.2657
HLA A*3101	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.392762	0.990022	-3.402740	24703.6783
HLA A*0206	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-3.438603	0.035827	-3.402776	2745.382568	
HLA B*3801	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.522904	1.119963	-3.402941	33335.2945
HLA A*0101	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.383484	0.980470	-3.403014	24181.5150
HLA B*4801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.419095	1.015721	-3.403374	26247.9053
HLA A*2603	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.626298	1.222842	-3.403456	42295.881801	
HLA A*0250	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.551044	1.147510	-3.403534	35566.7415
HLA A*0212	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.415657	1.012095	-3.403562	26040.9818
HLA A*3201	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.493160	1.089590	-3.403570	31128.616361	
HLA A*2602	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.529236	1.125530	-3.403707	33824.871806	
HLA A*0211	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-3.977063	0.573275	-3.403787	9485.55056
HLA B*1501	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.384078	0.980281	-3.403796	24214.635020	
HLA A*2402	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.572464	1.168653	-3.403812	37364.9438
HLA B*4402	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.431343	1.027504	-3.403838	26998.6791
HLA A*2301	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.436335	1.032480	-3.403855	27310.8472
HLA A*1101	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.216752	0.812772	-3.403981	16472.2264
HLA A*0216	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.463117	1.058921	-3.404196	29048.0479
HLA B*0803	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.493811	1.089590	-3.404221	31175.298785	
HLA B*4402	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.384503	0.980281	-3.404222	24238.357359	
HLA B*4601	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.366464	0.962074	-3.404390	23252.188680	
HLA A*6801	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.042514	0.638108	-3.404407	11028.4504
HLA A*0206	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.534833	1.130392	-3.404441	34263.571694	
HLA B*5701	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.413435	1.008953	-3.404482	25908.0509
HLA B*4001	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.362129	0.957621	-3.404508	23021.2572
HLA A*6801	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.590048	1.185494	-3.404553	38908.803839	
HLA A*3201	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.559211	1.154646	-3.404565	36241.8942
HLA A*2601	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.396394	0.991777	-3.404617	24911.1586
HLA B*4001	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.384907	0.980281	-3.404626	24260.921670	
HLA A*6801	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.073565	0.668648	-3.404918	11845.824403	
HLA B*0802	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.342558	0.937566	-3.404992	22006.8472
HLA A*1101	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.485033	1.080003	-3.405030	30551.5288
HLA A*2602	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.517176	1.112050	-3.405126	32898.5118
HLA B*5301	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.557409	1.152145	-3.405264	36091.8242
HLA B*3901	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.437945	1.032480	-3.405465	27412.2428
HLA A*0212	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.433008	1.027504	-3.405504	27102.4344
HLA A*3101	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.332678	0.927116	-3.405563	21511.873930	
HLA B*1517	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.286342	0.880566	-3.405776	19334.889786	
HLA B*3901	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.495488	1.089590	-3.405898	31295.951261	
HLA A*6901	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.025692	0.619672	-3.406020	10609.433236	
HLA B*3801	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.447345	1.041264	-3.406081	28012.0478
HLA A*3201	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.532467	1.126312	-3.406154	34077.4195
HLA B*5401	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.539658	1.133400	-3.406258	34646.4286
HLA B*3501	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.438269	1.031880	-3.406388	27432.7154
HLA B*2705	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.364011	0.957621	-3.406390	23121.2322
HLA B*1502	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.443111	1.036697	-3.406415	27740.2957
HLA A*8001	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.396540	0.990022	-3.406518	24919.5159
HLA A*2902	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.459454	1.052696	-3.406758	28804.0864
HLA A*0219	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.418907	1.012095	-3.406811	26236.5479
HLA B*4501	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.629728	1.222842	-3.406887	42631.276009	
HLA B*0702	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.279777	0.872645	-3.407132	19044.8361
HLA A*0250	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.473525	1.066259	-3.407266	29752.6169
HLA A*1101	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.496874	1.089590	-3.407285	31396.002349	
HLA B*0801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.381080	0.973692	-3.407388	24048.0569
HLA A*2403	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.334640	0.927116	-3.407524	21609.268415	
HLA A*3001	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.099663	0.692096	-3.407567	12579.499726	
HLA A*2301	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.519634	1.112050		
HLA A*1101	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.463939	1.056254		

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HLA B*1801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.421949	1.014245	-3.407704	26421.0015
HLA B*5301	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.541453	1.133400	-3.408053	34789.9241
HLA A*3001	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.219966	0.811904	-3.408062	16594.5851
HLA B*5401	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.516829	1.108664	-3.408165	32872.1817
HLA B*5401	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.538608	1.130392	-3.408217	34562.747214	
HLA B*4402	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-3.902006	0.493735	-3.408271	7980.05520
HLA B*1517	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.422795	1.014245	-3.408550	26472.5081
HLA A*6801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-3.855618	0.446772	-3.408845	7171.62650
HLA A*3002	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.198234	0.789295	-3.408939	15784.603014	
HLA B*4801	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.281732	0.872645	-3.409087	19130.7506
HLA B*4402	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.423608	1.014245	-3.409363	26522.1063
HLA B*5701	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.371466	0.962074	-3.409392	23521.547557	
HLA A*2902	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.314874	0.905427	-3.409447	20647.8029
HLA A*6801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.389935	0.980470	-3.409466	24543.4264
HLA A*2603	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.578253	1.168653	-3.409601	37866.3517
HLA A*2402	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.518325	1.108664	-3.409661	32985.6579
HLA A*6801	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.632517	1.222842	-3.409675	42905.915245	
HLA B*1517	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.441741	1.031880	-3.409861	27652.9416
HLA A*0203	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.399939	0.990022	-3.409917	25115.3538
HLA A*0301	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.315377	0.905427	-3.409950	20671.7210
HLA A*2403	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.422048	1.012095	-3.409953	26427.0054
HLA A*6802	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.444232	1.034236	-3.409995	27811.972542	
HLA A*2601	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.390478	0.980470	-3.410008	24574.1171
HLA B*5101	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.490035	1.080003	-3.410032	30905.4450
HLA A*0201	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.367751	0.957621	-3.410130	23321.2248
HLA A*8001	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.422386	1.012095	-3.410291	26447.6007
HLA B*5401	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.514500	1.104113	-3.410388	32696.418942	
HLA A*0216	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.291111	0.880633	-3.410478	19548.397227	
HLA A*0219	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.315952	0.905427	-3.410525	20699.1380
HLA B*4402	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.419647	1.008953	-3.410694	26281.2961
HLA A*2402	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.562888	1.152145	-3.410743	36550.0380
HLA B*1509	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.455002	1.044178	-3.410824	28510.3028
HLA B*2705	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.426557	1.015721	-3.410836	26702.7885
HLA B*0802	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.468732	1.057871	-3.410862	29426.0671
HLA B*1801	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.518962	1.108038	-3.410924	33034.053013	
HLA A*0250	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.257140	0.846009	-3.411131	18077.5658
HLA B*1509	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.401290	0.990022	-3.411268	25193.6014
HLA B*4501	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.578806	1.167504	-3.411301	37914.5227
HLA B*3801	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.537835	1.126312	-3.411523	34501.2852
HLA A*2603	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.563562	1.151985	-3.411577	36606.831079	
HLA A*3002	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.542017	1.130392	-3.411626	34835.123754	
HLA B*1801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.401704	0.990022	-3.411682	25217.6007
HLA B*0802	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.464397	1.052696	-3.411702	29133.8192
HLA B*3801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.468046	1.056254	-3.411793	29379.6198
HLA B*4601	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.403731	0.991777	-3.411955	25335.6102
HLA A*2902	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.284765	0.872645	-3.412120	19264.8306
HLA A*2301	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.537722	1.125530	-3.412193	34492.327352	
HLA B*4001	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.392759	0.980470	-3.412290	24703.5447
HLA B*1801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.468582	1.056254	-3.412328	29415.8806
HLA A*6802	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.295711	0.883157	-3.412554	19756.5654
HLA A*2602	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.542960	1.130392	-3.412568	34910.775900	
HLA B*0802	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.374847	0.962074	-3.412773	23705.373415	
HLA B*3901	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.422022	1.008953	-3.413069	26425.4328
HLA B*3901	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.404939	0.991777	-3.413162	25406.1585
HLA B*3801	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.521445	1.108038	-3.413407	33223.491192	
HLA A*0250	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.503089	1.089590	-3.413499	31848.482251	
HLA B*3801	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.539299	1.125530	-3.413769	34617.763259	
HLA B*1517	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.466620	1.052696	-3.413924	29283.3011
HLA A*2602	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.568646	1.154646	-3.414001	37037.9056
HLA A*0219	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.324180	0.910145	-3.414036	21095.0304
HLA B*3501	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.441694	1.027504	-3.414190	27649.9498
HLA A*0219	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.423448	1.008953	-3.414496	26512.3514
HLA A*0211	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.522597	1.108038	-3.414558	33311.678374	
HLA A*2902	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.449098	1.034236	-3.414861	28125.326670	
HLA B*0803	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.523022	1.108038	-3.414984	33344.312809	
HLA A*0212	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.395334	0.980281	-3.415053	24850.453010	
HLA A*0216	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.473187	1.057871	-3.415316	29729.4479
HLA B*4403	1:1-9 9	VAETAPLRV	1.127505	0.095337	-4.638189	1.222842	-3.415347	43469.918638	
HLA A*2601	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.395875	0.980281	-3.415593	24881.393040	
HLA A*0216	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.427722	1.012095	-3.415627	26774.5364
HLA A*1101	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.407446	0.991777	-3.415669	25553.2359
HLA A*3301	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.396208	0.980470	-3.415739	24900.5143
HLA A*2402	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.541409	1.125530	-3.415879	34786.348307	
HLA B*1517	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.450136	1.034236	-3.415900	28192.659605	
HLA A*6801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.228194	0.812136	-3.416058	16911.973775	
HLA B*3501	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.468786	1.052696	-3.416091	29429.7287
HLA B*3901	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.496315	1.080003	-3.416312	31355.6043
HLA A*2902	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.343491	0.927116	-3.416375	22054.162693	
HLA B*0803	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.491456	1.074983	-3.416473	31006.7637
HLA A*3002	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-3.976344	0.559811	-3.416533	9469.86093
HLA A*2601	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.378721	0.962074	-3.416647	23917.792930	
HLA A*0206	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.474540	1.057871	-3.416669	29822.2322
HLA A*2301	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.542995	1.126312	-3.416682	34913.6089
HLA A*2402	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.571353	1.154646	-3.416707	37269.4537
HLA B*5101	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.474860	1.057871	-3.416989	29844.1819
HLA A*2301	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.473318	1.056254	-3.417065	29738.4559
HLA A*6901	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.643149	0.225691	-3.417458	4396.924781	
HLA B*0802	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.375108	0.957621	-3.417487	23719.6127
HLA B*0803	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.475419	1.057871	-3.417548	29882.6326
HLA A*2501	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.433349	1.015721	-3.417628	27123.7028
HLA A*3201	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.473927	1.056254	-3.417673	29780.1535
HLA B*1509	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.332946	0.915034	-3.417912	21525.1449
HLA B*2705	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.391749	0.973692	-3.418057	24646.1448
HLA A*2403	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.408207	0.990022	-3.418185	25598.0650
HLA A*0250	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.527314	1.108664	-3.418650	33675.5176
HLA A*3001	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.171487	0.752698	-3.418789	14841.8188
HLA A*0203	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.166116	0.747233	-3.418883	14659.4002
HLA B*3801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.498902	1.080003	-3.418899	31542.9246
HLA B*3801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.463279	1.044178	-3.419101	29058.8930
HLA A*3201	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.399636	0.980470	-3.419167	25097.8325
HLA B*1509	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.453444	1.034236	-3.419208	28408.226545	
HLA A*2601	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.395550	0.976308	-3.419243	24862.824402	
HLA B*0702	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.399763	0.980470	-3.419294	25105.1655
HLA A*2402	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.566814	1.147510	-3.419304	36881.9455
HLA A*0206	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.472014	1.052696	-3.419319	29649.3005
HLA B*3901	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.420077	1.000751	-3.419325	26307.3278
HLA A*3001	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.262156	0.842742	-3.419414	18287.574241	
HLA A*0211	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.377044	0.957621	-3.419423	23825.5848
HLA B*5701	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.399916	0.980470	-3.419446	25113.9951
HLA A*0101	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.395835	0.976308	-3.419527	24879.104850	
HLA B*1502	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.553083	1.133400	-3.419683	35734.1480
HLA A*6802	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.181815	0.762047	-3.419768	15199.0156
HLA A*3301	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.605263	1.185494	-3.419769	40296.111960	
HLA A*3002	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.325299	0.905427	-3.419872	21149.4224
HLA A*2403	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.325463	0.905427	-3.420036	21157.4336
HLA A*3101	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.396387	0.976308	-3.4200		
HLA B*1503	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-3.654173	0.234045		

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HLA B*3501	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.429082	1.008953	-3.420130	26858.5345
HLA B*5801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.347471	0.927116	-3.420355	22257.203756	
HLA B*1517	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.478351	1.057871	-3.420480	30085.0690
HLA B*1503	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.232623	0.812136	-3.420487	17085.318363	
HLA A*2301	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.529159	1.108664	-3.420495	33818.8337
HLA B*5701	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.401206	0.980281	-3.420924	25188.695311	
HLA A*2501	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.448590	1.027504	-3.421086	28092.4804
HLA A*6802	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.348284	0.927116	-3.421168	22298.904288	
HLA B*1509	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.547485	1.126312	-3.421172	35276.4285
HLA A*2602	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.568745	1.147510	-3.421235	37046.3221
HLA B*1509	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.529276	1.108038	-3.421238	33827.982759	
HLA A*0216	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.156300	0.734934	-3.421367	14331.777444	
HLA B*0801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.326805	0.905427	-3.421378	21222.8904
HLA B*3901	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.458270	1.036697	-3.421573	28725.6566
HLA A*2602	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.541590	1.119963	-3.421627	34800.8419
HLA B*4601	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.402040	0.980281	-3.421758	25237.116951	
HLA B*2705	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.434084	1.012095	-3.421989	27169.6701
HLA A*3001	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.234230	0.812136	-3.422094	17148.657380	
HLA B*1509	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.478527	1.056254	-3.422274	30097.2783
HLA A*2602	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.380147	0.957621	-3.422526	23996.4633
HLA A*2902	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.303124	0.880566	-3.422558	20096.668659	
HLA B*1501	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.398901	0.976308	-3.422593	25055.370452	
HLA A*3001	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.266637	0.843953	-3.422684	18477.2174
HLA A*0216	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.403135	0.980281	-3.422853	25300.820198	
HLA A*3002	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.403964	0.980470	-3.423494	25349.1831
HLA A*2501	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.464825	1.041264	-3.423561	29162.5185
HLA B*1801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.424654	1.000751	-3.423902	26586.0326
HLA B*5701	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.413930	0.990022	-3.423908	25937.6415
HLA A*2402	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.504386	1.080003	-3.424382	31943.7322
HLA B*4801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.436554	1.012095	-3.424458	27324.5913
HLA B*0802	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.457006	1.032480	-3.424526	28642.1715
HLA A*2602	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.504708	1.080003	-3.424704	31967.4162
HLA B*4801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.382335	0.957621	-3.424714	24117.6289
HLA B*0801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.362308	0.937566	-3.424742	23030.7244
HLA A*0211	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.305495	0.880633	-3.424862	20206.667842	
HLA B*5801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.330402	0.905427	-3.424975	21399.3998
HLA B*0802	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.452490	1.027504	-3.424986	28345.8987
HLA B*0801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.405644	0.980470	-3.425174	25447.4254
HLA A*2602	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.439596	1.014245	-3.425351	27516.6942
HLA B*0801	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.298247	0.872645	-3.425601	19872.2270
HLA A*3201	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.538270	1.112498	-3.425772	34535.8324
HLA A*0216	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.402082	0.976308	-3.425774	25239.574611	
HLA A*2603	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.620575	1.194587	-3.425988	41742.142685	
HLA A*0211	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.470175	1.044178	-3.425997	29523.9733
HLA A*2501	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.460500	1.034236	-3.426263	28873.512934	
HLA B*0802	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.460575	1.034236	-3.426338	28878.511846	
HLA B*3901	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.341390	0.915034	-3.426356	21947.7565
HLA A*3002	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.535037	1.108664	-3.426373	34279.7019
HLA B*1501	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.046086	0.619672	-3.426413	11119.511645	
HLA B*0802	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.470631	1.044178	-3.426453	29554.9756
HLA B*4403	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.538510	1.112050	-3.426460	34554.8949
HLA A*0206	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.506580	1.080003	-3.426577	32105.5471
HLA B*4801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.440863	1.014245	-3.426617	27597.0480
HLA A*0211	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.407093	0.980281	-3.426812	25532.508345	
HLA B*1801	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.407129	0.980281	-3.426847	25534.580349	
HLA B*0802	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.441112	1.014245	-3.426866	27612.8781
HLA B*4002	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.174617	0.747233	-3.427383	14949.1548
HLA B*4501	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.459565	1.031880	-3.427684	28811.4112
HLA A*2402	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.365273	0.937566	-3.427707	23188.4996
HLA B*4002	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.596511	1.168653	-3.427859	39492.1986
HLA B*1801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.507950	1.080003	-3.427946	32206.9667
HLA A*3001	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.268044	0.839978	-3.428066	18537.190440	
HLA A*0101	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.355198	0.927121	-3.428077	22656.7732
HLA A*2602	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.540685	1.112498	-3.428188	34728.4339
HLA B*1503	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.351502	0.923260	-3.428243	22464.7876
HLA B*7301	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.561680	1.133400	-3.428280	36448.5451
HLA B*4801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.437251	1.008953	-3.428299	27368.5300
HLA A*6801	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.540810	1.112498	-3.428312	34738.3928
HLA B*1509	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.465156	1.036697	-3.428460	29184.7720
HLA B*5801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.355626	0.927121	-3.428504	22679.0920
HLA A*1101	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.481250	1.052696	-3.428555	30286.5829
HLA A*2902	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.084335	0.655774	-3.428561	12143.2610
HLA A*2602	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.437618	1.008953	-3.428665	27391.6372
HLA A*8001	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.409311	0.980470	-3.428842	25663.2347
HLA B*0803	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.456367	1.027504	-3.428863	28600.0559
HLA A*6801	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.485270	1.056254	-3.429017	30568.2267
HLA A*2603	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.583751	1.154646	-3.429106	38348.7541
HLA A*0216	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.419259	0.990022	-3.429237	26257.8471
HLA B*1509	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.504470	1.074983	-3.429487	31949.9540
HLA A*0203	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.405963	0.976308	-3.429656	25466.155126	
HLA A*0206	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.037082	0.607347	-3.429736	10891.369383	
HLA B*5101	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.445519	1.015721	-3.429798	27894.5467
HLA B*4601	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.406180	0.976308	-3.429872	25478.833035	
HLA B*4501	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.496179	1.066259	-3.429919	31345.7673
HLA B*5101	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.488865	1.058921	-3.429944	30822.2939
HLA A*2301	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.367547	0.937566	-3.429981	23310.2510
HLA A*8001	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.438962	1.008953	-3.430009	27476.5307
HLA A*0206	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.177915	0.747233	-3.430682	15063.1332
HLA B*2705	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.464982	1.034236	-3.430746	29173.090783	
HLA B*4001	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.407133	0.976308	-3.430826	25534.856629	
HLA A*6901	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.220422	0.789295	-3.431128	16612.010622	
HLA B*5801	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.354536	0.923260	-3.431276	22622.2346
HLA B*1801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.484079	1.052696	-3.431383	30484.4986
HLA A*1101	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.411875	0.980470	-3.431405	25815.1518
HLA B*3901	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.465741	1.034236	-3.431505	29224.112237	
HLA B*3501	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.465807	1.034236	-3.431571	29228.539350	
HLA B*2705	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.445933	1.014245	-3.431688	27921.1189
HLA B*1502	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.464271	1.032480	-3.431791	29125.3095
HLA A*0206	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.539856	1.108038	-3.431818	34662.176673	
HLA B*1509	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.393967	0.962074	-3.431893	24772.333027	
HLA A*0202	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.100683	0.668648	-3.432036	12609.069731	
HLA A*3101	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.244183	0.812136	-3.432046	17546.178450	
HLA A*2301	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.468810	1.036697	-3.432113	29431.3209
HLA A*2301	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.540227	1.108038	-3.432189	34691.817268	
HLA A*2603	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.491579	1.058921	-3.432658	31015.4876
HLA B*4402	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.347694	0.915034	-3.432660	22268.6459
HLA B*2705	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.409107	0.976308	-3.432799	25651.158910	
HLA B*0802	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.422828	0.990022	-3.432806	26474.5132
HLA A*0206	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.413148	0.980281	-3.432867	25890.957115	
HLA B*1517	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.469569	1.036697	-3.432872	29482.7940
HLA B*3901	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.448649	1.015721	-3.432928	28096.2800
HLA A*0301	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.360541	0.927121	-3.433419	22937.2203
HLA B*0802	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.449772	1.015721	-3.434051	28169.0290
HLA A*8001	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.407866	0.973692	-3.434175	25577.9929
HLA A*3001	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.237270	0.803085	-3.434186	17269.125954	
HLA A*1101	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.468450	1.034236	-3.4342		
HLA B*4001	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.339879	0.905427		

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HLA B*4402	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.424590	0.990022	-3.434568	26582.1495
HLA B*3501	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.426404	0.991777	-3.434627	26693.4003
HLA A*2301	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.514707	1.080003	-3.434704	32711.9884
HLA A*2902	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.414992	0.980281	-3.434711	26001.143676	
HLA B*1503	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.318020	0.883157	-3.434863	20797.9153
HLA B*4801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.415542	0.980470	-3.435073	26034.0797
HLA B*3801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.487794	1.052696	-3.435098	30746.3518
HLA B*5301	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.603830	1.168653	-3.435177	40163.3526
HLA A*0206	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.469430	1.034236	-3.435194	29473.385097	
HLA B*4001	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.362434	0.927116	-3.435319	23037.453498	
HLA A*3201	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.543740	1.108038	-3.435701	34973.534902	
HLA B*1517	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.247855	0.812136	-3.435719	17695.171943	
HLA B*3501	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-3.939974	0.504252	-3.435722	8709.105938	
HLA B*3901	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.488700	1.052696	-3.436005	30810.6240
HLA A*2902	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.055742	0.619672	-3.436070	11369.519146	
HLA A*2902	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.428206	0.991777	-3.436429	26804.3916
HLA B*7301	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.582154	1.145357	-3.436797	38207.9388
HLA B*4801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.426848	0.990022	-3.436826	26720.7074
HLA A*2501	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.503089	1.066259	-3.436829	31848.4822
HLA B*3901	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.464400	1.027504	-3.436896	29133.9768
HLA B*4402	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.417434	0.980470	-3.436964	26147.7043
HLA A*0301	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.364370	0.927116	-3.437255	23140.377911	
HLA B*5701	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.413580	0.976308	-3.437273	25916.742313	
HLA B*1502	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.584961	1.147510	-3.437451	38455.7463
HLA B*4402	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.413782	0.976308	-3.437475	25928.802895	
HLA A*0219	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.471754	1.034236	-3.437517	29631.501532	
HLA A*3002	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.453254	1.015721	-3.437533	28395.7807
HLA B*3801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.512541	1.074983	-3.437557	32549.2299
HLA A*0201	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.375237	0.937566	-3.437671	23726.6713
HLA A*0206	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.352724	0.915034	-3.437690	22528.0732
HLA B*4601	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.375258	0.937566	-3.437692	23727.8266
HLA B*4002	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.571330	1.133400	-3.437929	37267.4375
HLA B*0802	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.470081	1.031880	-3.438201	29517.5852
HLA A*0206	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.497180	1.058921	-3.438259	31418.0904
HLA A*0203	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.334584	0.896310	-3.438274	21606.462907	
HLA A*2402	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.470767	1.032480	-3.438287	29564.2506
HLA A*2602	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.583779	1.145357	-3.438423	38351.2438
HLA A*3301	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.590569	1.152145	-3.438425	38955.5612
HLA B*7301	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.564784	1.126312	-3.438471	36709.9562
HLA B*4501	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.624346	1.185494	-3.438851	42106.162451	
HLA A*2402	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.565209	1.126312	-3.438897	36745.9199
HLA B*1509	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.278953	0.839978	-3.438975	19008.706736	
HLA A*6901	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.319801	0.880633	-3.439168	20883.376425	
HLA A*3002	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.528811	1.089590	-3.439221	33791.767042	
HLA B*3901	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.471140	1.031880	-3.439260	29589.6919
HLA A*2602	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.455093	1.015721	-3.439373	28516.3187
HLA A*2501	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.471263	1.031880	-3.439382	29598.0171
HLA A*2603	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.565836	1.126312	-3.439524	36799.0359
HLA B*0801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.415897	0.976308	-3.439589	26055.355485	
HLA A*2902	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.448588	1.008953	-3.439635	28092.3284
HLA A*6802	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.415963	0.976308	-3.439655	26059.302568	
HLA B*4002	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.607347	1.167504	-3.439843	40489.9404
HLA A*3201	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.323175	0.883157	-3.440017	21046.2428
HLA A*0203	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.377899	0.937566	-3.440333	23872.5483
HLA A*8001	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.364067	0.923260	-3.440808	23124.2344
HLA A*8001	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.367930	0.927121	-3.440808	23330.8153
HLA A*2301	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.468584	1.027504	-3.441080	29416.0397
HLA A*3301	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.561246	1.119963	-3.441283	36412.0845
HLA B*0803	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.450312	1.008953	-3.441360	28204.1008
HLA B*5801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.356443	0.915034	-3.441409	22721.8288
HLA B*4501	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.588965	1.147510	-3.441455	38811.8877
HLA A*2501	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.494276	1.052696	-3.441580	31208.7103
HLA A*3301	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.399211	0.957621	-3.441590	25073.2690
HLA A*6802	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.421949	0.980281	-3.441668	26421.001528	
HLA A*6802	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.431859	0.990022	-3.441837	27030.8314
HLA B*1502	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.457711	1.015721	-3.441990	28688.6946
HLA B*5801	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.352397	0.910145	-3.442253	22511.1391
HLA A*0216	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.476634	1.034236	-3.442397	29966.328744	
HLA A*0101	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.357489	0.915034	-3.442455	22776.5953
HLA B*5401	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.554683	1.112050	-3.442633	35866.0402
HLA A*2301	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.508946	1.066259	-3.442687	32280.9276
HLA B*3801	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.475318	1.032480	-3.442838	29875.6819
HLA A*2902	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.455039	1.012095	-3.442944	28512.7707
HLA A*0301	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.366283	0.923260	-3.443023	23242.5047
HLA A*2601	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.326196	0.883157	-3.443039	21193.1745
HLA A*0202	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.551140	1.108038	-3.443102	35574.631325	
HLA B*1801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.423834	0.980470	-3.443364	26535.8841
HLA B*4501	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.612225	1.168653	-3.443572	40947.2432
HLA B*0803	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.476074	1.032480	-3.443594	29927.7703
HLA B*5101	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.353814	0.910145	-3.443670	22584.6940
HLA A*0201	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.371139	0.927121	-3.444018	23503.8665
HLA B*0801	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.112773	0.668648	-3.444126	12965.029112	
HLA B*1801	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.519162	1.074983	-3.444178	33049.2469
HLA B*1509	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.233563	0.789295	-3.444268	17122.330266	
HLA B*0803	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.434486	0.990022	-3.444464	27194.8162
HLA A*2501	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.453834	1.008953	-3.444881	28433.7497
HLA B*5701	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.382461	0.937566	-3.444896	24124.6755
HLA A*2501	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.489098	1.044178	-3.444920	30838.8061
HLA A*2402	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.557061	1.112050	-3.445011	36062.9384
HLA B*4801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.418940	0.973692	-3.445248	26238.5351
HLA A*2501	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.503180	1.057871	-3.445310	31855.2025
HLA A*0201	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.368616	0.923260	-3.445356	23367.6999
HLA A*6802	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.259656	0.814245	-3.445411	18182.6111
HLA A*0250	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.549726	1.104113	-3.445613	35458.961984	
HLA A*0212	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.422100	0.976308	-3.445792	26430.150932	
HLA B*1801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.461576	1.015721	-3.445855	28945.1423
HLA A*8001	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.258780	0.812772	-3.446008	18145.9576
HLA A*0101	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.369424	0.923260	-3.446165	23411.2277
HLA A*0301	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.331637	0.885414	-3.446223	21460.3807
HLA A*3201	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.576642	1.130392	-3.446250	37726.083202	
HLA B*0801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.006069	0.559811	-3.446259	10140.7315
HLA B*1801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.478163	1.031880	-3.446283	30072.0513
HLA A*2301	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.521330	1.074983	-3.446347	33214.6853
HLA B*5701	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.403983	0.957621	-3.446362	25350.2802
HLA A*2301	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.408592	0.962074	-3.446519	25620.786292	
HLA B*0702	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.373860	0.927121	-3.446739	23651.5723
HLA A*3301	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.572319	1.125530	-3.446789	37352.413252	
HLA A*6901	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.362016	0.915034	-3.446982	23015.2800
HLA A*0211	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.437080	0.990022	-3.447058	27357.7237
HLA B*4501	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.291020	0.843953	-3.447067	19544.2732
HLA A*2501	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.084866	0.637604	-3.447262	12158.1168
HLA A*2403	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.404930	0.957621	-3.447309	25405.6088
HLA B*2705	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.409556	0.962074	-3.447482	25677.677665	
HLA B*0803	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.481814	1.034236	-3.447578	30325.931806	
HLA B*4002	1:74-82 9	EHASVSFYI	0.978340	0.173645	-4.599843	1.151985	-3.4478[illegible]	39796.317092	
HLA B*4801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.424186	0.976308	-3.4478[illegible]		
HLA B*2705	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.438288	0.990022		

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HLA B*0803	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.410364	0.962074	-3.448290	25725.508363	
HLA A*2403	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.410622	0.962074	-3.448549	25740.821856	
HLA B*5301	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.232059	0.783495	-3.448564	17063.1496
HLA B*1509	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.538430	1.089590	-3.448840	34548.539607	
HLA A*3301	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.505166	1.056254	-3.448912	32001.1573
HLA B*5301	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.574863	1.125530	-3.449334	37571.900026	
HLA A*2402	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.450106	1.000751	-3.449354	28190.6769
HLA B*7301	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.569349	1.119963	-3.449386	37097.8650
HLA B*1501	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.141738	0.692096	-3.449642	13859.193150	
HLA B*4002	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.491003	1.041264	-3.449739	30974.4062
HLA A*3002	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.481723	1.031880	-3.449842	30319.5341
HLA A*3101	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.289948	0.839978	-3.449970	19496.118699	
HLA B*0702	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.355461	0.905427	-3.450034	22670.5052
HLA A*3101	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.377340	0.927121	-3.450218	23841.8309
HLA B*1502	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.440299	0.990022	-3.450277	27561.2400
HLA A*2301	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.540044	1.089590	-3.450454	34677.181403	
HLA A*0301	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.346940	0.896310	-3.450630	22230.007950	
HLA A*6901	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.378192	0.927116	-3.451077	23888.697305	
HLA A*3001	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.264083	0.812772	-3.451311	18368.8801
HLA A*6801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.356805	0.905427	-3.451378	22740.7668
HLA B*4801	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.431977	0.980281	-3.451695	27038.144093	
HLA A*3001	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.187351	0.735649	-3.451702	15393.9775
HLA A*2601	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.389533	0.937566	-3.451968	24520.7320
HLA B*5101	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.466359	1.014245	-3.452114	29265.7219
HLA A*2402	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.527209	1.074983	-3.452225	33667.3205
HLA A*0301	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.367361	0.915034	-3.452327	23300.2908
HLA A*0206	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.348753	0.896310	-3.452444	22323.044265	
HLA A*3002	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.600017	1.147510	-3.452507	39812.2520
HLA B*1502	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.561189	1.108664	-3.452525	36407.3572
HLA B*0802	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.464733	1.012095	-3.452638	29156.3663
HLA B*1503	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.237080	0.784286	-3.452794	17261.560263	
HLA B*4403	1:141-149	9	ATYSELLAK	0.738811	0.394589	-4.586216	1.133400	-3.452816	38567.0010
HLA A*0219	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.298874	0.846009	-3.452865	19900.9520
HLA B*5301	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.561589	1.108664	-3.452925	36440.8558
HLA B*1509	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-3.932046	0.478869	-3.453178	8551.58094
HLA A*0206	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.429670	0.976308	-3.453362	26894.884522	
HLA B*4403	1:47-55 9	WSKPNPKTA	1.389094	-0.203600	-4.638884	1.185494	-3.453390	43539.583964	
HLA B*4801	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.415469	0.962074	-3.453396	26029.714012	
HLA B*7301	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.528715	1.074983	-3.453731	33784.2726
HLA A*0211	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.506434	1.052696	-3.453739	32094.7803
HLA B*1502	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.573792	1.119963	-3.453829	37479.3277
HLA B*5101	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.491088	1.036697	-3.454391	30980.4392
HLA B*0802	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.434815	0.980281	-3.454534	27215.420948	
HLA B*0802	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.446689	0.991777	-3.454913	27969.7995
HLA B*1801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.335617	0.880566	-3.455051	21657.955138	
HLA A*0211	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.370204	0.915034	-3.455170	23453.3140
HLA B*5401	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.563306	1.108038	-3.455268	36585.251202	
HLA B*5301	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.609917	1.154646	-3.455272	40730.2873
HLA B*1503	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.086901	0.631559	-3.455342	12215.2108
HLA A*3002	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.464365	1.008953	-3.455412	29131.6127
HLA A*1101	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.445606	0.990022	-3.455584	27900.1308
HLA A*6802	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.295686	0.839978	-3.455708	19755.389772	
HLA A*1101	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.267879	0.812136	-3.455743	18530.171879	
HLA A*1101	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.467929	1.012095	-3.455833	29371.6738
HLA B*4403	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.608059	1.152145	-3.455914	40556.3658
HLA A*3101	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.379177	0.923260	-3.455917	23942.9082
HLA B*1502	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.500124	1.044178	-3.455946	31631.7843
HLA A*3101	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.341482	0.885414	-3.456067	21952.3877
HLA B*5101	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.488139	1.031880	-3.456259	30770.8127
HLA A*0219	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.432567	0.976308	-3.456259	27074.883645	
HLA A*0101	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.383385	0.927116	-3.456269	24176.021285	
HLA B*0803	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.472144	1.015721	-3.456423	29658.1238
HLA A*0212	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.414227	0.957621	-3.456605	25955.3278
HLA A*0219	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.379964	0.923260	-3.456704	23986.3396
HLA B*4601	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.331069	0.873495	-3.457574	21432.3033
HLA A*6801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.524201	1.066259	-3.457942	33434.9911
HLA B*4002	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.603452	1.145357	-3.458095	40128.3859
HLA A*6901	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.193873	0.735649	-3.458224	15626.9067
HLA A*3002	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.524486	1.066259	-3.458226	33456.8847
HLA B*4402	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.396013	0.937566	-3.458447	24889.3360
HLA A*3002	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.304459	0.846009	-3.458449	20158.5170
HLA A*6801	1:110-118	9	PEKDSRVVV	1.317651	-0.112924	-4.663258	1.204727	-3.458531	46052.9900
HLA B*3801	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.524901	1.066259	-3.458642	33488.9367
HLA A*2403	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.368858	0.910145	-3.458713	23380.7244
HLA B*7301	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.538803	1.080003	-3.458800	34578.2700
HLA A*3002	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.503016	1.044178	-3.458838	31843.1415
HLA A*2902	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.396641	0.937566	-3.459075	24925.3131
HLA A*2402	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.567209	1.108038	-3.459170	36915.481372	
HLA B*3501	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.295486	0.836190	-3.459296	19746.307530	
HLA B*0801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.221794	0.762047	-3.459747	16664.5771
HLA B*4601	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.369918	0.910145	-3.459773	23437.8397
HLA B*0702	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.472170	1.012095	-3.460074	29659.8887
HLA B*3501	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.436481	0.976308	-3.460173	27320.009179	
HLA A*0250	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.568261	1.108038	-3.460223	37005.059361	
HLA A*3301	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.605592	1.145357	-3.460235	40326.6431
HLA B*0803	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.452039	0.991777	-3.460262	28316.4712
HLA A*0206	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.263533	0.803085	-3.460448	18345.641412	
HLA B*4501	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.504726	1.044178	-3.460549	31968.7997
HLA B*4001	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.341153	0.880566	-3.460587	21935.767607	
HLA A*0201	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.375681	0.915034	-3.460647	23750.9435
HLA B*5701	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.370911	0.910145	-3.460767	23491.5359
HLA A*2603	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.540906	1.080003	-3.460903	34746.0988
HLA B*3901	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.167413	0.706243	-3.461170	14703.242480	
HLA B*5301	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.517456	1.056254	-3.461202	32919.6979
HLA B*5101	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.505431	1.044178	-3.461253	32020.7262
HLA A*2501	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.451337	0.990022	-3.461315	28270.7047
HLA B*0702	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.376656	0.915034	-3.461622	23804.3268
HLA A*3101	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-3.751817	0.290041	-3.461777	5646.99517
HLA A*0250	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.345034	0.883157	-3.461877	22132.6892
HLA A*2601	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.367451	0.905427	-3.462024	23305.0812
HLA A*3301	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.462936	1.000751	-3.462185	29035.9501
HLA B*4601	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.367723	0.905427	-3.462296	23319.7109
HLA B*5401	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.518616	1.056254	-3.462363	33007.7930
HLA B*3501	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.154585	0.692096	-3.462489	14275.289729	
HLA A*2601	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.372988	0.910145	-3.462844	23604.1495
HLA A*3201	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.610413	1.147510	-3.462903	40776.8069
HLA B*4601	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.378115	0.915034	-3.463081	23884.4329
HLA A*0211	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.386343	0.923260	-3.463083	24341.2474
HLA B*2705	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.443788	0.980470	-3.463318	27783.5501
HLA B*4002	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.589719	1.126312	-3.463406	38879.3460
HLA A*0219	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.421033	0.957621	-3.463412	26365.3157
HLA A*6901	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.390673	0.927121	-3.463551	24585.1539
HLA A*6901	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.299959	0.836190	-3.463769	19950.754104	
HLA B*0801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.216475	0.752698	-3.463777	16461.7145
HLA B*4801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.401380	0.937566	-3.463814	25198.7811
HLA B*1801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.508309	1.044178		
HLA B*5101	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.444685	0.980470		

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HLA B*1509	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.456202	0.991777	-3.464426	28589.2273
HLA B*3801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.522402	1.057871	-3.464531	33296.7240
HLA A*2902	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.454687	0.990022	-3.464665	28489.6425
HLA A*6802	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-3.824614	0.359849	-3.464765	6677.49943
HLA B*4501	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.576848	1.112050	-3.464798	37744.0477
HLA B*3801	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.523846	1.058921	-3.464926	33407.6895
HLA A*0212	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.388288	0.923260	-3.465029	24450.5258
HLA A*0219	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.392451	0.927116	-3.465336	24686.043616	
HLA B*3801	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.555226	1.089590	-3.465636	35910.889487	
HLA B*5301	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.573681	1.108038	-3.465643	37469.799320	
HLA A*0250	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.577838	1.112050	-3.465788	37830.1101
HLA A*3301	1:220-228	9	AAVAPAVFA	1.217581	-0.091269	-4.592132	1.126312	-3.465819	39095.9592
HLA A*2602	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.574804	1.108664	-3.466140	37566.8188
HLA A*2603	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.498700	1.032480	-3.466220	31528.2527
HLA A*0211	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.525174	1.058921	-3.466253	33509.9592
HLA B*4402	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.376428	0.910145	-3.466283	23791.8385
HLA B*4601	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.351862	0.885414	-3.466447	22483.3897
HLA A*2403	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.389862	0.923260	-3.466603	24539.3107
HLA A*0212	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.347313	0.880633	-3.466680	22249.137815	
HLA A*2601	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.393908	0.927116	-3.466793	24768.982864	
HLA A*0301	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.340328	0.873495	-3.466834	21894.1539
HLA A*2602	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.571064	1.104113	-3.466951	37244.662297	
HLA B*4501	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.382055	0.915034	-3.467021	24102.1075
HLA B*5701	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.394148	0.927116	-3.467032	24782.654375	
HLA A*6901	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.363381	0.896310	-3.467072	23087.734207	
HLA B*0803	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.481466	1.014245	-3.467221	30301.6606
HLA B*4001	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.363722	0.896310	-3.467412	23105.852114	
HLA B*0702	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.390694	0.923260	-3.467435	24586.3509
HLA A*3201	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.576148	1.108664	-3.467484	37683.2478
HLA B*3501	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-3.831676	0.364143	-3.467534	6786.97753
HLA B*1517	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.457558	0.990022	-3.467536	28678.6082
HLA A*0203	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.693508	0.225691	-3.467817	4937.508970	
HLA A*3101	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.364237	0.896310	-3.467927	23133.243359	
HLA A*2501	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.448487	0.980470	-3.468017	28085.7942
HLA A*2601	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.391357	0.923260	-3.468097	24623.8882
HLA B*1801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.348749	0.880633	-3.468116	22322.802736	
HLA B*5101	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.348695	0.880566	-3.468129	22320.025339	
HLA B*5101	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.502407	1.034236	-3.468171	31798.555366	
HLA B*1801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.441887	0.973692	-3.468195	27662.2184
HLA B*5401	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.469118	1.000751	-3.468366	29452.1861
HLA A*0201	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.314409	0.846009	-3.468400	20625.6977
HLA B*1801	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.215831	0.747233	-3.468598	16437.3312
HLA A*3201	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.548791	1.080003	-3.468788	35382.6961
HLA B*1517	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.252335	0.783495	-3.468840	17878.6719
HLA A*0101	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.378991	0.910145	-3.468847	23932.6777
HLA B*1502	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.503286	1.034236	-3.469050	31862.958468	
HLA B*0702	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.342722	0.873495	-3.469228	22015.1826
HLA A*1101	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.449551	0.980281	-3.469270	28154.707901	
HLA B*3501	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.384358	0.915034	-3.469323	24230.2288
HLA B*1517	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.449892	0.980281	-3.469610	28176.802074	
HLA A*2603	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.573839	1.104113	-3.469726	37483.383181	
HLA A*0301	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.282503	0.812772	-3.469731	19164.7272
HLA B*4402	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.431862	0.962074	-3.469788	27030.977648	
HLA A*1101	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.446172	0.976308	-3.469865	27936.530335	
HLA A*0101	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.366234	0.896310	-3.469924	23239.864354	
HLA A*2603	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.595522	1.125530	-3.469993	39402.355016	
HLA B*5301	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.600421	1.130392	-3.470029	39849.314591	
HLA A*8001	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.446548	0.976308	-3.470241	27960.722168	
HLA A*0211	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.482376	1.012095	-3.470280	30365.1674
HLA A*0301	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.343117	0.872645	-3.470472	22035.2004
HLA A*6802	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.408080	0.937566	-3.470514	25590.5880
HLA B*4601	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.397801	0.927116	-3.470686	24992.014797	
HLA B*4001	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.408299	0.937566	-3.470733	25603.4664
HLA A*0101	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.376186	0.905427	-3.470759	23778.5849
HLA B*0802	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.444540	0.973692	-3.470848	27831.6897
HLA A*2501	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.444659	0.973692	-3.470968	27839.3696
HLA A*6901	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.139666	0.668648	-3.471018	13793.221220	
HLA A*3201	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.502901	1.031880	-3.471020	31834.7014
HLA B*5801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.354270	0.883157	-3.471113	22608.4095
HLA B*5801	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.367575	0.896310	-3.471266	23311.764374	
HLA A*6801	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.638833	1.167504	-3.471328	43534.4022
HLA B*1801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.480285	1.008953	-3.471332	30219.3166
HLA B*3501	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.283323	0.811904	-3.471418	19200.9453
HLA A*6901	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.096473	0.625007	-3.471466	12487.4214
HLA B*0801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.345008	0.873495	-3.471514	22131.3721
HLA A*0201	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.352219	0.880633	-3.471586	22501.885518	
HLA A*2301	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.398797	0.927116	-3.471682	25049.407104	
HLA B*5101	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.445590	0.973692	-3.471898	27899.0743
HLA B*1509	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.448282	0.976308	-3.471975	28072.578445	
HLA B*5801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.352705	0.880633	-3.472072	22527.098302	
HLA A*0301	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.352762	0.880633	-3.472129	22530.023351	
HLA B*5801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.345673	0.873495	-3.472179	22165.2812
HLA B*7301	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.602594	1.130392	-3.472203	40049.226213	
HLA A*2902	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.399345	0.927121	-3.472223	25081.0018
HLA A*2501	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.452542	0.980281	-3.472260	28349.272624	
HLA B*5801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.353217	0.880566	-3.472651	22553.681440	
HLA A*3002	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.584759	1.112050	-3.472709	38437.8589
HLA B*4402	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.430382	0.957621	-3.472761	26939.0066
HLA B*3901	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.446469	0.973692	-3.472777	27955.5796
HLA A*2601	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.353575	0.880566	-3.473008	22572.235030	
HLA A*0211	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.276128	0.803085	-3.473044	18885.500092	
HLA B*1501	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.356237	0.883157	-3.473079	22711.0142
HLA B*7301	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.581787	1.108664	-3.473123	38175.7071
HLA B*0801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.400268	0.927116	-3.473153	25134.382998	
HLA B*4601	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.400374	0.927121	-3.473253	25140.5025
HLA A*3101	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.353960	0.880633	-3.473327	22592.270496	
HLA A*2402	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.449871	0.976308	-3.473563	28175.430207	
HLA A*2501	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.465394	0.991777	-3.473617	29200.7229
HLA A*8001	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.379142	0.905427	-3.473715	23940.9654
HLA A*2601	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.401055	0.927121	-3.473934	25179.9756
HLA A*2501	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.450437	0.976308	-3.474129	28212.188819	
HLA B*5401	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.554174	1.080003	-3.474170	35823.9601
HLA B*5101	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.177779	0.703256	-3.474523	15058.407562	
HLA B*5801	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.347219	0.872645	-3.474574	22244.3237
HLA A*0203	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.112280	0.637604	-3.474676	12950.3082
HLA A*0211	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.532727	1.057871	-3.474857	34097.8891
HLA B*1801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.487077	1.012095	-3.474982	30695.6617
HLA A*2402	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.541324	1.066259	-3.475065	34779.5741
HLA B*4001	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.390116	0.915034	-3.475082	24553.6524
HLA A*6901	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.258810	0.783495	-3.475315	18147.2338
HLA B*0801	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.315337	0.839978	-3.475359	20669.820028	
HLA A*0101	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.361081	0.885414	-3.475667	22965.7783
HLA A*3002	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.510008	1.034236	-3.475772	32359.959848	
HLA B*5101	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.484850	1.008953	-3.475897	30538.6397
HLA B*3501	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.356542	0.880633	-3.475909	22726.992216	
HLA A*0301	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.359112	0.883157		
HLA A*6801	1:59-67 9	GYLRHIIDV	0.947497	0.247090	-4.670762	1.194587	-3.4761		

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HLA A*3301	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.631002	1.154646	-3.476356	42756.4611
HLA A*0206	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.179851	0.703401	-3.476450	15130.430782	
HLA A*0301	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.288590	0.812136	-3.476454	19435.251188	
HLA B*3501	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.414530	0.937566	-3.476964	25973.4477
HLA A*6801	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.557024	1.080003	-3.477020	36059.8170
HLA B*4002	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.624606	1.147510	-3.477097	42131.4546
HLA A*3101	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.291417	0.814245	-3.477172	19562.1501
HLA B*4403	1:214-222	9	ECLRQLAAV	1.100507	0.066997	-4.644847	1.167504	-3.477343	44141.5183
HLA B*4402	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.363038	0.885414	-3.477624	23069.5057
HLA B*5701	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.383129	0.905427	-3.477702	24161.7694
HLA A*3301	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.510532	1.032480	-3.478052	32399.0226
HLA B*5101	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.213261	0.734934	-3.478327	16340.335523	
HLA A*3101	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.393434	0.915034	-3.478399	24741.9301
HLA B*3901	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.225662	0.747233	-3.478428	16813.6325
HLA B*1509	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.324476	0.846009	-3.478467	21109.4147
HLA A*2603	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.625995	1.147510	-3.478485	42266.3748
HLA A*0211	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.513034	1.034236	-3.478798	32586.229417	
HLA A*0203	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.086440	0.607347	-3.479094	12202.265448	
HLA B*4801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.394477	0.915034	-3.479443	24801.4314
HLA A*3201	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.591646	1.112050	-3.479595	39052.2022
HLA B*0702	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.365096	0.885414	-3.479682	23179.0930
HLA A*2501	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.492124	1.012095	-3.480028	31054.4394
HLA B*1501	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.326107	0.846009	-3.480098	21188.8181
HLA A*2403	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.365630	0.885414	-3.480215	23207.5754
HLA B*4403	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.634876	1.154646	-3.480230	43139.5939
HLA A*0101	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.363482	0.883157	-3.480325	23093.1056
HLA B*3801	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.442439	0.962074	-3.480365	27697.408408	
HLA A*2301	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.538239	1.057871	-3.480369	34533.4037
HLA A*6802	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.377062	0.896310	-3.480753	23826.615979	
HLA B*5301	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.366351	0.885414	-3.480937	23246.1514
HLA A*0212	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.391246	0.910145	-3.481102	24617.6280
HLA B*1509	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.508615	1.027504	-3.481110	32256.3133
HLA B*1801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.508685	1.027504	-3.481181	32261.5488
HLA B*1503	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.457518	0.976308	-3.481210	28675.970810	
HLA A*3301	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.522573	1.041264	-3.481309	33309.8762
HLA B*1517	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.461942	0.980470	-3.481473	28969.5807
HLA A*0212	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.419308	0.937566	-3.481743	26260.8304
HLA A*8001	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.354590	0.872645	-3.481944	22625.0496
HLA B*2705	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.405395	0.923260	-3.482135	25432.8368
HLA B*4801	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.405397	0.923260	-3.482138	25432.9744
HLA B*1502	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.590332	1.108038	-3.482294	38934.281747	
HLA A*0219	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.419933	0.937566	-3.482368	26298.6477
HLA A*6801	1:166-174	9	QARQAARAV	0.923681	0.228464	-4.634514	1.152145	-3.482370	43103.6683
HLA A*2603	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.318788	0.836190	-3.482598	20834.740168	
HLA B*4501	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.602601	1.119963	-3.482638	40049.8762
HLA B*5101	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.510172	1.027504	-3.482668	32372.2166
HLA A*0101	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.356173	0.873495	-3.482679	22707.6971
HLA B*4801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.409864	0.927121	-3.482742	25695.8817
HLA A*2403	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.398008	0.915034	-3.482974	25003.9155
HLA A*6802	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.266484	0.783495	-3.482988	18470.7212
HLA A*2402	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.520033	1.036697	-3.483337	33115.6456
HLA A*6901	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.295307	0.811904	-3.483403	19738.1904
HLA B*3501	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.366635	0.883157	-3.483478	23261.3732
HLA B*0803	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.356194	0.872645	-3.483549	22708.8028
HLA B*0702	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.459868	0.976308	-3.483560	28831.525019	
HLA A*0250	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.542621	1.058921	-3.483701	34883.5901
HLA B*1502	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.588142	1.104113	-3.484030	38738.468511	
HLA B*0803	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.298357	0.814245	-3.484112	19877.2805
HLA A*0206	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.152781	0.668648	-3.484133	14216.101871	
HLA B*3501	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.273607	0.789295	-3.484313	18776.190899	
HLA B*1509	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.411527	0.927121	-3.484406	25794.4909
HLA A*2601	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.399460	0.915034	-3.484426	25087.6513
HLA A*0301	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.365306	0.880566	-3.484739	23190.255967	
HLA B*4601	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.408061	0.923260	-3.484802	25589.4805
HLA B*5401	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.499123	1.014245	-3.484878	31558.9692
HLA A*2403	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.219825	0.734934	-3.484892	16589.199537	
HLA B*0802	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.465380	0.980470	-3.484910	29199.7750
HLA A*2601	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.381313	0.896310	-3.485003	24060.939638	
HLA B*3501	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.408426	0.923260	-3.485166	25610.9471
HLA A*2402	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.477040	0.991777	-3.485263	29994.3876
HLA B*2705	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.321577	0.836190	-3.485387	20968.961746	
HLA A*2301	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.501115	1.015721	-3.485394	31704.0813
HLA B*1509	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.465809	0.980281	-3.485528	29228.697474	
HLA B*1501	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.221296	0.735649	-3.485648	16645.4756
HLA B*1502	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.526967	1.041264	-3.485703	33648.5657
HLA B*4403	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.598248	1.112498	-3.485750	39650.4008
HLA B*0702	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.423427	0.937566	-3.485861	26511.0605
HLA B*4001	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.369093	0.883157	-3.485936	23393.3765
HLA A*2301	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.530136	1.044178	-3.485958	33895.0291
HLA B*3801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.486739	1.000751	-3.485987	30671.7583
HLA B*1509	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.289135	0.803085	-3.486051	19459.659575	
HLA B*4001	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.396197	0.910145	-3.486052	24899.8408
HLA A*2301	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.500753	1.014245	-3.486508	31677.6789
HLA B*3801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.514023	1.027504	-3.486519	32660.5311
HLA A*0211	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.424217	0.937566	-3.486651	26559.2941
HLA A*0211	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.463225	0.976308	-3.486917	29055.277571	
HLA B*0802	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.372406	0.885414	-3.486991	23572.5022
HLA A*2501	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.323355	0.836190	-3.487165	21055.011723	
HLA A*2501	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.367803	0.880566	-3.487237	23324.000649	
HLA A*3002	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.271664	0.784286	-3.487378	18692.374265	
HLA A*0101	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.270931	0.783495	-3.487436	18660.8502
HLA B*5401	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.531990	1.044178	-3.487812	34040.0160
HLA A*2902	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.411135	0.923260	-3.487875	25771.1973
HLA A*8001	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.425784	0.937566	-3.488218	26655.3037
HLA A*2403	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.361812	0.873495	-3.488317	23004.4501
HLA A*2403	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.368966	0.880633	-3.488333	23386.543581	
HLA B*4002	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.614139	1.125530	-3.488610	41128.180688	
HLA B*1517	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.194305	0.705319	-3.488987	15642.469788	
HLA A*0203	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.333026	0.843953	-3.489073	21529.1046
HLA B*3801	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.525935	1.036697	-3.489239	33568.7471
HLA B*1517	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.362016	0.872645	-3.489371	23015.2800
HLA A*0202	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.236643	0.747233	-3.489410	17244.1997
HLA A*2301	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.490181	1.000751	-3.489429	30915.8128
HLA B*1509	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.522014	1.032480	-3.489534	33267.0156
HLA A*0202	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.547623	1.057871	-3.489753	35287.6899
HLA B*5701	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.362547	0.872645	-3.489902	23043.4365
HLA B*3501	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.417058	0.927121	-3.489936	26125.0811
HLA B*4402	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.370611	0.880633	-3.489978	23475.274509	
HLA A*0212	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.336285	0.846009	-3.490276	21691.2561
HLA A*6801	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.517839	1.027504	-3.490335	32948.7397
HLA B*1509	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.499351	1.008953	-3.490398	31575.5344
HLA A*3002	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.304677	0.814245	-3.490432	20168.6617
HLA B*4001	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.364018	0.873495	-3.490523	23121.6074
HLA B*5701	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.405566	0.915034	-3.490532	25442.8827
HLA B*3801	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.524777	1.034236	-3.490540	33479.336062	
HLA B*4002	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.594658	1.104113	-3.4905		
HLA B*1509	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.522601	1.031880		

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HLA A*2402	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.580504	1.089590	-3.490915	38063.110133		
HLA A*2301	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.543716	1.052696	-3.491020	34971.6429	
HLA A*6901	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.238544	0.747233	-3.491310	17319.8361	
HLA B*7301	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.471765	0.980281	-3.491484	29632.303059		
HLA A*0219	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.372540	0.880633	-3.491907	23579.772279		
HLA B*0803	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.465654	0.973692	-3.491963	29218.2631	
HLA B*3901	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.504076	1.012095	-3.491980	31920.9291	
HLA B*1502	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.604037	1.112050	-3.491987	40182.4777	
HLA A*6801	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.637444	1.145357	-3.492087	43395.4344	
HLA B*5301	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.551014	1.058921	-3.492093	35564.2402	
HLA A*2602	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.551279	1.058921	-3.492359	35585.9879	
HLA A*2403	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.332363	0.839978	-3.492386	21496.285083		
HLA B*0801	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-3.619833	0.127125	-3.492707	4167.088720		
HLA B*4403	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.612786	1.119963	-3.492823	41000.2207	
HLA B*5701	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.419959	0.927121	-3.492838	26300.2127	
HLA B*4403	1:127-135	9	DLRHILTEA	1.440563	-0.271910	-4.661498	1.168653	-3.492845	45866.7605	
HLA A*0212	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.407942	0.915034	-3.492908	25582.4212	
HLA A*0250	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.483059	0.990022	-3.493037	30413.0083	
HLA B*0802	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.469536	0.976308	-3.493228	29480.561119		
HLA B*5401	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.552256	1.058921	-3.493336	35666.1649	
HLA A*2601	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.131090	0.637604	-3.493486	13523.5303	
HLA A*0301	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.307832	0.814245	-3.493587	20315.7303	
HLA B*5701	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.416924	0.923260	-3.493664	26117.0263	
HLA A*8001	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.408705	0.915034	-3.493671	25627.4402	
HLA B*1517	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.470053	0.976308	-3.493745	29515.669052		
HLA B*1509	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.474387	0.980470	-3.493918	29811.7473	
HLA B*4801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.421315	0.927116	-3.494199	26382.437334		
HLA B*4501	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.639843	1.145357	-3.494486	43635.7921	
HLA A*0219	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.377694	0.883157	-3.494537	23861.3151	
HLA B*4501	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.598717	1.104113	-3.494605	39693.324928		
HLA B*1502	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.486476	0.991777	-3.494699	30653.1797	
HLA B*5101	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.486607	0.991777	-3.494830	30662.4676	
HLA A*0201	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.391237	0.896310	-3.494927	24617.095374		
HLA A*2603	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.640463	1.145357	-3.495106	43698.1578	
HLA B*0803	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.475583	0.980470	-3.495114	29893.9511	
HLA B*1801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.452861	0.957621	-3.495240	28370.1381	
HLA B*0801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.376282	0.880566	-3.495716	23783.859803		
HLA A*0211	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.378897	0.883157	-3.495740	23927.4993	
HLA A*6802	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.422910	0.927121	-3.495789	26479.5265	
HLA A*0212	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.423162	0.927121	-3.496040	26494.8588	
HLA B*5301	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.376607	0.880566	-3.496040	23801.622623		
HLA B*5401	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.487902	0.991777	-3.496125	30754.0042	
HLA B*4002	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.571142	1.074983	-3.496158	37251.3120	
HLA A*6802	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.419424	0.923260	-3.496164	26267.7926	
HLA A*6801	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.497201	1.000751	-3.496450	31419.6202	
HLA A*0301	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.280856	0.784286	-3.496569	19092.185853		
HLA A*3101	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.377210	0.880566	-3.496644	23834.738022		
HLA B*0803	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.434345	0.937566	-3.496779	27185.9903	
HLA B*3501	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.339699	0.842742	-3.496957	21862.433689		
HLA A*3001	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.280849	0.783495	-3.497353	19091.8759	
HLA B*4001	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.382880	0.885414	-3.497465	24147.9178	
HLA A*2602	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.587367	1.089590	-3.497777	38669.371837		
HLA A*2301	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.529676	1.031880	-3.497795	33859.1080	
HLA B*4403	1:159-167	9	NAILRRKQA	1.372706	-0.225196	-4.645338	1.147510	-3.497828	44191.4559	
HLA B*7301	1:41-49 9	RACYQSWSK	0.781972	0.322141	-4.601967	1.104113	-3.497854	39991.419252		
HLA B*3901	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.478501	0.980470	-3.498032	30095.4873	
HLA B*2705	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.408207	0.910145	-3.498063	25598.0650	
HLA B*1509	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.513845	1.015721	-3.498124	32647.1059	
HLA B*5401	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.460323	0.962074	-3.498250	28861.800122		
HLA A*3301	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.611024	1.112498	-3.498526	40834.2028	
HLA A*3002	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.535248	1.036697	-3.498552	34296.3965	
HLA B*1509	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.379452	0.880633	-3.498819	23958.067902		
HLA B*4801	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.344990	0.846009	-3.498980	22130.4143	
HLA B*4002	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.619337	1.119963	-3.499374	41623.3048	
HLA B*3501	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.234378	0.734934	-3.499445	17154.503033		
HLA A*3301	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.607495	1.108038	-3.499457	40503.742675		
HLA B*1517	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.405186	0.905427	-3.499759	25420.5943	
HLA A*2603	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.607798	1.108038	-3.499760	40532.019118		
HLA A*0206	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.314155	0.814245	-3.499910	20613.6503	
HLA B*7301	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.556572	1.056254	-3.500319	36022.3811	
HLA B*7301	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.612556	1.112050	-3.500506	40978.4895	
HLA A*3101	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.383866	0.883157	-3.500709	24202.8480	
HLA A*6901	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.346900	0.846009	-3.500891	22227.9635	
HLA A*0203	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.373639	0.872645	-3.500994	23639.5478	
HLA A*0202	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.284519	0.783495	-3.501023	19253.8906	
HLA A*2501	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.424637	0.923260	-3.501378	26585.0258	
HLA B*3901	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.428711	0.927116	-3.501595	26835.586664		
HLA A*2601	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.387083	0.885414	-3.501669	24382.7630	
HLA B*5301	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.591556	1.089590	-3.501967	39044.174852		
HLA A*8001	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.194113	0.692096	-3.502017	15635.532156		
HLA A*1101	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.412171	0.910145	-3.502026	25832.7546	
HLA B*7301	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.591650	1.089590	-3.502060	39052.624752		
HLA B*1517	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.429524	0.927121	-3.502403	26885.8651	
HLA A*1101	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.398809	0.896310	-3.502500	25050.084685		
HLA B*3801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.511641	1.008953	-3.502688	32481.8582	
HLA B*1502	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.314876	0.812136	-3.502740	20647.914642		
HLA B*0702	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.430424	0.927116	-3.503308	26941.630067		
HLA A*0250	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.515731	1.012095	-3.503636	32789.2376	
HLA B*1509	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.477449	0.973692	-3.503757	30022.6353	
HLA A*2902	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.400146	0.896310	-3.503836	25127.313333		
HLA A*2602	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.387015	0.883157	-3.503858	24378.9380	
HLA A*8001	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.389510	0.885414	-3.504096	24519.4055	
HLA B*1502	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.557031	1.052696	-3.504335	36060.4022	
HLA B*1502	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.570672	1.066259	-3.504412	37211.0287	
HLA A*0250	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.557301	1.052696	-3.504605	36082.8437	
HLA A*2301	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.294015	0.789295	-3.504721	19679.547978		
HLA B*4002	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.563835	1.058921	-3.504914	36629.8108	
HLA B*4501	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.410578	0.905427	-3.505151	25738.1761	
HLA B*4403	1:175-183	9	LPNATETRI	1.064730	0.080627	-4.650632	1.145357	-3.505275	44733.3785	
HLA B*4601	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.388603	0.883157	-3.505446	24468.2571	
HLA A*3201	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.506373	1.000751	-3.505622	32090.2662	
HLA A*0101	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.386256	0.880633	-3.505623	24336.375628		
HLA B*1503	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-3.612939	0.107209	-3.505731	4101.46828	
HLA B*3801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.537769	1.031880	-3.505889	34496.0595	
HLA A*6801	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.614022	1.108038	-3.505984	41117.057248		
HLA B*3801	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.479695	0.973692	-3.506003	30178.3102	
HLA B*4002	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.416249	0.910145	-3.506105	26076.5075	
HLA A*3201	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.547797	1.041264	-3.506533	35301.8195	
HLA B*3801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.498404	0.991777	-3.506627	31506.7689	
HLA A*0202	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.351096	0.843953	-3.507143	22443.7724	
HLA B*5401	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.541425	1.034236	-3.507189	34787.665664		
HLA B*4601	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.387839	0.880566	-3.507273	24425.274486		
HLA A*2601	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.387957	0.880633	-3.507324	24431.882281		
HLA B*5701	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.403764	0.896310	-3.507455	25337.529204		
HLA A*0203	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.390633	0.883157	-3.507476	24582.8926	
HLA B*4002	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.638027	1.130392	-3.5076			
HLA A*2501	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.445261	0.937566			

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HLA B*7301	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.615751	1.108038	-3.507713	41281.098510	
HLA A*0301	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.347844	0.839978	-3.507866	22276.357024	
HLA A*3002	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.260584	0.752698	-3.507886	18221.5071
HLA A*8001	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.435055	0.927116	-3.507939	27230.442798	
HLA A*2902	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.422976	0.915034	-3.507942	26483.5378
HLA A*2501	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.435116	0.927121	-3.507994	27234.2732
HLA B*4402	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.380681	0.872645	-3.508036	24025.9501
HLA B*4002	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.509129	1.000751	-3.508378	32294.5521
HLA B*5401	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.435536	0.927116	-3.508421	27260.658854	
HLA A*2301	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.542800	1.034236	-3.508563	34897.935549	
HLA A*0219	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.423632	0.915034	-3.508597	26523.5412
HLA B*1502	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.489269	0.980470	-3.508799	30850.9875
HLA B*5801	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.351641	0.842742	-3.508899	22471.959190	
HLA A*2602	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.550276	1.041264	-3.509012	35503.8784
HLA B*4002	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.621590	1.112498	-3.509092	41839.8111
HLA A*2603	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.618061	1.108664	-3.509397	41501.2128
HLA A*2602	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.349573	0.839978	-3.509596	22365.231131	
HLA B*5801	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.349726	0.839978	-3.509748	22373.097086	
HLA A*2601	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.383352	0.873495	-3.509857	24174.1903
HLA A*3001	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.300791	0.790864	-3.509927	19988.998417	
HLA B*7301	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.568898	1.058921	-3.509977	37059.3515
HLA A*2603	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.544301	1.034236	-3.510065	35018.783652	
HLA B*5401	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.542163	1.031880	-3.510283	34846.8098
HLA B*4801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.390873	0.880566	-3.510307	24596.461783	
HLA B*3901	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.433614	0.923260	-3.510355	27140.2890
HLA B*5801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.354510	0.843953	-3.510557	22620.8884
HLA A*2603	1:198-206	9	MRASEHADV	0.792968	0.319530	-4.623115	1.112498	-3.510617	41986.9696
HLA A*2902	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.294967	0.784286	-3.510680	19722.713239	
HLA A*0301	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.203125	0.692096	-3.511029	15963.396159	
HLA B*3801	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.468739	0.957621	-3.511118	29426.5447
HLA A*1101	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.203337	0.692096	-3.511241	15971.170470	
HLA B*4002	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.384045	0.872645	-3.511400	24212.8011
HLA A*6901	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.325827	0.814245	-3.511582	21175.1817
HLA B*3501	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.273631	0.762047	-3.511584	18777.2066
HLA A*0216	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.449290	0.937566	-3.511724	28137.8061
HLA A*0201	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.394893	0.883157	-3.511735	24825.1914
HLA A*0216	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.438908	0.927121	-3.511786	27473.1121
HLA B*7301	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.435099	0.923260	-3.511840	27233.2419
HLA A*0203	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.315090	0.803085	-3.512005	20658.082111	
HLA A*6801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.527834	1.015721	-3.512113	33715.8037
HLA B*5301	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.524215	1.012095	-3.512120	33436.0764
HLA B*3901	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.449889	0.937566	-3.512323	28176.6496
HLA B*3901	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.143993	0.631559	-3.512435	13931.3580
HLA B*4801	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.422708	0.910145	-3.512564	26467.2097
HLA A*2403	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.439749	0.927121	-3.512628	27526.3719
HLA B*3901	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.489133	0.976308	-3.512825	30841.308805	
HLA B*5301	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.554178	1.041264	-3.512914	35824.3477
HLA B*5801	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.359018	0.846009	-3.513009	22856.9522
HLA B*1509	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.325273	0.812136	-3.513136	21148.163888	
HLA A*3002	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.393943	0.880633	-3.513311	24770.992907	
HLA A*0301	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.356161	0.842742	-3.513420	22707.082960	
HLA B*5801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.325623	0.812136	-3.513487	21165.217734	
HLA B*5101	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.440729	0.927116	-3.513613	27588.539480	
HLA B*3501	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.423784	0.910145	-3.513640	26532.8696
HLA A*0216	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.297170	0.783495	-3.513675	19823.0500
HLA B*1502	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.298016	0.784286	-3.513730	19861.694237	
HLA B*2705	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.399434	0.885414	-3.514020	25086.1584
HLA A*2902	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.303314	0.789295	-3.514020	20105.476969	
HLA A*2902	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.387924	0.873495	-3.514429	24430.0319
HLA B*2705	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.441589	0.927121	-3.514467	27643.2194
HLA B*0802	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.442122	0.927121	-3.515001	27677.1874
HLA B*0801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.327122	0.811904	-3.515217	21238.3958
HLA B*0803	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.495733	0.980281	-3.515451	31313.564208	
HLA B*1517	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.304820	0.789295	-3.515526	20175.318541	
HLA B*3901	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.420979	0.905427	-3.515552	26362.0354
HLA B*4402	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.421049	0.905427	-3.515623	26366.3142
HLA A*0216	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.430765	0.915034	-3.515730	26962.7722
HLA A*2402	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.573604	1.057871	-3.515733	37463.1105
HLA B*5301	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.582027	1.066259	-3.515767	38196.7786
HLA A*0202	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.568595	1.052696	-3.515899	37033.4977
HLA A*0101	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.360339	0.843953	-3.516386	22926.5512
HLA B*0803	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.492739	0.976308	-3.516432	31098.486929	
HLA A*6901	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.389266	0.872645	-3.516621	24505.6141
HLA B*4501	1:81-89 9	YITGISRSC	1.133968	-0.008438	-4.642155	1.125530	-3.516625	43868.699318	
HLA A*0201	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.389289	0.872645	-3.516644	24506.9398
HLA A*1101	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.443973	0.927116	-3.516858	27795.426900	
HLA B*5401	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.553607	1.036697	-3.516911	35777.2839
HLA A*0301	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.363158	0.846009	-3.517149	23075.8715
HLA A*0219	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.444706	0.927121	-3.517585	27842.3820
HLA B*0702	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.400752	0.883157	-3.517595	25162.4093
HLA B*0802	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.440931	0.923260	-3.517671	27601.3780
HLA A*0203	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.186557	0.668648	-3.517909	15365.854740	
HLA B*1501	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.358017	0.839978	-3.518040	22804.336446	
HLA B*5101	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.475752	0.957621	-3.518131	29905.5974
HLA B*3801	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.534036	1.015721	-3.518315	34200.7915
HLA B*5101	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.455970	0.937566	-3.518404	28573.9196
HLA A*2602	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.593497	1.074983	-3.518514	39219.0368
HLA B*5301	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.480592	0.962074	-3.518519	30240.740527	
HLA A*3002	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.508554	0.990022	-3.518532	32251.7765
HLA B*1502	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.593593	1.074983	-3.518610	39227.7367
HLA A*6802	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.253764	0.734934	-3.518830	17937.575489	
HLA B*5101	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.495159	0.976308	-3.518852	31272.257167	
HLA B*1801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.495176	0.976308	-3.518868	31273.441445	
HLA A*8001	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.415183	0.896310	-3.518873	26012.539900	
HLA A*3301	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.594016	1.074983	-3.519033	39265.9545
HLA B*1801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.511021	0.991777	-3.519244	32435.5003
HLA A*0203	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.255195	0.735649	-3.519546	17996.7704
HLA B*3501	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.332382	0.812772	-3.519610	21497.2154
HLA B*4801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.425222	0.905427	-3.519795	26620.8616
HLA A*0212	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.403034	0.883157	-3.519876	25294.9352
HLA A*0212	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.416202	0.896310	-3.519893	26073.686286	
HLA A*1101	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.447021	0.927121	-3.519899	27991.1428
HLA A*0101	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.392560	0.872645	-3.519915	24692.1876
HLA A*1101	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.443393	0.923260	-3.520134	27758.3102
HLA B*1801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.435506	0.915034	-3.520472	27258.7417
HLA B*4501	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.536268	1.015721	-3.520547	34377.0153
HLA B*4402	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.357179	0.836190	-3.520989	22760.336241	
HLA A*3101	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.363825	0.842742	-3.521084	23111.352773	
HLA A*6802	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.128543	0.607347	-3.521197	13444.456169	
HLA A*3002	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.401854	0.880566	-3.521288	25226.333385	
HLA B*0702	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.365294	0.843953	-3.521341	23189.6286
HLA B*0801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.402183	0.880633	-3.521550	25245.446656	
HLA A*0301	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.365526	0.843953	-3.521573	23202.0518
HLA B*4601	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.402540	0.880633	-3.521907	25266.214603	
HLA A*3201	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.588187	1.066259	-3.521928	38742.4505
HLA B*4501	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.652375	1.130392	-3.5219		
HLA B*4801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.274822	0.752698		

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HLA B*5101	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.437251	0.915034	-3.522217	27368.5300
HLA B*1509	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.459807	0.937566	-3.522241	28827.4699
HLA B*4002	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.575006	1.052696	-3.522311	37584.3009
HLA B*1801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.405663	0.883157	-3.522505	25448.5267
HLA B*5701	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.358739	0.836190	-3.522549	22842.242177
HLA A*6801	1:163-171	9	RRKQARQAA	1.170385	-0.015739	-4.677226	1.154646	-3.522580	47558.2122
HLA A*8001	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.432907	0.910145	-3.522763	27096.1304
HLA B*4002	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.503223	0.980281	-3.522941	31858.304681
HLA A*2402	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.537365	1.014245	-3.523120	34463.9758
HLA B*5701	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.406342	0.883157	-3.523184	25488.3456
HLA B*3801	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.537591	1.014245	-3.523346	34481.8793
HLA B*1801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.461028	0.937566	-3.523462	28908.6798
HLA B*4801	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.419856	0.896310	-3.523546	26293.953166
HLA A*1101	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.409208	0.885414	-3.523794	25657.1267
HLA A*0219	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.307299	0.783495	-3.523804	20290.7970
HLA A*3002	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.192496	0.668648	-3.523849	15577.444815
HLA A*0202	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.364255	0.839978	-3.524278	23134.244567
HLA A*2501	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.429738	0.905427	-3.524311	26899.1043
HLA B*5401	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.504851	0.980470	-3.524381	31977.9673
HLA B*1503	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.260037	0.735649	-3.524388	18198.5533
HLA A*3301	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.636568	1.112050	-3.524518	43307.9555
HLA A*0212	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.308157	0.783495	-3.524661	20330.9030
HLA B*4001	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.397658	0.872645	-3.525013	24983.7687
HLA B*1801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.398809	0.873495	-3.525315	25050.0846
HLA B*5301	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.605383	1.080003	-3.525380	40307.2313
HLA B*4402	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.368226	0.842742	-3.525484	23346.724157
HLA B*0802	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.430957	0.905427	-3.525530	26974.7359
HLA B*5801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.338326	0.812772	-3.525555	21793.4710
HLA B*4501	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.585098	1.058921	-3.526177	38467.8146
HLA A*8001	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.368947	0.842742	-3.526205	23385.531454
HLA B*1517	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.422588	0.896310	-3.526279	26459.908382
HLA B*1517	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.310793	0.784286	-3.526506	20454.684786
HLA A*0101	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.340765	0.814245	-3.526520	21916.1957
HLA B*4601	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.399192	0.872645	-3.526547	25072.1838
HLA B*2705	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.431977	0.905427	-3.526550	27038.1440
HLA B*7301	1:46-54	9	SWSKPNPKT	1.176779	-0.200471	-4.502858	0.976308	-3.526551	31831.601644
HLA B*3901	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.453841	0.927121	-3.526720	28434.2112
HLA B*7301	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.527512	1.000751	-3.526760	33690.8243
HLA A*2601	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.399444	0.872645	-3.526799	25086.7013
HLA B*5701	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.339652	0.812772	-3.526880	21860.0683
HLA A*2402	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.412502	0.885414	-3.527088	25852.4672
HLA B*1501	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.369873	0.842742	-3.527131	23435.430789
HLA B*0802	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.442416	0.915034	-3.527381	27695.9100
HLA B*4501	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.507952	0.980470	-3.527483	32207.1410
HLA B*0802	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.408327	0.880566	-3.527761	25605.128644
HLA A*2602	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.594145	1.066259	-3.527886	39277.6396
HLA A*3001	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-3.410968	-0.116983	-3.527952	2576.13269
HLA B*0801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.372110	0.843953	-3.528157	23556.4396
HLA A*6901	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.372147	0.843953	-3.528194	23558.4787
HLA B*7301	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.542452	1.014245	-3.528207	34870.0052
HLA B*1501	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.408780	0.880566	-3.528214	25631.877141
HLA B*0801	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.374285	0.846009	-3.528276	23674.7430
HLA B*5401	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.544505	1.015721	-3.528785	35035.2694
HLA B*0702	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.409441	0.880566	-3.528874	25670.871811
HLA A*8001	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.402531	0.873495	-3.529036	25265.6678
HLA B*4402	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.425398	0.896310	-3.529089	26631.665060
HLA A*0250	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.563407	1.034236	-3.529171	36593.762845
HLA A*2902	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.372056	0.842742	-3.529314	23553.508742
HLA B*7301	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.563557	1.034236	-3.529321	36606.435003
HLA B*0802	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.425965	0.896310	-3.529655	26666.409625
HLA B*5701	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.410268	0.880566	-3.529702	25719.802938
HLA A*3301	1:35-43	9	LVEFAGRAC	1.017577	0.072013	-4.619762	1.089590	-3.530172	41664.081919
HLA A*2902	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.440386	0.910145	-3.530241	27566.7574
HLA B*4403	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.638950	1.108664	-3.530286	43546.1797
HLA A*3002	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.588241	1.057871	-3.530370	38747.2714
HLA A*2902	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.415796	0.885414	-3.530382	26049.2950
HLA B*1517	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.453822	0.923260	-3.530563	28432.9806
HLA A*0202	1:2-10	9	AETAPLRVQ	1.072975	-0.038739	-4.564981	1.034236	-3.530745	36726.642213
HLA B*5101	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.427320	0.896310	-3.531011	26749.779035
HLA B*1509	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.436474	0.905427	-3.531047	27319.5657
HLA B*4601	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.375011	0.843953	-3.531058	23714.3521
HLA A*2603	1:224-232	9	PAVFADFEV	1.069788	0.050175	-4.651026	1.119963	-3.531063	44774.0534
HLA A*2403	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.427609	0.896310	-3.531300	26767.584699
HLA A*6801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.543422	1.012095	-3.531327	34948.0018
HLA B*4501	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.640202	1.108664	-3.531538	43671.9250
HLA A*3002	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.405280	0.873495	-3.531785	25426.0958
HLA A*2301	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.521899	0.990022	-3.531877	33258.1982
HLA B*5701	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.406036	0.873495	-3.532542	25470.4263
HLA A*2301	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.544686	1.012095	-3.532591	35049.8668
HLA A*2601	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.375512	0.842742	-3.532770	23741.694106
HLA B*4002	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.641445	1.108664	-3.532781	43797.0857
HLA B*0801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.345605	0.812772	-3.532833	22161.8040
HLA B*1509	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.545036	1.012095	-3.532941	35078.1310
HLA B*4402	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.372984	0.839978	-3.533006	23603.894196
HLA B*2705	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.413876	0.880566	-3.533310	25934.414380
HLA B*5101	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.336517	0.803085	-3.533433	21702.876673
HLA A*3301	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.642244	1.108664	-3.533580	43877.7185
HLA A*0250	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.577833	1.044178	-3.533655	37829.7008
HLA B*1801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.439230	0.905427	-3.533803	27493.4815
HLA A*2301	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.542849	1.008953	-3.533896	34901.9004
HLA B*3901	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.012887	0.478869	-3.534019	10301.1922
HLA B*5801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.348584	0.814245	-3.534339	22314.3508
HLA A*0216	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.417720	0.883157	-3.534563	26164.9677
HLA B*0702	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.318180	0.783495	-3.534684	20805.5677
HLA A*0212	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.407371	0.872645	-3.534726	25548.8126
HLA B*0801	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.371245	0.836190	-3.535055	23509.589195
HLA A*0250	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.592947	1.057871	-3.535076	39169.4203
HLA B*4402	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.379111	0.843953	-3.535158	23939.2817
HLA A*3101	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.381181	0.846009	-3.535172	24053.6513
HLA A*3002	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.587884	1.052696	-3.535188	38715.4225
HLA B*3901	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.338329	0.803085	-3.535244	21793.588954
HLA A*0250	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.318887	0.783495	-3.535391	20839.4746
HLA B*4403	1:41-49	9	RACYQSWSK	0.781972	0.322141	-4.639540	1.104113	-3.535427	43605.350450
HLA A*2403	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.408127	0.872645	-3.535482	25593.3570
HLA A*3201	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.593358	1.057871	-3.535488	39206.5207
HLA B*0803	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.450655	0.915034	-3.535621	28226.3864
HLA B*1501	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.297826	0.762047	-3.535779	19852.9927
HLA A*2403	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.372070	0.836190	-3.535880	23554.273285
HLA B*4403	1:81-89	9	YITGISRSC	1.133968	-0.008438	-4.661489	1.125530	-3.535959	45865.768015
HLA B*5301	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.347868	0.811904	-3.535963	22277.5621
HLA A*3101	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.409483	0.873495	-3.535988	25673.3717
HLA A*2402	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.588699	1.052696	-3.536004	38788.1686
HLA B*7301	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.321168	0.785066	-3.536102	20949.232515
HLA A*0203	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.372352	0.836190	-3.536162	23569.569371
HLA A*6901	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.349082	0.812772	-3.536311	22339.9575
HLA A*6802	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.417154	0.880633	-3.5365	
HLA B*5301	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.589277	1.052696		

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HLA B*7301	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.552329	1.015721	-3.536608	35672.1468
HLA B*0702	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.417295	0.880633	-3.536662	26139.359780	
HLA B*5101	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.442143	0.905427	-3.536716	27678.5350
HLA A*3002	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.549096	1.012095	-3.537001	35407.5890
HLA B*1517	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.410512	0.873495	-3.537017	25734.2777
HLA B*1501	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.381031	0.843953	-3.537078	24045.3246
HLA A*2501	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.377095	0.839978	-3.537118	23828.420638	
HLA B*3801	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.517508	0.980281	-3.537226	32923.616188	
HLA A*2402	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.569166	1.031880	-3.537285	37082.2140
HLA B*1503	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.285818	0.748410	-3.537408	19311.5781
HLA A*0201	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.272416	0.734934	-3.537483	18724.761866	
HLA B*4002	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.645858	1.108038	-3.537819	44244.322205	
HLA B*4001	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.384031	0.846009	-3.538022	24212.0151
HLA A*0101	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.380850	0.842742	-3.538108	24035.310395	
HLA B*4601	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.380998	0.842742	-3.538256	24043.503579	
HLA B*5301	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.596142	1.057871	-3.538272	39458.6700
HLA B*5301	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.554028	1.015721	-3.538307	35811.9463
HLA B*4501	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.646346	1.108038	-3.538308	44294.136458	
HLA B*0702	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.374772	0.836190	-3.538581	23701.269980	
HLA B*0702	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.434925	0.896310	-3.538616	27222.341752	
HLA B*4601	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.374969	0.836190	-3.538779	23712.043012	
HLA A*3101	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.382924	0.843953	-3.538971	24150.4001
HLA B*5401	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.566478	1.027504	-3.538974	36853.4241
HLA B*5701	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.419814	0.880633	-3.539181	26291.392838	
HLA A*3002	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.519575	0.980281	-3.539294	33080.729416	
HLA B*0803	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.435654	0.896310	-3.539344	27268.033709	
HLA A*8001	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.420077	0.880633	-3.539444	26307.327820	
HLA B*0801	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.329159	0.789295	-3.539864	21338.245896	
HLA B*3501	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.467222	0.927116	-3.540106	29323.884665	
HLA A*2301	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.532180	0.991777	-3.540403	34054.9356
HLA A*2601	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.324711	0.784286	-3.540425	21120.837753	
HLA B*2705	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.352435	0.811904	-3.540531	22513.0877
HLA A*6802	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.276192	0.735649	-3.540543	18888.2588
HLA A*2501	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.424090	0.883157	-3.540933	26551.5364
HLA B*1801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.034681	0.493735	-3.540947	10831.3181
HLA A*2402	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.550074	1.008953	-3.541121	35487.3640
HLA A*6801	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.550128	1.008953	-3.541175	35491.7799
HLA B*3801	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.478854	0.937566	-3.541288	30119.9192
HLA B*4002	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.035250	0.493735	-3.541515	10845.5077
HLA B*4002	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.533334	0.991777	-3.541557	34145.5145
HLA A*2403	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.355835	0.814245	-3.541590	22690.0142
HLA A*0201	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.385626	0.843953	-3.541673	24301.1170
HLA A*2601	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.353826	0.812136	-3.541690	22585.304935	
HLA B*4501	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.555940	1.014245	-3.541695	35969.9973
HLA A*8001	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.422480	0.880566	-3.541914	26453.324524	
HLA B*4002	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.515910	0.973692	-3.542218	32802.7217
HLA B*5801	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.161948	0.619672	-3.542276	14519.384870	
HLA B*1502	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.600160	1.057871	-3.542289	39825.3923
HLA B*4601	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.234618	0.692096	-3.542522	17163.971649	
HLA A*0201	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.345643	0.803085	-3.542558	22163.722415	
HLA A*2402	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.558299	1.015721	-3.542578	36165.9009
HLA B*1501	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.332098	0.789295	-3.542803	21483.148044	
HLA A*6801	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.632489	1.089590	-3.542899	42903.129941	
HLA B*0802	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.426164	0.883157	-3.543007	26678.6747
HLA A*2601	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.389087	0.846009	-3.543078	24495.5406
HLA A*2902	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.423794	0.880633	-3.543161	26533.443848	
HLA B*5401	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.552280	1.008953	-3.543327	35668.0944
HLA B*4801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.428857	0.885414	-3.543442	26844.5891
HLA A*1101	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.458526	0.915034	-3.543492	28742.6005
HLA A*2902	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.249824	0.706243	-3.543581	17775.574892	
HLA A*6901	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.386552	0.842742	-3.543810	24352.970077	
HLA A*3002	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.471098	0.927116	-3.543983	29586.810692	
HLA B*7301	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.454168	0.910145	-3.544023	28455.6010
HLA B*1801	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.416931	0.872645	-3.544286	26117.4502
HLA A*6901	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.356488	0.812136	-3.544352	22724.164531	
HLA B*4601	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.356530	0.812136	-3.544394	22726.377472	
HLA B*5301	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.588605	1.044178	-3.544428	38779.7759
HLA B*1517	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.425168	0.880633	-3.544535	26617.549515	
HLA A*3002	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.250933	0.706243	-3.544690	17821.022247	
HLA B*1502	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.521048	0.976308	-3.544741	33193.129790	
HLA B*4403	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.611001	1.066259	-3.544741	40831.9938
HLA A*0201	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.328304	0.783495	-3.544808	21296.2679
HLA A*2403	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.428058	0.883157	-3.544901	26795.2576
HLA B*3501	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.359211	0.814245	-3.544966	22867.0940
HLA A*2603	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.502591	0.957621	-3.544970	31811.9762
HLA A*2603	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.634669	1.089590	-3.545080	43119.061408	
HLA B*4002	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.589258	1.044178	-3.545081	38838.1426
HLA B*0802	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.334494	0.789295	-3.545200	21602.021598	
HLA B*3901	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.328893	0.783495	-3.545398	21325.2054
HLA B*3901	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.391422	0.846009	-3.545413	24627.6185
HLA A*3001	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.292690	0.747233	-3.545457	19619.5936
HLA A*6802	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.389461	0.843953	-3.545508	24516.6201
HLA A*2402	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.557651	1.012095	-3.545556	36111.9408
HLA B*4002	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.635247	1.089590	-3.545658	43176.483867	
HLA A*3001	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.105655	0.559811	-3.545844	12754.2391
HLA B*4403	1:6-14 9	PLRVQLIAK	1.039672	0.090720	-4.676281	1.130392	-3.545890	47454.896188	
HLA A*2602	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.603776	1.057871	-3.545905	40158.3555
HLA B*5801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.357820	0.811904	-3.545916	22793.9758
HLA B*4801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.419461	0.873495	-3.545967	26270.0664
HLA B*1501	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.293237	0.747233	-3.546004	19644.3398
HLA B*0803	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.469284	0.923260	-3.546025	29463.5009
HLA A*2402	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.418728	0.872645	-3.546083	26225.7630
HLA B*1502	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.573651	1.027504	-3.546147	37467.1642
HLA A*1101	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.427095	0.880633	-3.546462	26735.890161	
HLA A*2403	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.299231	0.752698	-3.546533	19917.3234
HLA B*4403	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.349681	0.803085	-3.546597	22370.797521	
HLA A*6801	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.382920	0.836190	-3.546730	24150.138810	
HLA A*2902	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.430245	0.883157	-3.547088	26930.5552
HLA A*2301	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.523468	0.976308	-3.547161	33378.604346	
HLA B*1502	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.453221	0.905427	-3.547794	28393.6301
HLA B*0702	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.390541	0.842742	-3.547800	24577.706895	
HLA A*0211	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.474930	0.927121	-3.547809	29849.0259
HLA B*4403	1:98-106	9	HFSYSQLSQ	1.017120	0.041801	-4.607065	1.058921	-3.548145	40463.6634
HLA B*5301	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.528865	0.980470	-3.548395	33795.9719
HLA B*4402	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.421992	0.873495	-3.548497	26423.5744
HLA B*5401	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.522286	0.973692	-3.548595	33287.8988
HLA B*4403	1:88-96 9	SCTHELIRH	1.266403	-0.158365	-4.656715	1.108038	-3.548676	45364.331624	
HLA B*5301	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.563059	1.014245	-3.548814	36564.4752
HLA B*0702	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.283776	0.734934	-3.548843	19221.003740	
HLA A*2602	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.486414	0.937566	-3.548849	30648.8684
HLA B*0801	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.333407	0.784286	-3.549120	21547.981023	
HLA B*0702	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.361088	0.811904	-3.549184	22966.1510
HLA B*1517	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.432360	0.883157	-3.549203	27061.9971
HLA A*2902	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.352466	0.803085	-3.549381	22514.671083	
HLA B*5401	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.363710	0.814245	-3.549465	23105.2271
HLA A*3201	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.302177	0.752698		
HLA B*5801	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.352595	0.803085	-3.5495		

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HLA A*2501	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.423556	0.873495	-3.550062	26518.9499
HLA B*3801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.526518	0.976308	-3.550210	33613.814973	
HLA B*4403	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.594472	1.044178	-3.550294	39307.1865
HLA A*3001	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.285235	0.734934	-3.550302	19285.686083	
HLA B*1801	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.446666	0.896310	-3.550356	27968.286412	
HLA A*0206	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.487923	0.937566	-3.550357	30755.5016
HLA A*2402	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.584625	1.034236	-3.550389	38426.007948	
HLA A*3201	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.584663	1.034236	-3.550426	38429.334179	
HLA A*2403	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.396495	0.846009	-3.550486	24916.9543
HLA B*4001	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.353607	0.803085	-3.550523	22573.944681	
HLA B*0803	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.433828	0.883157	-3.550671	27153.6535
HLA A*0219	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.390734	0.839978	-3.550756	24588.612253	
HLA B*0801	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.393619	0.842742	-3.550877	24752.506660	
HLA B*1502	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.583091	1.031880	-3.551211	38290.5015
HLA A*0250	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.531614	0.980281	-3.551332	34010.564330	
HLA A*0212	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.395325	0.843953	-3.551372	24849.9152
HLA A*6802	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.394397	0.842742	-3.551655	24796.870021	
HLA A*2501	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.461801	0.910145	-3.551657	28960.1789
HLA B*4801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.434832	0.883157	-3.551674	27216.4515
HLA B*1509	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.474968	0.923260	-3.551708	29851.6097
HLA B*5101	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.478884	0.927121	-3.551763	30122.0375
HLA B*4002	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.609774	1.057871	-3.551904	40716.8484
HLA B*5301	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.552722	1.000751	-3.551970	35704.3894
HLA B*5701	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.394780	0.842742	-3.552038	24818.745840	
HLA B*0803	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.479206	0.927116	-3.552091	30144.370965	
HLA B*4002	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.583972	1.031880	-3.552092	38368.2606
HLA B*1509	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.394972	0.842742	-3.552231	24829.758149	
HLA A*0219	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.448799	0.896310	-3.552490	28106.009634	
HLA A*0201	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.395261	0.842742	-3.552520	24846.285775	
HLA B*4402	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.433196	0.880566	-3.552630	27114.166643	
HLA A*0250	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-3.869470	0.316807	-3.552664	7404.065079	
HLA A*2301	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.533063	0.980281	-3.552782	34124.277924	
HLA B*1502	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.177845	0.625007	-3.552838	15060.6887
HLA B*4002	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.479967	0.927116	-3.552852	30197.254475	
HLA A*6901	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.256130	0.703256	-3.552873	18035.561727	
HLA B*4501	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.642502	1.089590	-3.552913	43903.837454	
HLA A*0101	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.342292	0.789295	-3.552998	21993.398164	
HLA A*2902	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.245136	0.692096	-3.553040	17584.759494	
HLA B*4001	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.389282	0.836190	-3.553092	24506.542132	
HLA B*4403	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.628347	1.074983	-3.553364	42495.8807
HLA A*3101	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.113272	0.559811	-3.553461	12979.9071
HLA A*2403	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.434028	0.880566	-3.553462	27166.142758	
HLA A*6802	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.399479	0.846009	-3.553470	25088.7371
HLA B*3501	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.257095	0.703401	-3.553694	18075.707772	
HLA A*0201	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.389947	0.836190	-3.553757	24544.090350	
HLA B*4801	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.396749	0.842742	-3.554007	24931.516734	
HLA B*1517	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.469294	0.915034	-3.554260	29464.1385
HLA A*0202	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.481516	0.927121	-3.554394	30305.1033
HLA B*0702	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.192069	0.637604	-3.554464	15562.1148
HLA B*1517	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.368844	0.814245	-3.554599	23379.9655
HLA A*0101	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.400639	0.846009	-3.554630	25155.8761
HLA B*2705	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.428234	0.873495	-3.554740	26806.1317
HLA B*4801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.287415	0.732654	-3.554761	19382.750948	
HLA B*4402	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.437949	0.883157	-3.554792	27412.5394
HLA A*3301	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.586768	1.031880	-3.554888	38616.0633
HLA A*2602	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.547113	0.991777	-3.555337	35246.2884
HLA A*2402	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.395337	0.839978	-3.555359	24850.587448	
HLA A*2601	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.399328	0.843953	-3.555375	25080.0521
HLA B*7301	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.582990	1.027504	-3.555486	38281.5952
HLA A*0301	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.317712	0.762047	-3.555665	20783.1812
HLA A*6901	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.259071	0.703401	-3.555670	18158.134490	
HLA A*3301	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.569974	1.014245	-3.555729	37151.2884
HLA B*4001	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.399810	0.843953	-3.555857	25107.8820
HLA A*0101	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.395849	0.839978	-3.555871	24879.912422	
HLA B*5801	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.345222	0.789295	-3.555928	22142.270116	
HLA B*4002	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.612239	1.056254	-3.555985	40948.5724
HLA B*5801	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.339534	0.783495	-3.556039	21854.1561
HLA A*0203	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.396027	0.839978	-3.556050	24890.143941	
HLA B*4001	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.396030	0.839978	-3.556052	24890.278594	
HLA B*5301	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.592825	1.036697	-3.556128	39158.4029
HLA B*3501	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.359223	0.803085	-3.556138	22867.712611	
HLA A*6802	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.392449	0.836190	-3.556259	24685.910068	
HLA A*6801	1:123-131	9	EDDADLRHI	1.163777	-0.051727	-4.668380	1.112050	-3.556330	46599.3339
HLA B*4501	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.614327	1.057871	-3.556457	41145.9844
HLA B*5101	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.479819	0.923260	-3.556560	30186.9643
HLA B*0803	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.466721	0.910145	-3.556576	29290.1140
HLA A*2602	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.609274	1.052696	-3.556578	40669.9572
HLA B*2705	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.439782	0.883157	-3.556625	27528.4568
HLA B*4403	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.548478	0.991777	-3.556702	35357.2469
HLA B*5701	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.400724	0.843953	-3.556771	25160.7758
HLA B*3801	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.568888	1.012095	-3.556793	37058.5495
HLA A*3201	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.430328	0.873495	-3.556833	26935.6549
HLA A*0201	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.396831	0.839978	-3.556853	24936.237867	
HLA B*3501	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.396843	0.839978	-3.556865	24936.912388	
HLA B*0802	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.484086	0.927116	-3.556970	30484.993449	
HLA A*2402	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.547026	0.990022	-3.557004	35239.2340
HLA A*0212	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.360210	0.803085	-3.557125	22919.730637	
HLA B*1517	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.484352	0.927116	-3.557236	30503.635156	
HLA A*3301	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.623507	1.066259	-3.557247	42024.9200
HLA A*2403	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.401365	0.843953	-3.557412	25197.9632
HLA A*0212	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.310118	0.752698	-3.557421	20422.9507
HLA A*2902	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.369607	0.812136	-3.557471	23421.108679	
HLA A*3001	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.306249	0.748410	-3.557839	20241.7887
HLA B*4601	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.372166	0.814245	-3.557921	23559.4983
HLA A*2501	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.485040	0.927116	-3.557924	30552.024733	
HLA A*0202	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.548025	0.990022	-3.558003	35320.3493
HLA B*4601	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.404049	0.846009	-3.558039	25354.1204
HLA A*2603	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.572471	1.014245	-3.558226	37365.5502
HLA B*1503	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.320442	0.762047	-3.558395	20914.2418
HLA A*2403	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.349378	0.790864	-3.558514	22355.190931	
HLA A*2403	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.183733	0.625007	-3.558726	15266.2595
HLA A*2602	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.590760	1.031880	-3.558879	38972.6353
HLA A*2902	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.405033	0.846009	-3.559024	25411.6569
HLA B*5801	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.349947	0.790864	-3.559083	22384.477361	
HLA B*0802	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.469348	0.910145	-3.559203	29467.8049
HLA A*3301	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.571400	1.012095	-3.559305	37273.4864
HLA B*7301	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.464762	0.905427	-3.559335	29158.2591
HLA A*2602	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.469486	0.910145	-3.559342	29477.2120
HLA B*0702	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.405486	0.846009	-3.559477	25438.2033
HLA B*1801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.184621	0.625007	-3.559614	15297.5100
HLA A*6801	1:176-184	9	PNATETRIV	1.219759	-0.111095	-4.668337	1.108664	-3.559673	46594.7964
HLA B*2705	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.373996	0.814245	-3.559751	23658.9947
HLA A*0301	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.363144	0.803085	-3.560059	23075.122543	
HLA A*6802	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.432830	0.872645	-3.560185	27091.2934
HLA B*5401	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.517848	0.957621	-3.560227	32949.4525
HLA A*2501	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.349752	0.789295	-3.5604		
HLA B*1801	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.363644	0.803085	-3.5605		

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HLA A*3301	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.569929	1.008953	-3.560977	37147.4699
HLA A*3001	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.293632	0.732654	-3.560978	19662.201967	
HLA B*5301	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.588568	1.027504	-3.561063	38776.4194
HLA B*5301	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.570021	1.008953	-3.561068	37155.3083
HLA A*2602	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.588680	1.027504	-3.561176	38786.4899
HLA B*3501	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.433866	0.872645	-3.561221	27156.0040
HLA B*1501	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.346322	0.785066	-3.561256	22198.401566	
HLA B*2705	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.457680	0.896310	-3.561371	28686.677042	
HLA A*0301	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.346470	0.785066	-3.561404	22205.968581	
HLA A*2602	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.787478	0.225691	-3.561787	6130.245960	
HLA A*3201	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.542215	0.980281	-3.561933	34850.957501	
HLA B*2705	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.346397	0.784286	-3.562111	22202.244807	
HLA A*6801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.375009	0.812772	-3.562237	23714.2238
HLA A*0250	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.538763	0.976308	-3.562456	34575.090139	
HLA B*5401	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.467969	0.905427	-3.562542	29374.3752
HLA A*0216	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.402629	0.839978	-3.562652	25271.409259	
HLA B*4801	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.398992	0.836190	-3.562802	25060.657334	
HLA B*0802	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.435731	0.872645	-3.563086	27272.9022
HLA B*3801	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.543617	0.980470	-3.563148	34963.6977
HLA B*4001	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.405905	0.842742	-3.563163	25462.711132	
HLA B*5801	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.347534	0.784286	-3.563248	22260.455037	
HLA B*3501	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.013202	0.449835	-3.563367	10308.6625
HLA B*5101	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.436998	0.873495	-3.563503	27352.5441
HLA A*6802	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.376376	0.812772	-3.563605	23789.0070
HLA B*5701	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.375822	0.812136	-3.563686	23758.654232	
HLA A*2402	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.543986	0.980281	-3.563705	34993.406855	
HLA A*0101	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.376557	0.812772	-3.563785	23798.9187
HLA A*2603	1:192-200	9	WRHFIAMRA	1.140260	-0.074001	-4.630128	1.066259	-3.563868	42670.5012
HLA B*5301	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.595891	1.031880	-3.564011	39435.8357
HLA A*2501	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.479079	0.915034	-3.564045	30135.5660
HLA B*5401	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.501679	0.937566	-3.564113	31745.2717
HLA A*2603	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.447434	0.883157	-3.564277	28017.8070
HLA A*8001	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.408299	0.843953	-3.564346	25603.4664
HLA B*5801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.349470	0.785066	-3.564404	22359.908054	
HLA B*4601	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.404551	0.839978	-3.564574	25383.490370	
HLA A*8001	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.447794	0.883157	-3.564636	28041.0073
HLA B*4501	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.617408	1.052696	-3.564712	41438.8440
HLA A*2602	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.609295	1.044178	-3.565117	40671.9374
HLA A*6801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.497674	-0.067515	-3.565189	3145.38364
HLA B*4002	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.645364	1.080003	-3.565361	44194.0858
HLA A*0219	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.369142	0.803085	-3.566058	23396.034401	
HLA A*3002	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.462619	0.896310	-3.566309	29014.751915	
HLA A*2603	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.447091	0.880566	-3.566525	27995.686089	
HLA B*3501	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.410528	0.843953	-3.566575	25735.2522
HLA B*0803	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.472022	0.905427	-3.566595	29649.7817
HLA A*2603	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.406781	0.839978	-3.566803	25514.143923	
HLA B*1517	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.379708	0.812772	-3.566936	23972.1996
HLA A*0203	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.351098	0.783495	-3.567603	22443.8938
HLA A*0101	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.379842	0.812136	-3.567706	23979.592908	
HLA B*7301	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.494833	0.927121	-3.567711	31248.7500
HLA A*0101	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.380079	0.811904	-3.568175	23992.6989
HLA A*0101	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.352555	0.784286	-3.568269	22519.300030	
HLA A*6801	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.600263	1.031880	-3.568383	39834.8733
HLA B*5701	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.237313	0.668648	-3.568665	17270.807669	
HLA A*3301	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.596438	1.027504	-3.568934	39485.5761
HLA A*0202	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.549625	0.980281	-3.569344	35450.714294	
HLA B*5101	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.381287	0.811904	-3.569382	24059.5078
HLA B*4601	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.358875	0.789295	-3.569580	22849.410594	
HLA B*2705	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-3.457023	-0.112631	-3.569654	2864.32856
HLA B*1517	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.238447	0.668648	-3.569800	17315.994893	
HLA A*6901	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.360684	0.790864	-3.569820	22944.790954	
HLA A*0219	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.442545	0.872645	-3.569900	27704.1520
HLA A*2902	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.384205	0.814245	-3.569960	24221.7095
HLA A*0250	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.497098	0.927116	-3.569982	31412.142141	
HLA A*3201	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.622750	1.052696	-3.570055	41951.7769
HLA A*2301	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.543777	0.973692	-3.570085	34976.5622
HLA B*4402	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.143561	0.573275	-3.570286	13917.4973
HLA A*2601	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.384541	0.814245	-3.570296	24240.4554
HLA B*4002	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.586035	1.015721	-3.570314	38550.9388
HLA B*5301	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.604551	1.034236	-3.570315	40230.112826	
HLA A*2501	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.466712	0.896310	-3.570402	29289.480208	
HLA A*2603	1:140-148	9	RATYSELLA	1.126115	-0.051132	-4.645458	1.074983	-3.570475	44203.6502
HLA B*1501	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.383448	0.812772	-3.570676	24179.5528
HLA A*2501	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.456299	0.885414	-3.570884	28595.5692
HLA A*2501	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.443809	0.872645	-3.571164	27784.9029
HLA B*5701	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.417180	0.846009	-3.571171	26132.4315
HLA B*0803	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.498298	0.927121	-3.571177	31499.0996
HLA B*7301	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.583274	1.012095	-3.571179	38306.6624
HLA B*4601	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.374281	0.803085	-3.571196	23674.486884	
HLA B*5401	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-3.870885	0.299515	-3.571370	7428.217601	
HLA A*2402	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.528997	0.957621	-3.571375	33806.2120
HLA B*4801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.415627	0.843953	-3.571674	26039.1505
HLA A*0216	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.407991	0.836190	-3.571801	25585.327815	
HLA B*5801	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.240473	0.668648	-3.571825	17396.933570	
HLA A*3001	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.278245	0.706243	-3.572002	18977.778591	
HLA A*6801	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.616245	1.044178	-3.572067	41328.0236
HLA B*5701	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.412164	0.839978	-3.572186	25832.335420	
HLA B*0802	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.408475	0.836190	-3.572285	25613.856949	
HLA B*4801	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.307933	0.735649	-3.572285	20320.4568
HLA B*7301	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.604488	1.031880	-3.572608	40224.2369
HLA A*8001	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.418665	0.846009	-3.572656	26221.9325
HLA B*4002	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.478201	0.905427	-3.572774	30074.6544
HLA A*6802	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-3.632919	0.060047	-3.572872	4294.566959	
HLA B*0802	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.415744	0.842742	-3.573002	26046.194918	
HLA A*2501	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.453898	0.880633	-3.573265	28437.903309	
HLA A*0206	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.211574	0.638108	-3.573467	16276.9878
HLA B*4403	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.614783	1.041264	-3.573519	41189.1905
HLA A*2601	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.385704	0.811904	-3.573799	24305.4558
HLA A*2601	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.386646	0.812772	-3.573874	24358.2405
HLA B*4601	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.386763	0.812772	-3.573992	24364.8301
HLA B*1501	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.322491	0.748410	-3.574081	21013.1362
HLA A*2403	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.416910	0.842742	-3.574168	26116.178655	
HLA B*4501	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.574983	1.000751	-3.574232	37582.2677
HLA A*3301	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.632195	1.057871	-3.574325	42874.1271
HLA B*3901	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.447953	0.873495	-3.574459	28051.3247
HLA A*2603	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.606346	1.031880	-3.574466	40396.7342
HLA B*4501	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.607112	1.032480	-3.574632	40468.0417
HLA A*6802	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.364058	0.789295	-3.574763	23123.734044	
HLA B*4501	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.230718	0.655774	-3.574943	17010.5220
HLA A*3101	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.378091	0.803085	-3.575007	23883.140837	
HLA B*5701	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.389259	0.814245	-3.575013	24505.2163
HLA B*4501	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.655216	1.080003	-3.575212	45208.0261
HLA A*0301	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.359300	0.783495	-3.575805	22871.7954
HLA B*5401	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.499146	0.923260	-3.575887	31560.6765
HLA A*6901	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.360990	0.785066	-3.575924	22960.933371	
HLA B*1517	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.311075	0.734934	-3.5761		
HLA A*0301	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.367140	0.790864	-3.5762		

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HLA B*4403	1:35-43 9	LVEFAGRAC	1.017577	0.072013	-4.665901	1.089590	-3.576311	46334.128943	
HLA B*4601	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.361387	0.785066	-3.576321	22981.935492	
HLA B*7301	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.379708	0.803085	-3.576623	23972.199612	
HLA A*0201	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.389505	0.812772	-3.576733	24519.1402
HLA A*0212	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.419767	0.842742	-3.577025	26288.548322	
HLA B*7301	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.550941	0.973692	-3.577249	35558.2764
HLA B*5301	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.473664	0.896310	-3.577354	29762.115008	
HLA B*3901	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.487662	0.910145	-3.577517	30737.0385
HLA A*2902	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.339745	0.762047	-3.577698	21864.7992
HLA B*7301	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.614490	1.036697	-3.577793	41161.3463
HLA A*8001	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.389942	0.812136	-3.577806	24543.824790	
HLA B*4601	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.362181	0.784286	-3.577894	23023.997382	
HLA A*3301	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.622118	1.044178	-3.577941	41890.7706
HLA B*4801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.389987	0.811904	-3.578082	24546.3477
HLA B*4002	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.592404	1.014245	-3.578159	39120.5014
HLA B*1801	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.488318	0.910145	-3.578173	30783.4668
HLA B*1801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.505441	0.927116	-3.578325	32021.419136	
HLA A*0201	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.367909	0.789295	-3.578614	23329.679451	
HLA A*2603	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.631465	1.052696	-3.578769	42802.0530
HLA B*4801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.391721	0.812772	-3.578949	24644.5448
HLA A*0203	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.421771	0.842742	-3.579029	26410.140725	
HLA B*4801	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.368334	0.789295	-3.579039	23352.534827	
HLA A*1101	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.452641	0.873495	-3.579146	28355.7147
HLA A*0101	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.382520	0.803085	-3.579435	24127.938593	
HLA A*2603	1:189-197	9	YRAWRHFIA	1.123021	-0.081757	-4.620800	1.041264	-3.579536	41763.8270
HLA B*5101	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.463364	0.883157	-3.580206	29064.5530
HLA B*0702	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.420291	0.839978	-3.580313	26320.282103	
HLA A*0201	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.392379	0.811904	-3.580474	24681.9039
HLA B*1501	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.364016	0.783495	-3.580520	23121.4824
HLA A*3301	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.596704	1.015721	-3.580983	39509.7217
HLA A*2603	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.590147	1.008953	-3.581194	38917.6455
HLA A*0202	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.518922	0.937566	-3.581356	33031.0150
HLA A*3101	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.201034	0.619672	-3.581362	15886.720315	
HLA B*4601	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.364981	0.783495	-3.581486	23172.9494
HLA B*7301	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.454140	0.872645	-3.581495	28453.7538
HLA A*2602	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.593593	1.012095	-3.581498	39227.7367
HLA A*0201	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.393777	0.812136	-3.581640	24761.480143	
HLA A*8001	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.366064	0.784286	-3.581778	23230.813910	
HLA B*3901	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.393986	0.812136	-3.581850	24773.405174	
HLA A*6801	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.544132	0.962074	-3.582058	35005.146071	
HLA B*0802	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.394232	0.811904	-3.582328	24787.4814
HLA B*0702	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.220714	0.638108	-3.582606	16623.1581
HLA A*0216	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.479014	0.896310	-3.582704	30131.001558	
HLA B*5301	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.488313	0.905427	-3.582886	30783.1337
HLA A*2403	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.395177	0.812136	-3.583041	24841.447283	
HLA A*0219	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.425852	0.842742	-3.583110	26659.485932	
HLA B*0801	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-3.900225	0.316807	-3.583418	7947.398428	
HLA A*0250	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.521081	0.937566	-3.583515	33195.6438
HLA A*2301	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.541136	0.957621	-3.583515	34764.5250
HLA B*4403	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.557374	0.973692	-3.583682	36088.8955
HLA A*3301	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.636875	1.052696	-3.584180	43338.6586
HLA B*0801	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.368193	0.783495	-3.584698	23344.9559
HLA A*6901	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.319726	0.734934	-3.584792	20879.761482	
HLA B*5401	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.561105	0.976308	-3.584797	36400.267388	
HLA B*4801	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.424851	0.839978	-3.584873	26598.116884	
HLA A*2601	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.387959	0.803085	-3.584875	24432.014455	
HLA B*3501	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.204624	0.619672	-3.584952	16018.589164	
HLA B*4501	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.597061	1.012095	-3.584966	39542.2240
HLA A*0202	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.508817	0.923260	-3.585557	32271.3241
HLA B*4501	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.513022	0.927116	-3.585907	32585.347989	
HLA B*4501	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.622814	1.036697	-3.586117	41957.9052
HLA B*4402	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.398285	0.812136	-3.586149	25019.882353	
HLA B*1502	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.598525	1.012095	-3.586430	39675.7204
HLA A*0101	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.371722	0.785066	-3.586656	23535.421784	
HLA B*1502	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.567021	0.980281	-3.586739	36899.508136	
HLA A*1101	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.459456	0.872645	-3.586811	28804.2422
HLA B*4403	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.567138	0.980281	-3.586857	36909.490599	
HLA B*0802	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.467879	0.880633	-3.587247	29368.337234	
HLA B*5101	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.255921	0.668648	-3.587273	18026.880052	
HLA B*3801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.514514	0.927116	-3.587399	32697.480263	
HLA A*0219	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.423928	0.836190	-3.587737	26541.627060	
HLA A*0216	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.431721	0.843953	-3.587768	27022.2049
HLA A*2603	1:168-176	9	RQAARAVLP	0.787201	0.256977	-4.632390	1.044178	-3.588213	42893.3827
HLA B*4001	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.340937	0.752698	-3.588239	21924.8526
HLA B*4403	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.515675	0.927116	-3.588559	32784.980666	
HLA A*2902	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.432513	0.843953	-3.588560	27071.5149
HLA A*2402	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.562448	0.973692	-3.588757	36513.0808
HLA B*4001	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.403156	0.814245	-3.588911	25302.0520
HLA B*5101	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.469599	0.880633	-3.588966	29484.867571	
HLA A*3201	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.546604	0.957621	-3.588983	35204.9354
HLA A*2602	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.562881	0.973692	-3.589189	36549.4448
HLA B*3901	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.485644	0.896310	-3.589334	30594.532025	
HLA A*3001	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.105105	0.515530	-3.589575	12738.1036
HLA A*1101	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.470316	0.880566	-3.589750	29533.558239	
HLA A*0101	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.380845	0.790864	-3.589981	24035.050340	
HLA B*4001	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.379337	0.789295	-3.590042	23951.717830	
HLA A*3101	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.295542	0.705319	-3.590224	19748.871505	
HLA B*3901	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.228063	0.637604	-3.590458	16906.8510
HLA B*4402	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.403283	0.812772	-3.590511	25309.4447
HLA A*2603	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.591326	1.000751	-3.590575	39023.4803
HLA B*5301	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.564288	0.973692	-3.590596	36668.0762
HLA B*4001	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.402914	0.812136	-3.590778	25287.957253	
HLA A*2602	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.571102	0.980281	-3.590820	37247.886269	
HLA B*1501	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.394268	0.803085	-3.591183	24789.492961	
HLA B*5701	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.403323	0.811904	-3.591418	25311.7725
HLA B*5801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.353565	0.762047	-3.591518	22571.7465
HLA B*0801	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.394780	0.803085	-3.591695	24818.745840	
HLA A*0250	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.817392	0.225691	-3.591701	6567.370879	
HLA A*0203	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.381066	0.789295	-3.591771	24047.275982	
HLA B*0702	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.376160	0.784286	-3.591874	23777.170006	
HLA B*4403	1:161-169	9	ILRRKQARQ	1.020477	0.059526	-4.671899	1.080003	-3.591896	46978.5099
HLA A*2501	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.394998	0.803085	-3.591914	24831.235782	
HLA B*0702	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.216954	0.625007	-3.591947	16479.8919
HLA A*0212	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.428305	0.836190	-3.592115	26810.482697	
HLA B*0802	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.465699	0.873495	-3.592204	29221.2665
HLA B*5701	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.375935	0.783495	-3.592439	23764.8245
HLA A*3001	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.295918	0.703401	-3.592517	19765.973178	
HLA B*4001	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.376099	0.783495	-3.592604	23773.8258
HLA A*0219	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.436596	0.843953	-3.592643	27327.2522
HLA B*4002	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.601607	1.008953	-3.592655	39958.3315
HLA B*4001	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.377819	0.785066	-3.592753	23868.157742	
HLA B*3801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.507886	0.915034	-3.592852	32202.2627
HLA A*2501	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.405169	0.812136	-3.593033	25419.631726	
HLA B*4601	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.404967	0.811904	-3.593063	25407.8079
HLA A*2501	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.439190	0.846009	-3.593181	27490.9531
HLA B*4002	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.625664	1.032480		
HLA A*3101	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.376691	0.783495		

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HLA B*1502	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.602364	1.008953	-3.593411	40027.998
HLA B*5401	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.474000	0.880566	-3.593434	29785.148309	
HLA A*2301	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.499313	0.905427	-3.593886	31572.8014
HLA A*0101	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.249774	0.655774	-3.594000	17773.5555
HLA A*2603	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.652239	1.057871	-3.594368	44899.2149
HLA A*3101	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.378956	0.784286	-3.594670	23930.735691	
HLA B*0702	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.356763	0.762047	-3.594716	22738.5525
HLA A*0212	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.434745	0.839978	-3.594767	27211.004335	
HLA A*2601	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.357024	0.762047	-3.594977	22752.2110
HLA B*1801	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.434965	0.839978	-3.594988	27224.845454	
HLA A*6802	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.407986	0.812136	-3.595850	25585.050989	
HLA A*2902	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.386721	0.790864	-3.595857	24362.457700	
HLA A*0216	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.169142	0.573275	-3.595867	14761.9027
HLA B*4403	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.653869	1.057871	-3.595999	45068.1042
HLA A*3201	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.533597	0.937566	-3.596031	34166.2098
HLA B*0803	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.469844	0.873495	-3.596349	29501.4612
HLA B*7301	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.605381	1.008953	-3.596428	40307.0133
HLA B*4002	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.633168	1.036697	-3.596471	42970.2596
HLA B*3801	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.439427	0.842742	-3.596685	27505.978242	
HLA B*2705	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.409687	0.812772	-3.596916	25685.4579
HLA B*5301	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.588843	0.991777	-3.597066	38800.9709
HLA B*1517	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.300587	0.703401	-3.597185	19979.592602	
HLA B*0702	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.386512	0.789295	-3.597217	24350.730484	
HLA A*8001	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.400322	0.803085	-3.597238	25137.510600	
HLA B*3901	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.480569	0.883157	-3.597412	30239.1045
HLA B*5701	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.386768	0.789295	-3.597473	24365.093806	
HLA B*0803	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.478114	0.880633	-3.597481	30068.635132	
HLA B*4402	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.409521	0.811904	-3.597616	25675.5940
HLA B*4501	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.382008	0.784286	-3.597722	24099.499940	
HLA A*0101	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.217467	0.619672	-3.597794	16499.339085	
HLA A*2601	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.387273	0.789295	-3.597979	24393.449972	
HLA B*1801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.412267	0.814245	-3.598022	25838.4851
HLA A*1101	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.350753	0.752698	-3.598055	22426.0523
HLA A*0202	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.333066	0.734934	-3.598132	21531.084683	
HLA B*1502	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.434500	0.836190	-3.598310	27195.698955	
HLA B*5401	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.102596	0.504252	-3.598344	12664.718096	
HLA B*3901	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.483767	0.885414	-3.598352	30462.5725
HLA B*4403	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.651104	1.052696	-3.598408	44782.0475
HLA A*3101	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.383507	0.785066	-3.598441	24182.823301	
HLA B*4801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.410789	0.812136	-3.598653	25750.710859	
HLA A*3201	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.588875	0.990022	-3.598853	38803.9098
HLA A*2603	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.626662	1.027504	-3.599158	42331.3631
HLA A*3001	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.302483	0.703256	-3.599226	20067.009801	
HLA B*3501	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.445425	0.846009	-3.599416	27888.5111
HLA A*0216	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.206814	0.607347	-3.599467	16099.559112	
HLA A*3002	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.485172	0.885414	-3.599757	30561.2819
HLA A*0250	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.402881	0.803085	-3.599796	25286.042055	
HLA A*3001	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-3.959756	0.359849	-3.599908	9114.99085
HLA A*3301	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.634521	1.034236	-3.600285	43104.367943	
HLA A*2603	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.562460	0.962074	-3.600386	36514.068566	
HLA B*4001	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.413165	0.812772	-3.600393	25891.9376
HLA A*2301	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.485867	0.885414	-3.600453	30610.2598
HLA A*2603	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.616346	1.015721	-3.600625	41337.6387
HLA B*5801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.353330	0.752698	-3.600632	22559.5388
HLA A*0202	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.403832	0.803085	-3.600748	25341.504639	
HLA A*3301	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.019334	0.418270	-3.601065	10455.2513
HLA A*3101	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.307360	0.706243	-3.601117	20293.651296	
HLA A*0211	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.208618	0.607347	-3.601272	16166.588628	
HLA A*0206	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.445329	0.843953	-3.601376	27882.3260
HLA B*1517	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.386479	0.785066	-3.601413	24348.886267	
HLA B*2705	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.307132	0.705319	-3.601814	20283.004809	
HLA A*0216	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.474554	0.872645	-3.601909	29823.2003
HLA B*1501	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.413867	0.811904	-3.601963	25933.8531
HLA B*0702	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.414896	0.812136	-3.602760	25995.377120	
HLA B*0803	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.488379	0.885414	-3.602964	30787.7970
HLA B*5801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.351472	0.748410	-3.603062	22463.2077
HLA B*5701	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.406180	0.803085	-3.603095	25478.833035	
HLA B*1517	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.445909	0.842742	-3.603167	27919.608506	
HLA B*4501	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.659525	1.056254	-3.603271	45658.8007
HLA A*0211	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.443290	0.839978	-3.603312	27751.703603	
HLA B*1502	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.484032	0.880633	-3.603399	30481.200515	
HLA A*0203	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.415359	0.811904	-3.603454	26023.0964
HLA A*3002	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.447427	0.843953	-3.603474	28017.3523
HLA B*0702	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.107915	0.504252	-3.603663	12820.789252	
HLA A*0203	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.417037	0.812772	-3.604265	26123.8091
HLA B*5401	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.484920	0.880633	-3.604287	30543.596460	
HLA A*2601	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.395163	0.790864	-3.604299	24840.640959	
HLA B*4801	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.407413	0.803085	-3.604328	25551.300670	
HLA B*0802	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.448646	0.843953	-3.604694	28096.1280
HLA A*0301	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.357524	0.752698	-3.604826	22778.4436
HLA B*1517	1:241-249	9	VATSPLATE	1.089931	-0.716788	-3.978416	0.373143	-3.605273	9515.15455
HLA B*3901	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.274134	0.668648	-3.605486	18798.957964	
HLA B*4403	1:173-181	9	AVLPNATET	1.134394	-0.118673	-4.621357	1.015721	-3.605636	41817.4086
HLA A*0212	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.395182	0.789295	-3.605887	24841.716063	
HLA B*0801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.391030	0.785066	-3.605964	24605.378696	
HLA A*0203	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.418120	0.812136	-3.605983	26189.042210	
HLA B*0803	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.445996	0.839978	-3.606019	27925.197619	
HLA A*0101	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.368167	0.762047	-3.606120	23343.5667
HLA B*3801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.418115	0.811904	-3.606210	26188.7588
HLA A*6901	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.358981	0.752698	-3.606283	22854.9738
HLA A*0201	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.397548	0.790864	-3.606684	24977.417027	
HLA B*1801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.492128	0.885414	-3.606714	31054.7754
HLA A*6802	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.418836	0.811904	-3.606932	26232.2902
HLA A*3002	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.449711	0.842742	-3.606969	28165.067148	
HLA B*4801	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.390767	0.783495	-3.607272	24590.4746
HLA B*7301	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.587825	0.980470	-3.607356	38710.1867
HLA A*6801	1:216-224	9	LRQLAAVAP	0.939514	0.118357	-4.665603	1.057871	-3.607732	46302.3057
HLA A*0201	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.392849	0.785066	-3.607783	24708.623677	
HLA B*4002	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.619891	1.012095	-3.607796	41676.4806
HLA B*1517	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.232809	0.625007	-3.607802	17092.6218
HLA B*1502	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.581834	0.973692	-3.608142	38179.8378
HLA A*0250	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.531640	0.923260	-3.608380	34012.5883
HLA B*0802	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.420655	0.812136	-3.608519	26342.361779	
HLA B*4002	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.024837	0.416215	-3.608622	10588.5617
HLA A*0202	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.481415	0.872645	-3.608770	30298.0544
HLA B*4403	1:108-116	9	YVPEKDSRV	0.818350	0.237904	-4.665112	1.056254	-3.608858	46249.9828
HLA A*2603	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.514437	0.905427	-3.609010	32691.6434
HLA A*1101	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.492187	0.883157	-3.609030	31058.9757
HLA B*1801	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.445623	0.836190	-3.609433	27901.187463	
HLA B*0803	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.490016	0.880566	-3.609450	30904.107525	
HLA A*0216	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.312764	0.703256	-3.609508	20547.737512	
HLA B*4001	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.421623	0.811904	-3.609718	26401.1410
HLA A*1101	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.452488	0.842742	-3.609746	28345.745416	
HLA B*0702	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.422534	0.812772	-3.609763	26456.6162
HLA A*2602	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.394056	0.784286	-3.609770	24777.426142	
HLA B*5101	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.455996	0.846009		
HLA A*2601	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.393513	0.783495		

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HLA B*0803	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.446255	0.836190	-3.610065	27941.820509	
HLA B*1517	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.456287	0.846009	-3.610278	28594.7957
HLA A*2602	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.600670	0.990022	-3.610648	39872.1726
HLA A*6901	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.359375	0.748410	-3.610966	22875.7552
HLA A*8001	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.450980	0.839978	-3.611002	28247.467190	
HLA B*4402	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.425278	0.814245	-3.611033	26624.3182
HLA B*3801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.538251	0.927121	-3.611130	34534.3378
HLA A*0206	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.314660	0.703256	-3.611404	20637.640530	
HLA A*0212	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.424252	0.812772	-3.611480	26561.4495
HLA A*3201	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.623662	1.012095	-3.611567	42039.9278
HLA B*5801	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.346505	0.734934	-3.611571	22207.770632	
HLA B*3901	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.314961	0.703256	-3.611704	20651.936339	
HLA A*0211	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.448031	0.836190	-3.611841	28056.333107	
HLA B*7301	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.601875	0.990022	-3.611853	39982.9825
HLA A*0206	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.495035	0.883157	-3.611878	31263.2919
HLA B*4002	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.639674	1.027504	-3.612169	43618.7988
HLA A*0250	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.452150	0.839978	-3.612172	28323.671998	
HLA B*4501	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.639718	1.027504	-3.612214	43623.2825
HLA B*5701	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.396504	0.784286	-3.612218	24917.493498	
HLA A*0301	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.237240	0.625007	-3.612233	17267.9114
HLA A*2602	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.574365	0.962074	-3.612291	37528.833647	
HLA A*0250	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.527425	0.915034	-3.612391	33684.0812
HLA A*0201	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.365200	0.752698	-3.612502	23184.6111
HLA B*3901	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.374551	0.762047	-3.612504	23689.2202
HLA A*2601	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.397637	0.785066	-3.612571	24982.552307	
HLA A*2301	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.536111	0.923260	-3.612851	34364.5572
HLA B*0801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.238180	0.625007	-3.613173	17305.3189
HLA A*3002	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.305290	0.692096	-3.613194	20197.159602	
HLA A*3002	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.375444	0.762047	-3.613397	23737.9696
HLA B*1502	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.427659	0.814245	-3.613413	26770.6258
HLA B*7301	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.575657	0.962074	-3.613583	37640.664694	
HLA B*4403	1:212-220	9	AIECLRQLA	1.186528	-0.154648	-4.645519	1.031880	-3.613639	44209.8682
HLA A*2403	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.397158	0.783495	-3.613662	24954.9963
HLA B*3901	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.450336	0.836190	-3.614146	28205.626715	
HLA A*3301	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.587875	0.973692	-3.614183	38714.5848
HLA B*0802	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.454445	0.839978	-3.614467	28473.772006	
HLA A*2301	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.529692	0.915034	-3.614658	33860.3902
HLA A*8001	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.429059	0.814245	-3.614814	26857.0815
HLA A*0212	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.427311	0.812136	-3.615175	26749.200187	
HLA A*3101	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.307297	0.692096	-3.615201	20290.687280	
HLA A*8001	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.427106	0.811904	-3.615202	26736.6133
HLA B*4403	1:101-109	9	YSQLSQRYV	0.847430	0.153321	-4.615972	1.000751	-3.615221	41302.0965
HLA A*2301	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.542384	0.927121	-3.615262	34864.5350
HLA A*6802	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.400590	0.785066	-3.615524	25153.018372	
HLA B*5801	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.351458	0.735649	-3.615809	22462.4786
HLA B*3901	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.458611	0.842742	-3.615869	28748.198848	
HLA B*0803	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.405237	0.789295	-3.615943	25423.620043	
HLA A*6801	1:2-10 9	AETAPLRVQ	1.072975	-0.038739	-4.650206	1.034236	-3.615970	44689.597494	
HLA A*3201	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.378023	0.762047	-3.615976	23879.3941
HLA A*3001	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.075619	0.459518	-3.616101	11901.966964	
HLA B*1501	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.407068	0.790864	-3.616204	25530.988981	
HLA B*5701	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.351185	0.734934	-3.616252	22448.386825	
HLA B*3501	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.241366	0.625007	-3.616358	17432.7342
HLA B*7301	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.352036	0.735649	-3.616387	22492.3923
HLA B*1501	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.285040	0.668648	-3.616393	19277.028353	
HLA B*4601	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.407462	0.790864	-3.616598	25554.203659	
HLA A*2402	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.543815	0.927116	-3.616699	34979.589920	
HLA B*5301	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.574363	0.957621	-3.616742	37528.6306
HLA B*4801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.431096	0.814245	-3.616851	26983.3471
HLA A*1101	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.462931	0.846009	-3.616922	29035.6359
HLA A*0101	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.320421	0.703401	-3.617020	20913.223596	
HLA B*4002	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.272924	0.655774	-3.617150	18746.6552
HLA B*5301	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.554759	0.937566	-3.617193	35872.2497
HLA A*0301	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.364725	0.747233	-3.617492	23159.2888
HLA B*0801	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.364934	0.747233	-3.617701	23170.4422
HLA A*2602	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.598349	0.980470	-3.617879	39659.6256
HLA B*3801	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.528024	0.910145	-3.617879	33730.5812
HLA A*3101	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.408766	0.790864	-3.617902	25631.045161	
HLA B*0803	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.460878	0.842742	-3.618136	28898.672492	
HLA B*3501	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.409600	0.790864	-3.618736	25680.317155	
HLA A*3201	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.595135	0.976308	-3.618827	39367.198918	
HLA B*4403	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.464954	0.846009	-3.618945	29171.1969
HLA A*0301	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.367916	0.748410	-3.619506	23330.0580
HLA A*0101	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.372244	0.752698	-3.619546	23563.7046
HLA B*1503	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.431883	0.811904	-3.619978	27032.2937
HLA A*0101	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.257720	0.637604	-3.620116	18101.7379
HLA B*4001	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.411118	0.790864	-3.620254	25770.221436	
HLA B*4801	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.411200	0.790864	-3.620336	25775.101389	
HLA A*2301	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.530721	0.910145	-3.620576	33940.7186
HLA B*5801	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.368014	0.747233	-3.620781	23335.3596
HLA A*0250	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.501540	0.880633	-3.620908	31735.140845	
HLA B*4001	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.405228	0.784286	-3.620942	25423.069893	
HLA B*4403	1:183-191	9	IVVTGNYRA	1.102754	-0.070274	-4.653604	1.032480	-3.621124	45040.5617
HLA A*0219	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.368616	0.747233	-3.621383	23367.6999
HLA B*3901	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.435666	0.814245	-3.621421	27268.7713
HLA A*2602	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.597914	0.976308	-3.621606	39619.952946	
HLA A*6802	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.246659	0.625007	-3.621652	17646.5129
HLA B*3901	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.410949	0.789295	-3.621654	25760.185579	
HLA B*1503	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.502243	0.880566	-3.621677	31786.515780	
HLA A*2301	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.494344	0.872645	-3.621699	31213.6069
HLA B*5301	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.598231	0.976308	-3.621923	39648.899355	
HLA A*2403	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.434749	0.812772	-3.621977	27211.2987
HLA A*0301	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.327328	0.705319	-3.622010	21248.509270	
HLA B*7301	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.505264	0.883157	-3.622107	32008.4293
HLA B*5801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.354975	0.732654	-3.622321	22645.132008	
HLA B*4501	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.598640	0.976308	-3.622332	39686.239257	
HLA A*2601	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.358248	0.735649	-3.622599	22816.4298
HLA A*0203	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.407742	0.785066	-3.622676	25570.660159	
HLA B*5101	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.406461	0.783495	-3.622966	25495.3789
HLA B*4601	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.385138	0.762047	-3.623091	24273.7874
HLA B*0702	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.326424	0.703256	-3.623168	21204.298776	
HLA B*7301	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.508664	0.885414	-3.623250	32259.9781
HLA B*4403	1:145-153	9	ELLAKLEAK	0.882949	0.153748	-4.660091	1.036697	-3.623394	45718.3687
HLA B*1509	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.533602	0.910145	-3.623457	34166.5794
HLA B*1517	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.463686	0.839978	-3.623708	29086.102334	
HLA A*2902	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.359394	0.735649	-3.623746	22876.7453
HLA A*0216	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.359575	0.735649	-3.623927	22886.2769
HLA A*2902	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.436006	0.811904	-3.624102	27290.1702
HLA B*1501	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.327723	0.703401	-3.624322	21267.829998	
HLA A*0219	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.359375	0.734934	-3.624442	22875.755291	
HLA B*0802	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.470459	0.846009	-3.624450	29543.3060
HLA A*6801	1:162-170	9	LRRKQARQA	1.167553	-0.114857	-4.677275	1.052696	-3.624579	47563.6159
HLA B*5101	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.497372	0.872645	-3.624727	31432.0309
HLA A*3002	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.244537	0.619672	-3.624865	17560.517661	
HLA A*0301	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.360531	0.735649	-3.624883	22936.7246
HLA A*0212	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.437099	0.811904		
HLA B*3801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.506338	0.880633	-3.6257		

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HLA B*5801	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.331426	0.705319	-3.626107	21449.934410		
HLA B*0702	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.141682	0.515530	-3.626152	13857.393	
HLA A*0202	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.361901	0.735649	-3.626253	23009.179	
HLA B*4002	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.470262	0.843953	-3.626309	29529.883	
HLA B*4403	1:178-186	9	ATETRIVVT	1.263708	-0.254755	-4.635301	1.008953	-3.626349	43181.856	
HLA B*4403	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.638461	1.012095	-3.626366	43497.206	
HLA A*3001	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.264019	0.637604	-3.626415	18366.197	
HLA A*0216	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.379224	0.752698	-3.626526	23945.498	
HLA A*2403	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.438718	0.811904	-3.626813	27461.076	
HLA A*3001	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.287340	0.660487	-3.626854	19379.395765		
HLA A*2501	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.470851	0.843953	-3.626899	29570.009	
HLA A*2403	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.330174	0.703256	-3.626917	21388.173234		
HLA A*0219	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.439709	0.812772	-3.626937	27523.840	
HLA A*2403	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.430165	0.803085	-3.627081	26925.602201		
HLA B*1801	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.469836	0.842742	-3.627095	29500.982469		
HLA A*0216	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.416404	0.789295	-3.627110	26085.819903		
HLA B*5701	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.412274	0.785066	-3.627208	25838.904509		
HLA A*0201	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.374457	0.747233	-3.627223	23684.094	
HLA A*0211	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.523569	0.896310	-3.627260	33386.369955		
HLA B*4402	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.418216	0.790864	-3.627352	26194.851727		
HLA A*0216	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.412530	0.785066	-3.627464	25854.145634		
HLA B*4402	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.380258	0.752698	-3.627560	24002.565	
HLA A*0201	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.363266	0.735649	-3.627618	23081.614	
HLA B*3801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.508817	0.880566	-3.628251	32271.324115		
HLA A*2603	1:242-250	9	ATSPLATEA	1.133303	-0.159611	-4.602075	0.973692	-3.628383	40001.372	
HLA B*5101	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.472412	0.843953	-3.628459	29676.420	
HLA B*1517	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.390548	0.762047	-3.628501	24578.105	
HLA B*4501	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.501148	0.872645	-3.628503	31706.482	
HLA A*6901	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.201866	0.573275	-3.628591	15917.174	
HLA A*0301	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.363550	0.734934	-3.628617	23096.728909		
HLA B*1509	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.441466	0.812772	-3.628695	27635.444	
HLA B*1509	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.440609	0.811904	-3.628704	27580.928	
HLA A*1101	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.413073	0.784286	-3.628787	25886.475353		
HLA A*3002	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.440952	0.812136	-3.628816	27602.721963		
HLA A*2402	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.525296	0.896310	-3.628986	33519.387408		
HLA A*2601	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.376508	0.747233	-3.629274	23796.215	
HLA A*0219	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.420556	0.790864	-3.629692	26336.377071		
HLA B*0803	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.441800	0.811904	-3.629896	27656.681	
HLA B*1517	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.474115	0.843953	-3.630162	29793.044	
HLA B*4002	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.610759	0.980470	-3.630289	40809.247	
HLA B*5701	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.392503	0.762047	-3.630456	24688.981	
HLA A*2403	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.419893	0.789295	-3.630599	26296.229223		
HLA A*2403	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.336029	0.705319	-3.630710	21678.469096		
HLA B*5801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.334215	0.703401	-3.630813	21588.119193		
HLA A*0206	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.467008	0.836190	-3.630818	29309.452072		
HLA A*0203	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.190635	0.559811	-3.630825	15510.843	
HLA A*3002	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.856525	0.225691	-3.630834	7186.618070		
HLA A*2501	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.473708	0.842742	-3.630967	29765.174350		
HLA B*4002	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.593464	0.962074	-3.631390	39216.066543		
HLA A*2403	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.416003	0.784286	-3.631716	26061.699304		
HLA A*3201	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-3.445167	-0.186575	-3.631742	2787.194863		
HLA B*1502	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.512607	0.880566	-3.632040	32554.160811		
HLA A*2501	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.444927	0.812772	-3.632155	27856.544	
HLA B*3501	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.379581	0.747233	-3.632348	23965.197	
HLA A*2603	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.608778	0.976308	-3.632470	40623.559479		
HLA B*1509	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.517963	0.885414	-3.632549	32958.188	
HLA A*3201	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.559749	0.927116	-3.632633	36286.820888		
HLA A*2402	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.513269	0.880566	-3.632703	32603.862975		
HLA B*5401	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-3.497293	-0.135764	-3.633057	3142.628228		
HLA B*5701	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.424031	0.790864	-3.633167	26547.945652		
HLA A*2402	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.538632	0.905427	-3.633205	34564.617	
HLA B*0802	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.436291	0.803085	-3.633206	27308.040146		
HLA A*8001	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.422518	0.789295	-3.633223	26455.614376		
HLA A*4501	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.469470	0.836190	-3.633280	29476.095833		
HLA A*1101	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.477442	0.843953	-3.633489	30022.148	
HLA B*3901	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.446642	0.812772	-3.633871	27966.773	
HLA B*1501	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.339565	0.705319	-3.634246	21855.693148		
HLA B*0801	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.254229	0.619672	-3.634557	17956.799762		
HLA B*3501	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.370385	0.735649	-3.634737	23463.085	
HLA A*0216	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.382020	0.747233	-3.634786	24100.151	
HLA A*3101	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.397024	0.762047	-3.634977	24947.302	
HLA B*7301	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.592696	0.957621	-3.635075	39146.753	
HLA A*2501	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.447089	0.811904	-3.635184	27995.534	
HLA A*2403	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.383662	0.748410	-3.635252	24191.459	
HLA B*0803	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.481264	0.846009	-3.635255	30287.566	
HLA A*3002	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.550320	0.915034	-3.635286	35507.527	
HLA A*0301	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.367977	0.732654	-3.635323	23333.339857		
HLA A*0101	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.371292	0.735649	-3.635643	23512.133	
HLA B*4403	1:210-218	9	RLAIECLRQ	0.895004	0.132500	-4.663192	1.027504	-3.635688	46046.014	
HLA B*4801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.420951	0.785066	-3.635885	26360.324067		
HLA B*3501	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.420265	0.784286	-3.635978	26318.715862		
HLA B*1503	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.448853	0.812772	-3.636081	28109.507	
HLA B*5801	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.328367	0.692096	-3.636271	21299.378884		
HLA B*5101	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.450594	0.814245	-3.636349	28222.416	
HLA A*2902	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.419886	0.783495	-3.636391	26295.802	
HLA A*0250	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.563609	0.927121	-3.636488	36610.792	
HLA B*1517	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.152033	0.515530	-3.636503	14191.666	
HLA A*8001	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.292340	0.655774	-3.636566	19603.785	
HLA A*0202	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.519732	0.883157	-3.636575	33092.722	
HLA A*2601	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.862525	0.225691	-3.636834	7286.603696		
HLA A*3002	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.563959	0.927121	-3.636838	36640.314	
HLA B*4002	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.574410	0.937566	-3.636844	37532.691	
HLA A*0211	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.509491	0.872645	-3.636846	32321.468	
HLA B*3901	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.448820	0.811904	-3.636916	28107.378	
HLA B*4801	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.421442	0.784286	-3.637155	26390.145667		
HLA A*0101	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.385598	0.748410	-3.637188	24299.539	
HLA A*0101	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.384433	0.747233	-3.637199	24234.423	
HLA B*1801	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.428422	0.790864	-3.637558	26817.735765		
HLA B*0802	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.450392	0.812772	-3.637620	28209.289	
HLA A*6801	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.518198	0.880566	-3.637632	32976.023109		
HLA B*4001	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.131452	0.493735	-3.637717	13534.801	
HLA A*2301	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.534452	0.896310	-3.638142	34233.556185		
HLA A*2402	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.565428	0.927121	-3.638306	36764.412	
HLA B*4402	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.422701	0.784286	-3.638415	26466.780243		
HLA B*4402	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.427774	0.789295	-3.638479	26777.723295		
HLA B*3501	1:137-145	9	DAARATYSE	0.875934	-0.718414	-3.796035	0.157520	-3.638514	6252.226	
HLA B*2705	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.478635	0.839978	-3.638658	30104.769118		
HLA A*1101	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.478680	0.839978	-3.638702	30107.863683		
HLA A*6901	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.371381	0.732654	-3.638727	23516.967040		
HLA A*0212	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.429639	0.790864	-3.638775	26892.993110		
HLA B*4501	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.453146	0.814245	-3.638901	28388.715	
HLA A*0206	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.511589	0.872645	-3.638944	32477.992	
HLA A*2301	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.519728	0.880633	-3.639095	33092.364062		
HLA B*4001	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.401325	0.762047	-3.639278	25195.645	
HLA A*0219	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.428817	0.789295	-3.639			
HLA A*3001	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.295432	0.655774			
HLA A*3301	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.308331	0.668648	-3.6396			

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HLA B*5301	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.549968	0.910145	-3.639823	35478.7258
HLA A*2603	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.620380	0.980470	-3.639910	41723.4038
HLA B*3801	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.476201	0.836190	-3.640011	29936.514514	
HLA A*3301	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.525444	0.885414	-3.640030	33530.8135
HLA A*0201	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.308871	0.668648	-3.640223	20364.366877	
HLA A*0219	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.452385	0.811904	-3.640480	28338.9989
HLA B*0802	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.454741	0.814245	-3.640496	28493.1876
HLA B*0702	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.425664	0.785066	-3.640598	26647.950440	
HLA B*4601	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.375566	0.734934	-3.640632	23744.648408	
HLA A*0216	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.483393	0.842742	-3.640651	30436.380722	
HLA B*3901	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.480705	0.839978	-3.640728	30248.594301	
HLA B*1503	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.214224	0.573275	-3.640949	16376.6195
HLA A*8001	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.403005	0.762047	-3.640958	25293.2932
HLA B*1501	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.375921	0.734934	-3.640987	23764.053176	
HLA A*3001	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.092262	0.451144	-3.641119	12366.9467
HLA A*3301	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.568404	0.927121	-3.641283	37017.2731
HLA B*4402	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.426392	0.785066	-3.641326	26692.678297	
HLA A*3301	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.633361	0.991777	-3.641584	42989.3259
HLA A*0219	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.377290	0.735649	-3.641642	23839.1224
HLA A*2601	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.376665	0.734934	-3.641732	23804.841944	
HLA B*5401	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.514514	0.872645	-3.641869	32697.4802
HLA A*0212	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.867816	0.225691	-3.642126	7375.919869	
HLA B*4801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.390908	0.748410	-3.642498	24598.4578
HLA A*2403	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.404685	0.762047	-3.642638	25391.3189
HLA A*0201	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.391187	0.748410	-3.642778	24614.2988
HLA B*3801	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.566038	0.923260	-3.642779	36816.1603
HLA A*3201	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.558140	0.915034	-3.643105	36152.5989
HLA B*4501	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.633184	0.990022	-3.643162	42971.8869
HLA B*1509	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.540178	0.896310	-3.643868	34687.876235	
HLA B*1801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.396671	0.752698	-3.643973	24927.0661
HLA A*3001	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.251520	0.607347	-3.644173	17845.140992	
HLA A*2603	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.635985	0.991777	-3.644208	43249.8903
HLA A*2601	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.396951	0.752698	-3.644253	24943.1188
HLA A*3301	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.620577	0.976308	-3.644269	41742.368506	
HLA A*2403	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.429484	0.785066	-3.644418	26883.392609	
HLA B*1801	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.456696	0.811904	-3.644791	28621.7253
HLA B*0801	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.435706	0.790864	-3.644842	27271.279277	
HLA B*4403	1:226-234	9	VFADFEVTT	1.113175	-0.132705	-4.625412	0.980470	-3.644943	42209.7060
HLA A*6802	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.435832	0.790864	-3.644968	27279.247309	
HLA B*3801	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.541350	0.896310	-3.645041	34781.643868	
HLA A*0203	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.397811	0.752698	-3.645113	24992.5556
HLA B*1509	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.481333	0.836190	-3.645142	30292.318163	
HLA A*3101	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.380805	0.735649	-3.645157	24032.8399
HLA B*1502	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.572298	0.927121	-3.645176	37350.5946
HLA A*3001	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.218547	0.573275	-3.645272	16540.4496
HLA A*3201	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.572570	0.927121	-3.645449	37374.0412
HLA A*0202	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.541808	0.896310	-3.645499	34818.355371	
HLA B*1502	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.568794	0.923260	-3.645535	37050.5311
HLA A*3301	1:5-13 9	APLRVQLIA	1.268990	-0.288709	-4.625908	0.980281	-3.645627	42257.915390	
HLA A*2601	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.394047	0.748410	-3.645637	24776.8899
HLA A*0212	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.381726	0.735649	-3.646078	24083.8599
HLA A*2501	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.284237	0.638108	-3.646129	19241.3953
HLA B*1509	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.437002	0.790864	-3.646138	27352.840095	
HLA B*2705	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.458284	0.812136	-3.646148	28726.589059	
HLA A*3101	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.378846	0.732654	-3.646192	23924.651721	
HLA A*3201	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.526772	0.880566	-3.646205	33633.460189	
HLA B*5101	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.489316	0.842742	-3.646574	30854.325700	
HLA B*1501	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.284316	0.637604	-3.646712	19244.9348
HLA B*0803	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.490679	0.843953	-3.646726	30951.2904
HLA A*0219	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.459069	0.812136	-3.646933	28778.542141	
HLA B*5301	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.562263	0.915034	-3.647229	36497.4792
HLA A*2902	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.432494	0.785066	-3.647428	27070.343390	
HLA B*4501	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.585004	0.937566	-3.647438	38459.4912
HLA A*8001	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.432856	0.785066	-3.647790	27092.905711	
HLA B*4601	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.396476	0.748410	-3.648066	24915.8759
HLA B*4501	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.610272	0.962074	-3.648198	40763.573267	
HLA B*4501	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.451391	0.803085	-3.648306	28274.222595	
HLA A*0211	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.433535	0.785066	-3.648469	27135.297460	
HLA B*4403	1:234-242	9	TLADGTEVA	1.234837	-0.220592	-4.663053	1.014245	-3.648808	46031.3198
HLA B*5301	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.575986	0.927116	-3.648871	37669.183948	
HLA A*0216	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.461059	0.812136	-3.648923	28910.713073	
HLA A*0211	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.492981	0.843953	-3.649028	31115.8204
HLA A*0212	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.396450	0.747233	-3.649217	24914.3932
HLA A*0212	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.317872	0.668648	-3.649224	20790.828191	
HLA B*0801	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.287070	0.637604	-3.649466	19367.3428
HLA B*4002	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.402164	0.752698	-3.649466	25244.3540
HLA A*2403	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.385199	0.735649	-3.649550	24277.2019
HLA B*1503	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.433095	0.783495	-3.649600	27107.8599
HLA B*4601	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.397120	0.747233	-3.649886	24952.8363
HLA B*4002	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.639996	0.990022	-3.649974	43651.1390
HLA A*3301	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.640043	0.990022	-3.650021	43655.8623
HLA A*0301	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.356302	0.706243	-3.650059	22714.454724	
HLA B*1517	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.453165	0.803085	-3.650080	28389.943873	
HLA A*3001	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-3.875800	0.225691	-3.650109	7512.763888	
HLA A*0203	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.288294	0.638108	-3.650187	19422.0077
HLA A*1101	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.453322	0.803085	-3.650237	28400.236030	
HLA B*1502	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.565371	0.915034	-3.650337	36759.6390
HLA B*1801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.463138	0.812772	-3.650366	29049.4622
HLA B*3501	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.435713	0.785066	-3.650647	27271.721884	
HLA B*1801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.462861	0.812136	-3.650725	29030.923980	
HLA A*2301	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.453815	0.803085	-3.650731	28432.519212	
HLA B*5801	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.357221	0.706243	-3.650978	22762.552705	
HLA B*1509	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.524514	0.873495	-3.651019	33459.0568
HLA B*2705	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.434785	0.783495	-3.651289	27213.5069
HLA B*5801	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.354615	0.703256	-3.651359	22626.396092	
HLA B*7301	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.465791	0.814245	-3.651546	29227.4325
HLA A*3201	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.537206	0.885414	-3.651791	34451.2998
HLA A*2301	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.532737	0.880566	-3.652171	34098.626980	
HLA B*1509	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.535892	0.883157	-3.652735	34347.2720
HLA B*4501	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.535960	0.883157	-3.652803	34352.6611
HLA A*8001	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.388462	0.735649	-3.652814	24460.3161
HLA A*6802	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.356213	0.703256	-3.652957	22709.785662	
HLA A*0203	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.356396	0.703256	-3.653140	22719.370563	
HLA A*3002	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.576574	0.923260	-3.653314	37720.1649
HLA A*0212	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.356608	0.703256	-3.653351	22730.435091	
HLA B*4402	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.437367	0.783495	-3.653871	27375.7859
HLA A*2603	1:147-155	9	LAKLEAKFA	1.198786	-0.186691	-4.666075	1.012095	-3.653980	46352.6816
HLA A*3301	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.537147	0.883157	-3.653990	34446.6407
HLA B*2705	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.416198	0.762047	-3.654151	26073.4041
HLA A*2501	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.468401	0.814245	-3.654156	29403.6296
HLA A*0212	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.439298	0.785066	-3.654232	27497.795223	
HLA B*5401	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.500258	0.846009	-3.654249	31641.5399
HLA A*0203	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.387168	0.732654	-3.654513	24387.512231	
HLA A*2501	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.390184	0.735649	-3.654536	24557.5048
HLA A*0202	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.490820	0.836190	-3.654630	30961.338679	
HLA B*1517	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.466578	0.811904		
HLA A*2402	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.577946	0.923260		

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HLA A*3201	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.439105	0.784286	-3.654819	27485.599607	
HLA A*6801	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.631169	0.976308	-3.654861	42772.887172	
HLA B*0802	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.438443	0.783495	-3.654947	27443.6998
HLA B*4002	1:46-54 9	SWSKPNPKT	1.176779	-0.200471	-4.631272	0.976308	-3.654964	42783.069833	
HLA A*2402	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.535721	0.880633	-3.655088	34333.710267	
HLA B*2705	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.440214	0.785066	-3.655148	27555.872879	
HLA A*0101	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.390191	0.734934	-3.655258	24557.903440	
HLA A*6802	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.387938	0.732654	-3.655284	24430.824914	
HLA B*4001	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.358739	0.703401	-3.655337	22842.242177	
HLA A*0212	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-3.972270	0.316807	-3.655463	9381.441920	
HLA B*1502	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.540925	0.885414	-3.655510	34747.6027
HLA B*7301	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.402827	0.747233	-3.655593	25282.8959
HLA A*2603	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.528327	0.872645	-3.655682	33754.1292
HLA A*2403	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.403193	0.747233	-3.655960	25304.2422
HLA A*3001	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.294100	0.638108	-3.655992	19683.3810
HLA A*0203	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.404497	0.748410	-3.656088	25380.3321
HLA B*4601	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.408886	0.752698	-3.656188	25638.1178
HLA B*6801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.530145	0.873495	-3.656651	33895.7626
HLA A*3101	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.403910	0.747233	-3.656676	25346.0291
HLA B*0702	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.459898	0.803085	-3.656813	28833.552770	
HLA B*5401	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.500796	0.843953	-3.656843	31680.7637
HLA A*6801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.540067	0.883157	-3.656910	34679.0574
HLA B*4002	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.537805	0.880633	-3.657172	34498.858959	
HLA A*6801	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.584343	0.927116	-3.657228	38401.070391	
HLA B*1502	1:68-76 9	GHFSVLEHA	1.164569	-0.237453	-4.584346	0.927116	-3.657230	38401.278137	
HLA A*3001	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.281643	0.624086	-3.657557	19126.8182
HLA B*4801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.419630	0.762047	-3.657583	26280.3009
HLA B*5101	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.497579	0.839978	-3.657602	31446.998388	
HLA A*0206	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.497593	0.839978	-3.657616	31448.019153	
HLA B*5701	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.404861	0.747233	-3.657628	25401.6233
HLA A*2902	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.295444	0.637604	-3.657839	19744.3847
HLA A*0216	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.448834	0.790864	-3.657970	28108.290483	
HLA B*0801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.390830	0.732654	-3.658176	24594.066746	
HLA B*4501	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.539029	0.880633	-3.658396	34596.232957	
HLA B*5701	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.406821	0.748410	-3.658411	25516.4905
HLA B*7301	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.596016	0.937566	-3.658450	39447.1445
HLA B*5101	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.494640	0.836190	-3.658450	31234.890851	
HLA A*0101	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.327298	0.668648	-3.658650	21247.014946	
HLA A*8001	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.442277	0.783495	-3.658782	27687.0713
HLA A*0101	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.391538	0.732654	-3.658884	24634.147774	
HLA A*3001	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.170176	0.511259	-3.658917	14797.083136	
HLA B*5701	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.411717	0.752698	-3.659019	25805.7965
HLA A*3002	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.499059	0.839978	-3.659082	31554.359849	
HLA A*0212	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.362491	0.703401	-3.659089	23040.444814	
HLA A*0219	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.411861	0.752698	-3.659163	25814.3139
HLA B*3801	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.532756	0.873495	-3.659261	34100.1027
HLA A*8001	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.450169	0.790864	-3.659305	28194.794954	
HLA B*4402	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.392007	0.732654	-3.659353	24660.815800	
HLA B*4001	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.365982	0.706243	-3.659739	23226.415662	
HLA A*6801	1:165-173	9	KQARQAARA	1.079552	-0.087775	-4.651959	0.991777	-3.660182	44870.3191
HLA A*2601	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.392994	0.732654	-3.660340	24716.912664	
HLA B*0801	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.365938	0.705319	-3.660619	23224.028391	
HLA A*2403	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.364070	0.703401	-3.660668	23124.359537	
HLA A*0201	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.363955	0.703256	-3.660698	23118.230439	
HLA B*3801	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.543864	0.883157	-3.660707	34983.5640
HLA A*3301	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.566179	0.905427	-3.660753	36828.1125
HLA B*0702	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.413735	0.752698	-3.661038	25925.9976
HLA A*2301	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.544348	0.883157	-3.661191	35022.5728
HLA A*0212	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.409685	0.748410	-3.661275	25685.3190
HLA A*0216	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.364887	0.703401	-3.661486	23167.935420	
HLA A*2902	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.414224	0.752698	-3.661526	25955.1874
HLA B*4501	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.546949	0.885414	-3.661535	35232.9434
HLA B*3501	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.414403	0.752698	-3.661705	25965.8611
HLA A*2902	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.365153	0.703401	-3.661751	23182.102714	
HLA B*5701	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.367150	0.705319	-3.661831	23288.948902	
HLA B*1509	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.414628	0.752698	-3.661930	25979.3500
HLA B*5301	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.589355	0.927121	-3.662233	38846.7581
HLA B*3801	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.368477	0.706243	-3.662234	23360.242511	
HLA B*1509	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.409509	0.747233	-3.662275	25674.8995
HLA B*1502	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.502285	0.839978	-3.662308	31789.611238	
HLA A*2402	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.572493	0.910145	-3.662348	37367.3696
HLA B*1502	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.535023	0.872645	-3.662378	34278.5893
HLA A*0219	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.365829	0.703256	-3.662573	23218.249696	
HLA B*4402	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.424656	0.762047	-3.662609	26586.1764
HLA A*0206	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.505518	0.842742	-3.662776	32027.136313	
HLA A*3201	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.586141	0.923260	-3.662881	38560.3250
HLA B*5401	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.546044	0.883157	-3.662887	35159.6363
HLA A*0201	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.236312	0.573275	-3.663037	17231.0509
HLA A*2301	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.536691	0.873495	-3.663196	34410.5072
HLA A*8001	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.410693	0.747233	-3.663459	25744.9998
HLA B*3801	1:225-233	9	AVFADFEVT	1.103824	-0.198397	-4.568961	0.905427	-3.663534	37064.7650
HLA B*1801	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.509571	0.846009	-3.663562	32327.4143
HLA A*3301	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.559899	0.896310	-3.663590	36299.386755	
HLA A*0203	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.454614	0.790864	-3.663750	28484.865043	
HLA A*0216	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.476589	0.812772	-3.663817	29963.2487
HLA A*2603	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.653966	0.990022	-3.663944	45078.1017
HLA B*1502	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.574205	0.910145	-3.664061	37515.0303
HLA B*4601	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.399874	0.735649	-3.664225	25111.5497
HLA A*0202	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.412699	0.748410	-3.664290	25864.2180
HLA B*4601	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.397226	0.732654	-3.664572	24958.911753	
HLA B*1509	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.400266	0.735649	-3.664617	25134.2470
HLA B*3801	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.510656	0.846009	-3.664647	32408.3135
HLA A*2403	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.397360	0.732654	-3.664706	24966.609361	
HLA A*6802	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.413146	0.748410	-3.664736	25890.8170
HLA A*0301	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.368188	0.703401	-3.664787	23344.703393	
HLA B*0801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.413249	0.748410	-3.664839	25896.9807
HLA A*0301	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.368280	0.703256	-3.665024	23349.629311	
HLA B*1503	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.412279	0.747233	-3.665045	25839.1840
HLA A*0201	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.397841	0.732654	-3.665187	24994.313371	
HLA A*0219	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.450298	0.785066	-3.665232	28203.185392	
HLA A*1101	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.479514	0.814245	-3.665269	30165.7417
HLA B*1502	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.450456	0.785066	-3.665390	28213.409844	
HLA A*3201	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.575817	0.910145	-3.665672	37654.5142
HLA A*0211	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.401464	0.735649	-3.665816	25203.6892
HLA A*0101	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.357928	0.692096	-3.665832	22799.648909	
HLA B*0801	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.400891	0.734934	-3.665957	25170.442009	
HLA A*6901	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.372648	0.706243	-3.666405	23585.640951	
HLA B*7301	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.291569	0.625007	-3.666562	19569.0302
HLA B*3801	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.552235	0.885414	-3.666821	35664.4284
HLA A*1101	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.450467	0.783495	-3.666972	28214.1730
HLA A*0301	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.335655	0.668648	-3.667008	21659.829893	
HLA B*1502	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.604737	0.937566	-3.667171	40247.3100
HLA A*3301	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.577382	0.910145	-3.667237	37790.4275
HLA A*2402	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.456635	0.789295	-3.667340	28617.699778	
HLA A*2402	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.582774	0.915034	-3.667740	38262.5466
HLA A*0250	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.564246	0.896310	-3.6679		
HLA B*1801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.511932	0.843953		

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HLA B*1509	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.451628	0.783495	-3.668133	28289.6758
HLA B*5401	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.417041	0.748410	-3.668631	26124.0918
HLA A*0219	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.372382	0.703401	-3.668981	23571.227043
HLA A*2602	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.307099	0.638108	-3.668992	20281.4686
HLA A*2603	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.606757	0.937566	-3.669192	40434.9971
HLA A*0301	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.229104	0.559811	-3.669293	16947.4182
HLA A*8001	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.375596	0.706243	-3.669353	23746.318393
HLA B*1501	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.402162	0.732654	-3.669508	25244.217510
HLA A*3001	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.301073	0.631559	-3.669514	20001.9792
HLA B*0702	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.373395	0.703401	-3.669993	23626.251306
HLA B*2705	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.473159	0.803085	-3.670074	29727.518037
HLA B*5301	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.593565	0.923260	-3.670306	39225.1902
HLA A*0203	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.373879	0.703401	-3.670477	23652.595956
HLA A*8001	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.418965	0.748410	-3.670556	26240.0966
HLA B*7301	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.566913	0.896310	-3.670603	36890.326655
HLA A*6901	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.376087	0.705319	-3.670769	23773.182752
HLA B*1509	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.485197	0.814245	-3.670952	30563.1007
HLA B*1502	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.513769	0.842742	-3.671028	32641.454269
HLA A*3101	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.406013	0.734934	-3.671079	25469.048441
HLA B*3901	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.455636	0.784286	-3.671350	28551.977463
HLA B*4601	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.309491	0.638108	-3.671384	20393.4722
HLA B*4403	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.661663	0.990022	-3.671641	45884.1332
HLA B*0803	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.484617	0.812772	-3.671845	30522.2882
HLA A*6901	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.364060	0.692096	-3.671964	23123.859142
HLA A*2501	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.456353	0.784286	-3.672066	28599.127577
HLA B*7301	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.545788	0.873495	-3.672294	35138.9096
HLA A*0219	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.420826	0.748410	-3.672417	26352.7670
HLA B*5101	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.484554	0.812136	-3.672417	30517.830288
HLA A*3301	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.484424	0.811904	-3.672520	30508.7512
HLA A*2501	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.425297	0.752698	-3.672599	26625.4705
HLA A*3001	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-3.962947	0.290041	-3.672906	9182.20189
HLA B*1503	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.512907	0.839978	-3.672930	32576.711261
HLA A*2602	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.558391	0.885414	-3.672977	36173.5322
HLA A*0206	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.462696	0.789295	-3.673402	29019.932275
HLA B*3801	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.462708	0.789295	-3.673414	29020.717259
HLA B*0801	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.409116	0.735649	-3.673468	25651.7139
HLA B*4002	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.488101	0.814245	-3.673856	30768.1494
HLA A*2602	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.554451	0.880566	-3.673885	35846.836282
HLA B*5401	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.516791	0.842742	-3.674049	32869.336482
HLA A*8001	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.426968	0.752698	-3.674270	26728.0808
HLA A*2602	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.436516	0.762047	-3.674469	27322.2262
HLA B*4402	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.410019	0.734934	-3.675085	25705.058190
HLA A*2603	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.489335	0.814245	-3.675090	30855.6610
HLA B*0801	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.367286	0.692096	-3.675190	23296.257505
HLA A*0250	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.300312	0.625007	-3.675305	19966.9503
HLA A*2902	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.422584	0.747233	-3.675350	26459.6220
HLA B*5301	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.556138	0.880633	-3.675505	35986.346938
HLA A*2603	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.590710	0.915034	-3.675676	38968.2079
HLA B*1801	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.465321	0.789295	-3.676026	29195.826177
HLA A*0101	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.379532	0.703256	-3.676275	23962.475064
HLA B*5701	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.412892	0.735649	-3.677243	25875.6942
HLA A*2301	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.517242	0.839978	-3.677264	32903.495557
HLA B*0802	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.462506	0.785066	-3.677440	29007.218497
HLA A*0301	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.315116	0.637604	-3.677511	20659.3114
HLA A*3002	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.193060	0.515530	-3.677530	15597.6832
HLA A*2603	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.657934	0.980281	-3.677652	45491.881509
HLA A*2602	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.413322	0.734934	-3.678388	25901.324164
HLA A*6802	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.431110	0.752698	-3.678412	26984.2230
HLA B*4801	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.425657	0.747233	-3.678423	26647.5179
HLA A*3201	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.574826	0.896310	-3.678516	37568.648010
HLA B*0801	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.384787	0.706243	-3.678545	24254.228899
HLA A*0211	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.425791	0.747233	-3.678557	26655.7363
HLA A*2602	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.468009	0.789295	-3.678714	29377.076904
HLA A*0203	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.339236	0.660487	-3.678749	21839.146252
HLA A*2602	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.606034	0.927116	-3.678918	40367.678616
HLA A*2603	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.491245	0.812136	-3.679109	30991.670558
HLA B*4402	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.234357	0.555227	-3.679130	17153.6678
HLA A*2602	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.606339	0.927121	-3.679218	40396.0786
HLA B*4601	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.382668	0.703401	-3.679267	24136.163351
HLA B*5101	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.464743	0.785066	-3.679677	29156.997259
HLA A*0216	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.412377	0.732654	-3.679723	25845.055808
HLA A*0201	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.383695	0.703401	-3.680294	24193.291677
HLA A*0211	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.412960	0.732654	-3.680306	25879.754163
HLA A*0212	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.240282	0.559811	-3.680472	17389.3118
HLA B*1501	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.336271	0.655774	-3.680496	21690.5521
HLA A*2603	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.591110	0.910145	-3.680965	39004.0627
HLA A*3301	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.608122	0.927116	-3.681007	40562.290191
HLA A*2403	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.387703	0.706243	-3.681460	24417.611683
HLA A*2403	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.350485	0.668648	-3.681837	22412.225883
HLA A*2501	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.465513	0.783495	-3.682018	29208.7806
HLA B*1517	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-3.980986	0.298936	-3.682051	9571.636200
HLA B*4001	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.351025	0.668648	-3.682378	22440.130201
HLA B*4601	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.385711	0.703256	-3.682454	24305.850343
HLA B*5401	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.485691	0.803085	-3.682606	30597.842464
HLA A*0216	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.494856	0.811904	-3.682952	31250.4406
HLA A*0202	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.251348	0.568388	-3.682960	17838.094947
HLA B*1502	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.566236	0.883157	-3.683079	36832.8945
HLA A*3001	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.238375	0.555227	-3.683147	17313.0911
HLA A*3101	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.386531	0.703256	-3.683274	24351.784384
HLA A*0206	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.415953	0.732654	-3.683299	26058.738663
HLA B*1503	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.321034	0.637604	-3.683430	20942.7735
HLA A*2602	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.557103	0.873495	-3.683609	36066.4503
HLA A*6801	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.526767	0.842742	-3.684025	33633.096285
HLA A*0250	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.616529	-0.067515	-3.684044	4135.51281
HLA B*4002	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.641762	0.957621	-3.684141	43829.0839
HLA B*5101	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.473459	0.789295	-3.684165	29748.110456
HLA A*2601	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.390431	0.706243	-3.684188	24571.458444
HLA A*0202	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.526950	0.842742	-3.684208	33647.291483
HLA A*0301	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.303977	0.619672	-3.684305	20136.173068
HLA A*0211	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.437012	0.752698	-3.684314	27353.4320
HLA A*2602	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.599434	0.915034	-3.684400	39758.8736
HLA A*2601	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.389949	0.705319	-3.684631	24544.223131
HLA A*0212	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.417288	0.732654	-3.684634	26138.935551
HLA B*0803	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.496778	0.812136	-3.684642	31389.039317
HLA A*0101	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.390981	0.706243	-3.684738	24602.583495
HLA B*5101	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.497563	0.812772	-3.684791	31445.8075
HLA B*3801	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.497755	0.812772	-3.684984	31459.7603
HLA B*4403	1:46-54	9	SWSKPNPKT	1.176779	-0.200471	-4.661475	0.976308	-3.685167	45864.279267
HLA A*2501	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.447333	0.762047	-3.685286	28011.2901
HLA A*6801	1:5-13	9	APLRVQLIA	1.268990	-0.288709	-4.665875	0.980281	-3.685594	46331.371738
HLA B*0702	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.476497	0.790864	-3.685633	29956.927577
HLA B*0803	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.447932	0.762047	-3.685885	28049.9590
HLA A*1101	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.310981	0.625007	-3.685974	20463.5393
HLA B*0803	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.489180	0.803085	-3.686095	30844.645947
HLA A*2602	1:144-152	9	SELLAKLEA	1.205349	-0.282089	-4.609358	0.923260	-3.686099	40677.8786
HLA B*3801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.530056	0.843953		
HLA A*0101	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.391888	0.705319	-3.6865	

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HLA B*3801	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.526819	0.839978	-3.686841	33637.099452		
HLA B*5701	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.393105	0.706243	-3.686862	24723.198103		
HLA B*3501	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-3.941881	0.255019	-3.686862	8747.44771	
HLA A*3002	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.570183	0.883157	-3.687026	37169.1803	
HLA B*5801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.312155	0.625007	-3.687148	20518.9669	
HLA B*4403	1:104-112	9	LSQRYVPEK	0.751083	0.186483	-4.624860	0.937566	-3.687294	42156.0779	
HLA A*3201	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.499565	0.812136	-3.687428	31591.082903		
HLA B*1502	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.478403	0.790864	-3.687539	30088.649952		
HLA A*6801	1:109-117	9	VPEKDSRVV	1.044987	-0.054965	-4.677890	0.990022	-3.687868	47631.0795	
HLA A*0250	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.524192	0.836190	-3.688002	33434.267669		
HLA A*2402	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.571177	0.883157	-3.688020	37254.3350	
HLA B*1801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.450143	0.762047	-3.688096	28193.1171	
HLA B*1502	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.450145	0.762047	-3.688098	28193.2696	
HLA B*5801	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.343890	0.655774	-3.688116	22074.4548	
HLA A*0212	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.423103	0.734934	-3.688169	26491.275753		
HLA B*5301	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.534508	0.846009	-3.688499	34238.0012	
HLA B*1503	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.479787	0.790864	-3.688923	30184.678082		
HLA B*0803	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.474524	0.785066	-3.689458	29821.102953		
HLA A*2602	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.586174	0.896310	-3.689864	38563.245649		
HLA B*4001	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.422673	0.732654	-3.690019	26465.062110		
HLA A*0206	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.502421	0.812136	-3.690285	31799.587543		
HLA A*2402	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.481506	0.790864	-3.690642	30304.447569		
HLA A*2501	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.423573	0.732654	-3.690919	26519.954238		
HLA A*2301	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.536935	0.846009	-3.690926	34429.8730	
HLA B*2705	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.426794	0.735649	-3.691145	26717.3828	
HLA A*1101	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.476415	0.785066	-3.691349	29951.255886		
HLA A*0219	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.329457	0.638108	-3.691350	21352.9115	
HLA B*4402	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.397656	0.706243	-3.691413	24983.633553		
HLA A*2603	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.618733	0.927121	-3.691611	41565.4744	
HLA A*0211	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.480999	0.789295	-3.691704	30269.056411		
HLA A*6801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.395370	0.703401	-3.691968	24852.469664		
HLA B*0702	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.439540	0.747233	-3.692306	27513.1217	
HLA A*3101	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.440778	0.748410	-3.692368	27591.6739	
HLA A*0301	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.207904	0.515530	-3.692374	16140.0228	
HLA A*0201	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.398746	0.706243	-3.692503	25046.425962		
HLA B*5101	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.483492	0.790864	-3.692628	30443.297121		
HLA B*5301	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.427764	0.734934	-3.692831	26777.143843		
HLA B*1517	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.440071	0.747233	-3.692837	27546.7808	
HLA B*5101	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.428676	0.735649	-3.693027	26833.4090	
HLA B*1502	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.589367	0.896310	-3.693057	38847.808927		
HLA B*0802	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.477505	0.784286	-3.693219	30026.533627		
HLA A*3201	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.496536	0.803085	-3.693451	31371.553633		
HLA A*2601	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.397068	0.703256	-3.693812	24949.866721		
HLA B*5801	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.354333	0.660487	-3.693847	22611.712104		
HLA B*1501	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-3.958271	0.263887	-3.694385	9083.87945	
HLA A*2402	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.568430	0.873495	-3.694936	37019.4760	
HLA B*4501	1:195-203	9	FIAMRASEH	1.177080	-0.219459	-4.652622	0.957621	-3.695001	44938.8250	
HLA B*5101	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.479300	0.784286	-3.695014	30150.894779		
HLA A*2902	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.363807	0.668648	-3.695159	23110.352556		
HLA A*2301	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.539127	0.843953	-3.695175	34604.0946	
HLA A*0211	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.538357	0.842742	-3.695615	34542.746076		
HLA B*0801	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.327303	0.631559	-3.695744	21247.2448	
HLA A*1101	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.443015	0.747233	-3.695781	27734.1435	
HLA B*0802	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.486741	0.790864	-3.695877	30671.924329		
HLA B*5401	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.430837	0.734934	-3.695904	26967.294500		
HLA A*0203	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.251165	0.555227	-3.695938	17830.5693	
HLA B*4402	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.399354	0.703256	-3.696098	25081.544642		
HLA B*1801	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.479601	0.783495	-3.696106	30171.7804	
HLA A*1101	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.315795	0.619672	-3.696122	20691.636713		
HLA B*3801	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.508340	0.812136	-3.696204	32235.902958		
HLA A*2301	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.508342	0.812136	-3.696206	32236.077351		
HLA A*0202	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.448966	0.752698	-3.696268	28116.8072	
HLA A*3201	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.540300	0.843953	-3.696347	34697.6358	
HLA A*2301	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.539273	0.842742	-3.696531	34615.703260		
HLA B*3901	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.481770	0.785066	-3.696704	30322.814828		
HLA B*4001	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.402117	0.705319	-3.696799	25241.622843		
HLA B*2705	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.429540	0.732654	-3.696886	26886.883304		
HLA B*1501	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.335138	0.638108	-3.697031	21634.0662	
HLA B*4403	1:170-178	9	AARAVLPNA	1.056252	-0.146107	-4.607288	0.910145	-3.697144	40484.4646	
HLA B*0803	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.481636	0.784286	-3.697349	30313.465814		
HLA B*4001	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.432339	0.734934	-3.697405	27060.679577		
HLA B*5701	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.400985	0.703256	-3.697729	25175.889371		
HLA B*0702	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.430548	0.732654	-3.697894	26949.355990		
HLA B*1502	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.510734	0.812772	-3.697962	32414.0998	
HLA A*1101	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.404460	0.706243	-3.698217	25378.135382		
HLA B*0802	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.404474	0.706243	-3.698231	25378.959152		
HLA B*4403	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.578958	0.880633	-3.698326	37927.857484		
HLA B*5401	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.538331	0.839978	-3.698353	34540.690540		
HLA B*4001	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.390553	0.692096	-3.698457	24578.371717		
HLA A*0219	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.336087	0.637604	-3.698483	21681.4012	
HLA A*0201	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.403891	0.705319	-3.698573	25344.932239		
HLA B*5701	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.431378	0.732654	-3.698724	27000.870101		
HLA B*4601	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.405075	0.706243	-3.698832	25414.131625		
HLA A*0201	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.391166	0.692096	-3.699070	24613.100425		
HLA B*1503	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.318748	0.619672	-3.699076	20832.824125		
HLA B*4801	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.404413	0.705319	-3.699094	25375.389672		
HLA B*1509	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.368120	0.668648	-3.699473	23341.041205		
HLA B*1517	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.490376	0.790864	-3.699512	30929.697847		
HLA B*1509	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.484596	0.785066	-3.699530	30520.802199		
HLA A*0250	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.572222	0.872645	-3.699577	37344.1292	
HLA A*0301	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.355706	0.655774	-3.699931	22683.2639	
HLA B*3901	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.490951	0.790864	-3.700087	30970.719955		
HLA B*1517	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.337753	0.637604	-3.700149	21764.7223	
HLA A*8001	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.405555	0.705319	-3.700236	25442.194585		
HLA A*3301	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.572967	0.872645	-3.700322	37408.2268	
HLA B*1517	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.436267	0.735649	-3.700618	27306.5628	
HLA A*2301	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.536881	0.836190	-3.700691	34425.589319		
HLA A*2301	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.491830	0.790864	-3.700966	31033.446403		
HLA A*2601	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.393398	0.692096	-3.701302	24739.922478		
HLA B*1501	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.000304	0.298936	-3.701368	10006.994227		
HLA A*0216	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.450007	0.748410	-3.701597	28184.2722	
HLA A*6901	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.357374	0.655774	-3.701600	22770.5584	
HLA A*2501	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.486877	0.785066	-3.701811	30681.549879		
HLA A*2902	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.450275	0.748410	-3.701865	28201.6596	
HLA A*0206	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.257417	0.555227	-3.702190	18089.1096	
HLA B*5101	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.450615	0.748410	-3.702206	28223.7906	
HLA B*1517	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.340354	0.638108	-3.702246	21895.4568	
HLA B*4601	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.370895	0.668648	-3.702247	23490.646374		
HLA B*3901	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.435372	0.732654	-3.702718	27250.337409		
HLA B*5301	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.576235	0.873495	-3.702741	37690.7914	
HLA B*4801	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.437954	0.734934	-3.703020	27412.836009		
HLA B*5701	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.395189	0.692096	-3.703093	24842.119239		
HLA B*2705	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.494264	0.790864	-3.703400	31207.866182		
HLA A*6801	1:12-20 9	IAKTDFLAP	0.799705	0.096605	-4.600061	0.896310	-3.703752	39816.344440		
HLA B*4601	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.409163	0.705319	-3.703845	25654.489605		
HLA B*0802	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.456571	0.752698			
HLA A*2902	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.438823	0.734934	-3.7038			

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HLA B*1801	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.488195	0.784286	-3.703909	30774.808227	
HLA A*2601	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.323959	0.619672	-3.704287	21084.305739	
HLA B*4403	1:64-72 9	IIDVGHFSV	0.847576	0.114498	-4.666477	0.962074	-3.704403	46395.581973	
HLA B*3501	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.453275	0.748410	-3.704865	28397.1633	
HLA A*2501	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.408393	0.703401	-3.704991	25609.007524	
HLA A*3301	1:215-223	9 CLRQLAAVA	1.106552	-0.292307	-4.519335	0.814245	-3.705090	33062.4802	
HLA A*6802	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.397315	0.692096	-3.705219	24964.043228	
HLA A*2602	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.586058	0.880633	-3.705426	38553.024483	
HLA A*0203	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.410775	0.705319	-3.705457	25749.875022	
HLA A*3201	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.586258	0.880633	-3.705625	38570.756804	
HLA A*2501	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.496588	0.790864	-3.705724	31375.287621	
HLA B*1801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.491163	0.785066	-3.706097	30985.802961	
HLA B*5701	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.409654	0.703401	-3.706253	25683.512690	
HLA A*0212	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.411694	0.705319	-3.706375	25804.400522	
HLA A*1101	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.497302	0.790864	-3.706438	31426.930071	
HLA A*8001	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.439192	0.732654	-3.706538	27491.101837	
HLA A*1101	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.442211	0.735649	-3.706563	27682.8777	
HLA B*5801	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.344358	0.637604	-3.706753	22098.2322	
HLA A*3301	1:144-152	9 SELLAKLEA	1.205349	-0.282089	-4.630337	0.923260	-3.707077	42691.0511	
HLA A*2501	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.442145	0.734934	-3.707212	27678.684751	
HLA A*2602	1:80-88 9	FYITGISRS	1.033042	-0.849138	-3.891316	0.183904	-3.707411	7786.024016	
HLA A*2301	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.519389	0.811904	-3.707485	33066.5943	
HLA A*1101	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.376275	0.668648	-3.707628	23783.473802	
HLA B*0802	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.376647	0.668648	-3.707999	23803.811714	
HLA B*2705	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.411583	0.703401	-3.708182	25797.840205	
HLA B*0702	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.376921	0.668648	-3.708274	23818.883273	
HLA B*4402	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.413644	0.705319	-3.708325	25920.528170	
HLA A*0206	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.456839	0.748410	-3.708429	28631.1721	
HLA B*4001	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.411698	0.703256	-3.708442	25804.679721	
HLA B*4403	1:195-203	9 FIAMRASEH	1.177080	-0.219459	-4.666075	0.957621	-3.708454	46352.6816	
HLA B*2705	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.456921	0.748410	-3.708512	28636.5938	
HLA B*0702	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.414781	0.706243	-3.708538	25988.487060	
HLA B*4801	1:129-137	9 RHILTEAAD	1.107553	-0.628684	-4.187450	0.478869	-3.708581	15397.4757	
HLA A*2501	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.455888	0.747233	-3.708654	28568.5097	
HLA A*0301	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.369224	0.660487	-3.708738	23400.464769	
HLA A*3301	1:128-136	9 LRHILTEAA	1.102392	-0.187358	-4.623817	0.915034	-3.708783	42054.9409	
HLA B*4403	1:204-212	9 ADVEIRRLA	0.833844	-0.278617	-4.264024	0.555227	-3.708797	18366.3959	
HLA A*3002	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.511892	0.803085	-3.708808	32500.666034	
HLA A*0206	1:149-157	9 KLEAKFADQ	0.547523	0.012288	-4.268678	0.559811	-3.708867	18564.2869	
HLA B*5301	1:207-215	9 EIRRLAIEC	0.869270	0.013887	-4.592341	0.883157	-3.709184	39114.7876	
HLA B*4402	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-4.334194	0.625007	-3.709187	21587.0681	
HLA B*4403	1:128-136	9 LRHILTEAA	1.102392	-0.187358	-4.624296	0.915034	-3.709262	42101.3791	
HLA A*3301	1:131-139	9 ILTEAADAA	1.112012	-0.238517	-4.582795	0.873495	-3.709300	38264.4098	
HLA B*4501	1:102-110	9 SQLSQRYVP	0.667890	0.084808	-4.462020	0.752698	-3.709322	28974.7530	
HLA A*0206	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.347090	0.637604	-3.709486	22237.7060	
HLA B*2705	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.416198	0.706243	-3.709955	26073.404176	
HLA A*2402	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.546401	0.836190	-3.710211	35188.560156	
HLA A*1101	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.472844	0.762047	-3.710797	29705.9756	
HLA B*5101	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.473062	0.762047	-3.711015	29720.9250	
HLA B*0803	1:102-110	9 SQLSQRYVP	0.667890	0.084808	-4.463871	0.752698	-3.711173	29098.5358	
HLA B*3901	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.366976	0.655774	-3.711202	23279.6274	
HLA B*0801	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.414795	0.703256	-3.711539	25989.330643	
HLA A*6801	1:170-178	9 AARAVLPNA	1.056252	-0.146107	-4.622003	0.910145	-3.711859	41879.6675	
HLA A*2402	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.524178	0.812136	-3.712042	33433.182432	
HLA A*0201	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.319484	0.607347	-3.712137	20868.130131	
HLA A*6901	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.372638	0.660487	-3.712152	23585.130574	
HLA B*1503	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.447115	0.734934	-3.712181	27997.200665	
HLA A*2501	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.415655	0.703256	-3.712399	26040.841001	
HLA A*0203	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.404533	0.692096	-3.712436	25382.391818	
HLA B*4403	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.548934	0.836190	-3.712744	35394.374486	
HLA B*0702	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.418263	0.705319	-3.712944	26197.686105	
HLA A*6802	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.419367	0.706243	-3.713124	26264.382353	
HLA A*2603	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.555884	0.842742	-3.713142	35965.327407	
HLA A*2603	1:144-152	9 SELLAKLEA	1.205349	-0.282089	-4.636457	0.923260	-3.713198	43296.9452	
HLA A*3001	1:169-177	9 QAARAVLPN	0.840310	-0.476167	-4.077451	0.364143	-3.713309	11952.2959	
HLA B*7301	1:28-36 9	DADGGPALV	0.931987	-0.051421	-4.594023	0.880566	-3.713457	39266.591851	
HLA B*1501	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.416736	0.703256	-3.713479	26105.725611	
HLA B*5301	1:95-103	9 RHRHFSYSQ	0.785584	0.087061	-4.586246	0.872645	-3.713601	38569.7135	
HLA B*0802	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.475825	0.762047	-3.713778	29910.6132	
HLA A*8001	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.448867	0.734934	-3.713934	28110.419441	
HLA A*0201	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.351592	0.637604	-3.713987	22469.4063	
HLA B*4801	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.406133	0.692096	-3.714036	25476.076431	
HLA B*4801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.417817	0.703401	-3.714415	26170.771890	
HLA A*3201	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.560743	0.846009	-3.714734	36369.9541	
HLA B*1801	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.421167	0.706243	-3.714924	26373.447124	
HLA B*5401	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.504301	0.789295	-3.715006	31937.511584	
HLA A*0206	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.500269	0.785066	-3.715204	31642.395808	
HLA B*0702	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.371031	0.655774	-3.715257	23498.0182	
HLA A*2301	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.528184	0.812772	-3.715412	33742.9920	
HLA B*0702	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.451102	0.735649	-3.715453	28255.4147	
HLA B*0803	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.498949	0.783495	-3.715454	31546.3377	
HLA B*1502	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.561800	0.846009	-3.715791	36458.6028	
HLA B*0802	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.463063	0.747233	-3.715829	29044.4337	
HLA A*2902	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.419128	0.703256	-3.715871	26249.893437	
HLA B*1501	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.323386	0.607347	-3.716039	21056.492543	
HLA A*3201	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.528886	0.812772	-3.716114	33797.6174	
HLA A*1101	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.464698	0.748410	-3.716288	29154.0004	
HLA B*4801	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.422539	0.706243	-3.716296	26456.902505	
HLA A*6802	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.421768	0.705319	-3.716450	26409.997849	
HLA A*0206	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.529408	0.812772	-3.716636	33838.2326	
HLA A*6801	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.597277	0.880633	-3.716644	39561.909486	
HLA A*3301	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.507628	0.790864	-3.716764	32183.105266	
HLA A*2601	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.377330	0.660487	-3.716844	23841.315037	
HLA A*0211	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.529626	0.812136	-3.717490	33855.261591	
HLA B*1509	1:97-105	9 RHFSYSQLS	0.762603	-0.828693	-3.651598	-0.066090	-3.717687	4483.2998	
HLA A*2601	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.386592	0.668648	-3.717944	24355.209877	
HLA B*4403	1:225-233	9 AVFADFEVT	1.103824	-0.198397	-4.623472	0.905427	-3.718045	42021.5099	
HLA B*0801	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.356302	0.638108	-3.718195	22714.4547	
HLA A*2402	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.521283	0.803085	-3.718198	33211.091763	
HLA A*2301	1:215-223	9 CLRQLAAVA	1.106552	-0.292307	-4.532507	0.814245	-3.718262	34080.5537	
HLA B*2705	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.465589	0.747233	-3.718355	29213.8375	
HLA A*2602	1:171-179	9 ARAVLPNAT	0.924326	-0.080373	-4.562860	0.843953	-3.718907	36547.6653	
HLA B*4403	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.558891	0.839978	-3.718914	36215.239282	
HLA B*0803	1:149-157	9 KLEAKFADQ	0.547523	0.012288	-4.278776	0.559811	-3.718966	19000.9956	
HLA B*4601	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.374753	0.655774	-3.718979	23700.2442	
HLA A*0219	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.387837	0.668648	-3.719190	24425.142348	
HLA A*0211	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.532013	0.812772	-3.719241	34041.8575	
HLA A*3201	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.502741	0.783495	-3.719246	31822.9925	
HLA B*3901	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.467851	0.748410	-3.719441	29366.4307	
HLA A*8001	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.422870	0.703256	-3.719614	26477.091380	
HLA A*2601	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.375772	0.655774	-3.719998	23755.9552	
HLA A*0206	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.531966	0.811904	-3.720062	34038.1745	
HLA B*3501	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.452962	0.732654	-3.720308	28376.738510	
HLA B*7301	1:228-236	9 ADFEVTTLA	0.872294	-0.299019	-4.293700	0.573275	-3.720425	19665.2869	
HLA A*3001	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.288846	0.568388	-3.720458	19446.715106	
HLA A*2602	1:95-103	9 RHRHFSYSQ	0.785584	0.087061	-4.593147	0.872645			
HLA A*0101	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.381127	0.660487	-3.7206		

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HLA B*4002	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.594521	0.873495	-3.721027	39311.6524	
HLA B*3801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.535295	0.814245	-3.721050	34300.1074	
HLA B*1801	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.424444	0.703256	-3.721188	26573.235063	
HLA B*1501	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.428027	0.706243	-3.721785	26793.373234	
HLA B*5701	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.346810	0.625007	-3.721803	22223.3945	
HLA B*0702	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.470654	0.748410	-3.722244	29556.5745	
HLA B*1502	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.455629	0.732654	-3.722975	28551.514078	
HLA A*0211	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.535192	0.811904	-3.723288	34291.9438	
HLA A*0219	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.456029	0.732654	-3.723375	28577.784446	
HLA B*0803	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.514315	0.790864	-3.723451	32682.448091	
HLA A*0216	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.283264	0.559811	-3.723453	19198.3486	
HLA B*3501	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.429869	0.706243	-3.723627	26907.254725	
HLA B*1509	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.472266	0.748410	-3.723856	29666.4682	
HLA B*4801	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.427135	0.703256	-3.723878	26738.349123	
HLA B*5401	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.560167	0.836190	-3.723977	36321.780485	
HLA B*4501	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.598163	0.873495	-3.724668	39642.6794	
HLA A*2403	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.416771	0.692096	-3.724675	26107.844133	
HLA B*3801	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.508189	0.783495	-3.724694	32224.7437	
HLA B*1509	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.427987	0.703256	-3.724731	26790.909211	
HLA B*1517	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-3.923485	0.198739	-3.724745	8384.64901	
HLA A*8001	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.428316	0.703401	-3.724915	26811.207916	
HLA A*2602	1:152-160	9	AKFADQPNA	1.017259	-0.171250	-4.570961	0.846009	-3.724952	37235.7978	
HLA B*4001	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.363113	0.638108	-3.725006	23073.4997	
HLA A*6801	1:128-136	9	LRHILTEAA	1.102392	-0.187358	-4.640087	0.915034	-3.725053	43660.3498	
HLA A*0206	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-3.892754	0.167651	-3.725103	7811.845112	
HLA B*2705	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.393927	0.668648	-3.725279	24770.054867	
HLA B*5801	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.363541	0.638108	-3.725434	23096.2291	
HLA B*3501	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.431819	0.705319	-3.726501	27028.345553	
HLA A*0301	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.364746	0.638108	-3.726639	23160.4164	
HLA A*3002	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.538629	0.811904	-3.726725	34564.4300	
HLA B*1509	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.489248	0.762047	-3.727201	30849.4854	
HLA B*0802	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.383232	0.655774	-3.727458	24167.5214	
HLA A*0203	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.433758	0.706243	-3.727515	27149.246945	
HLA B*3801	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.530712	0.803085	-3.727627	33939.984208	
HLA B*5301	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.567671	0.839978	-3.727694	36954.844951	
HLA A*3301	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.563966	0.836190	-3.727776	36640.909622	
HLA A*3002	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.512856	0.785066	-3.727790	32572.834291	
HLA B*4501	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.624162	0.896310	-3.727853	42088.398605	
HLA A*2603	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.624292	0.896310	-3.727982	42100.923615	
HLA B*1502	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.572018	0.843953	-3.728065	37326.5569	
HLA B*2705	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.431507	0.703256	-3.728251	27008.905241	
HLA A*2402	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.572305	0.843953	-3.728352	37351.2008	
HLA A*0211	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.519265	0.790864	-3.728401	33057.114722	
HLA B*1501	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.288470	0.559811	-3.728660	19429.8896	
HLA A*8001	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.366353	0.637604	-3.728749	23246.2772	
HLA A*0212	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.420901	0.692096	-3.728805	26357.329502	
HLA A*2301	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.513875	0.785066	-3.728809	32649.401635	
HLA B*1517	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.481692	0.752698	-3.728994	30317.4018	
HLA B*1801	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.397822	0.668648	-3.729175	24993.231663	
HLA A*8001	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.348861	0.619672	-3.729189	22328.600155	
HLA A*2902	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.461907	0.732654	-3.729253	28967.229998	
HLA B*1502	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.482047	0.752698	-3.729349	30342.1780	
HLA A*2501	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.477792	0.748410	-3.729382	30046.3578	
HLA B*4402	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.433177	0.703401	-3.729776	27112.993192	
HLA B*0803	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.436103	0.706243	-3.729860	27296.224025	
HLA A*0250	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.573973	0.843953	-3.730020	37494.9434	
HLA B*1509	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-3.964084	0.234045	-3.730039	9206.27595	
HLA A*3201	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.544428	0.814245	-3.730183	35029.0153	
HLA B*5101	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.477505	0.747233	-3.730272	30026.5336	
HLA B*0803	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.477552	0.747233	-3.730319	30029.7826	
HLA A*3101	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.386594	0.655774	-3.730820	24355.3416	
HLA B*4801	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.399472	0.668648	-3.730824	25088.329978	
HLA A*3002	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.514355	0.783495	-3.730859	32685.4539	
HLA B*4402	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.423084	0.692096	-3.730988	26490.129259	
HLA B*4002	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.616449	0.885414	-3.731035	41347.4796	
HLA B*4403	1:95-103	9	RHRHFSYSQ	0.785584	0.087061	-4.603872	0.872645	-3.731227	40167.2638	
HLA A*3002	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.356692	0.625007	-3.731685	22734.8624	
HLA A*1101	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.464607	0.732654	-3.731953	29147.849999	
HLA A*2602	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.522998	0.790864	-3.732134	33342.508967	
HLA A*0211	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.369948	0.637604	-3.732344	23439.4881	
HLA A*2501	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.438647	0.706243	-3.732404	27456.619556	
HLA A*0216	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.370141	0.637604	-3.732536	23449.8885	
HLA B*1801	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.437888	0.705319	-3.732570	27408.683912	
HLA B*1502	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.424999	0.692096	-3.732903	26607.183679	
HLA A*2902	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.438288	0.705319	-3.732969	27433.902757	
HLA A*2603	1:68-76	9	GHFSVLEHA	1.164569	-0.237453	-4.660283	0.927116	-3.733168	45738.654450	
HLA A*0201	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.393741	0.660487	-3.733255	24759.470872	
HLA B*5801	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.364845	0.631559	-3.733286	23165.6794	
HLA B*5301	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.576172	0.842742	-3.733430	37685.286491	
HLA B*0702	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.353415	0.619672	-3.733742	22563.932854	
HLA B*5101	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.371987	0.638108	-3.733880	23549.8137	
HLA B*4002	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.617088	0.883157	-3.733931	41408.3668	
HLA A*3301	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.546841	0.812772	-3.734069	35224.1766	
HLA B*4002	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.630483	0.896310	-3.734173	42705.372711	
HLA A*2603	1:44-52	9	YQSWSKPNP	0.817579	0.063054	-4.614962	0.880633	-3.734329	41206.129075	
HLA A*2603	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.607902	0.873495	-3.734407	40541.6683	
HLA B*0802	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.483217	0.748410	-3.734807	30424.0339	
HLA A*0202	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.547640	0.812772	-3.734868	35289.0262	
HLA B*5801	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.359150	0.624086	-3.735064	22863.8778	
HLA B*0801	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.395595	0.660487	-3.735109	24865.380131	
HLA A*0212	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.441629	0.706243	-3.735386	27645.761852	
HLA A*0202	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.438976	0.703401	-3.735575	27477.422651	
HLA B*1517	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.484168	0.748410	-3.735759	30490.7662	
HLA A*6801	1:213-221	9	IECLRQLAA	1.136851	-0.209730	-4.662917	0.927121	-3.735796	46016.8786	
HLA B*2705	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.355496	0.619672	-3.735824	22672.345045	
HLA A*2602	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.550090	0.814245	-3.735845	35488.7079	
HLA A*0212	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.373486	0.637604	-3.735882	23631.2366	
HLA A*0301	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.367446	0.631559	-3.735887	23304.8291	
HLA B*1501	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.396382	0.660487	-3.735896	24910.484838	
HLA A*2402	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.550224	0.814245	-3.735979	35499.6530	
HLA B*5301	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.572441	0.836190	-3.736251	37362.922496	
HLA B*5401	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.548495	0.812136	-3.736359	35358.585899	
HLA B*2705	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.471453	0.734934	-3.736519	29610.989833	
HLA A*2902	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-3.962214	0.225691	-3.736523	9166.716464	
HLA B*7301	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.485045	0.748410	-3.736635	30552.3553	
HLA A*2403	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.343989	0.607347	-3.736642	22079.471045	
HLA B*1502	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.539745	0.803085	-3.736661	34653.364423	
HLA A*8001	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.405663	0.668648	-3.737015	25448.526788	
HLA A*3301	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-3.962820	0.225691	-3.737129	9179.519855	
HLA A*2402	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.549089	0.811904	-3.737185	35407.0143	
HLA B*7301	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.526492	0.789295	-3.737197	33611.814716	
HLA B*4403	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.622649	0.885414	-3.737235	41942.0190	
HLA B*4402	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.375345	0.638108	-3.737237	23732.5766	
HLA A*0202	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.526790	0.789295	-3.737496	33634.915847	
HLA B*4002	1:55-63	9	ATNAGYLRH	1.050890	-0.214700	-4.573710	0.836190	-3.737519	37472.231888	
HLA A*2603	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.581531	0.843953			
HLA B*1502	1:45-53	9	QSWSKPNPK	0.511632	0.277663	-4.526943	0.789295	-3.7376		

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HLA B*0802	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.472661	0.734934	-3.737727	29693.443195
HLA A*0250	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.441093	0.703256	-3.737837	27611.683078
HLA B*0702	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.430217	0.692096	-3.738121	26928.807011
HLA A*3101	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.441694	0.703401	-3.738293	27649.949863
HLA A*2501	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.394150	0.655774	-3.738376	24782.7884
HLA A*0201	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.394399	0.655774	-3.738625	24797.0041
HLA A*2602	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.551143	0.812136	-3.739007	35574.823780
HLA A*0101	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.346639	0.607347	-3.739292	22214.619758
HLA B*2705	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.431643	0.692096	-3.739547	27017.381251
HLA A*2402	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.552522	0.812772	-3.739750	35687.9749
HLA A*0219	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.445454	0.705319	-3.740135	27890.321732
HLA B*0801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.443933	0.703401	-3.740532	27792.870724
HLA B*7301	1:55-63 9	ATNAGYLRH	1.050890	-0.214700	-4.577011	0.836190	-3.740820	37758.139560
HLA B*4601	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.378484	0.637604	-3.740879	23904.7278
HLA B*1801	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.433170	0.692096	-3.741074	27112.553160
HLA B*4801	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.396925	0.655774	-3.741151	24941.6345
HLA B*5301	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.553927	0.812136	-3.741791	35803.616545
HLA B*5301	1:171-179	9 ARAVLPNAT	0.924326	-0.080373	-4.585910	0.843953	-3.741957	38539.8869
HLA B*0803	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.490517	0.748410	-3.742107	30939.7390
HLA A*6802	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.402608	0.660487	-3.742122	25270.178850
HLA A*1101	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.477397	0.734934	-3.742464	30019.062307
HLA A*3301	1:44-52 9	YQSWSKPNP	0.817579	0.063054	-4.623613	0.880633	-3.742980	42035.152020
HLA A*0211	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.446403	0.703401	-3.743001	27951.345348
HLA A*2902	1:149-157	9 KLEAKFADQ	0.547523	0.012288	-4.302910	0.559811	-3.743099	20086.7775
HLA A*0301	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.367498	0.624086	-3.743412	23307.6029
HLA A*6801	1:144-152	9 SELLAKLEA	1.205349	-0.282089	-4.666838	0.923260	-3.743579	46434.2513
HLA B*0802	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.479714	0.735649	-3.744065	30179.6163
HLA B*5701	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.363743	0.619672	-3.744071	23106.977143
HLA A*2402	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.590130	0.846009	-3.744121	38916.1717
HLA B*5401	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.556930	0.812772	-3.744158	36052.0146
HLA A*0202	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.529248	0.785066	-3.744182	33825.786762
HLA B*0802	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.476883	0.732654	-3.744229	29983.517811
HLA A*2602	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.556138	0.811904	-3.744233	35986.3469
HLA B*5801	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.351831	0.607347	-3.744485	22481.808583
HLA B*4501	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.584517	0.839978	-3.744540	38416.446638
HLA B*0803	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.449950	0.705319	-3.744632	28180.613166
HLA B*4402	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.405230	0.660487	-3.744744	25423.207430
HLA B*0702	1:172-180	9 RAVLPNATE	0.899712	-0.448568	-4.196227	0.451144	-3.745083	15711.8456
HLA B*0801	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.401046	0.655774	-3.745272	25179.4307
HLA A*3101	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.383025	0.637604	-3.745421	24156.0187
HLA A*2402	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.448740	0.703256	-3.745484	28102.208631
HLA A*0201	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.383796	0.638108	-3.745688	24198.9203
HLA B*7301	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.478464	0.732654	-3.745810	30092.882433
HLA A*0219	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.438236	0.692096	-3.746140	27430.637835
HLA A*0202	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.558271	0.811904	-3.746367	36163.5532
HLA A*6901	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.377965	0.631559	-3.746406	23876.1647
HLA A*0101	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-4.371414	0.625007	-3.746407	23518.7482
HLA B*0802	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.449889	0.703256	-3.746633	28176.649641
HLA A*3201	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.589425	0.842742	-3.746683	38853.063341
HLA B*5401	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.494370	0.747233	-3.747136	31215.4645
HLA A*0101	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.385455	0.638108	-3.747347	24291.5219
HLA A*2601	1:180-188	9 ETRIVVTGN	0.840941	-0.642202	-3.946228	0.198739	-3.747488	8835.43431
HLA A*0250	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.494779	0.747233	-3.747545	31244.8621
HLA B*4402	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.416642	0.668648	-3.747994	26100.077059
HLA B*5401	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-4.373005	0.625007	-3.747998	23605.0434
HLA A*0211	1:149-157	9 KLEAKFADQ	0.547523	0.012288	-4.307995	0.559811	-3.748184	20323.3152
HLA B*1509	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.481121	0.732654	-3.748467	30277.572726
HLA A*2402	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.591347	0.842742	-3.748605	39025.380382
HLA B*4001	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.380208	0.631559	-3.748650	23999.8388
HLA A*0250	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.591636	0.842742	-3.748894	39051.357150
HLA A*3002	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.452533	0.703401	-3.749131	28348.659165
HLA B*4601	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-4.374311	0.625007	-3.749304	23676.1519
HLA B*5401	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.533639	0.784286	-3.749353	34169.537008
HLA B*0803	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.485226	0.735649	-3.749577	30565.0848
HLA B*4001	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.387421	0.637604	-3.749817	24401.7652
HLA B*5101	1:102-110	9 SQLSQRYVP	0.667890	0.084808	-4.502619	0.752698	-3.749921	31814.0415
HLA B*5401	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.541082	0.790864	-3.750218	34760.199689
HLA A*3201	1:37-45 9	EFAGRACYQ	0.875308	-0.035330	-4.590515	0.839978	-3.750538	38950.714366
HLA B*3801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.536144	0.785066	-3.751078	34367.160033
HLA B*4002	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.593939	0.842742	-3.751197	39258.945191
HLA B*1501	1:228-236	9 ADFEVTTLA	0.872294	-0.299019	-4.324587	0.573275	-3.751311	21114.7827
HLA A*2603	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.564474	0.812772	-3.751702	36683.7508
HLA A*2403	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.407728	0.655774	-3.751954	25569.8301
HLA B*4601	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.412979	0.660487	-3.752492	25880.874240
HLA A*6801	1:95-103	9 RHRHFSYSQ	0.785584	0.087061	-4.625311	0.872645	-3.752666	42199.8881
HLA A*3301	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.565007	0.812136	-3.752871	36728.827835
HLA A*0216	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.421566	0.668648	-3.752919	26397.713443
HLA A*3001	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.257189	0.504252	-3.752938	18079.619698
HLA B*1801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.456466	0.703401	-3.753064	28606.555010
HLA B*5401	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.538279	0.785066	-3.753214	34536.579836
HLA A*0219	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.409873	0.655774	-3.754099	25696.4378
HLA A*6802	1:204-212	9 ADVEIRRLA	0.833844	-0.278617	-4.309886	0.555227	-3.754659	20412.0159
HLA A*2301	1:102-110	9 SQLSQRYVP	0.667890	0.084808	-4.507426	0.752698	-3.754728	32168.1355
HLA A*2501	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.423667	0.668648	-3.755019	26525.693659
HLA A*2602	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.597811	0.842742	-3.755069	39610.523128
HLA B*5301	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.567906	0.812772	-3.755135	36974.8425
HLA B*5401	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.393669	0.638108	-3.755561	24755.3188
HLA A*3101	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.379647	0.624086	-3.755561	23968.8279
HLA B*3501	1:172-180	9 RAVLPNATE	0.899712	-0.448568	-4.206772	0.451144	-3.755628	16097.9914
HLA A*2301	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.540135	0.784286	-3.755849	34684.498563
HLA B*5701	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.412009	0.655774	-3.756234	25823.1135
HLA A*0216	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.461620	0.705319	-3.756302	28948.117746
HLA A*0206	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.547327	0.790864	-3.756463	35263.644435
HLA B*0802	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.459933	0.703401	-3.756532	28835.892660
HLA A*0202	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.569502	0.812136	-3.757365	37110.912515
HLA A*3101	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.389294	0.631559	-3.757735	24507.2050
HLA A*0202	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.395398	0.637604	-3.757793	24854.0831
HLA A*3101	1:115-123	9 RVVVPPGME	0.970430	-0.454900	-4.273387	0.515530	-3.757857	18766.6450
HLA A*2403	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.418517	0.660487	-3.758030	26212.997048
HLA A*0101	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.389679	0.631559	-3.758120	24528.9580
HLA B*3901	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.396467	0.638108	-3.758359	24915.3367
HLA A*0301	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.365867	0.607347	-3.758520	23220.259514
HLA B*3801	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.543068	0.784286	-3.758781	34919.464699
HLA B*7301	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.521267	0.762047	-3.759220	33209.8341
HLA A*6901	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.366588	0.607347	-3.759242	23258.856599
HLA A*3201	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.396923	0.637604	-3.759318	24941.4996
HLA A*3002	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.495004	0.735649	-3.759356	31261.0933
HLA B*1517	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.465619	0.706243	-3.759376	29215.892234
HLA A*2301	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.543404	0.783495	-3.759908	34946.4893
HLA B*1509	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.391850	0.631559	-3.760291	24651.8787
HLA A*2602	1:115-123	9 RVVVPPGME	0.970430	-0.454900	-4.275856	0.515530	-3.760326	18873.6522
HLA A*3101	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.398539	0.638108	-3.760431	25034.5049
HLA B*4002	1:112-120	9 KDSRVVVPP	0.498317	-0.117809	-4.141508	0.380508	-3.761000	13851.8473
HLA A*6801	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.467435	0.706243	-3.761192	29338.324365
HLA B*3901	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.466794	0.705319	-3.761475	29295.026582
HLA A*3101	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.421994	0.660487	-3.7615	
HLA B*5101	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.494471	0.732654	-3.7618	

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HLA B*1517	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.494567	0.732654	-3.761913	31229.652994	
HLA A*2601	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.393605	0.631559	-3.762046	24751.7032	
HLA A*2601	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.387189	0.625007	-3.762182	24388.6996	
HLA A*3101	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.273455	0.511259	-3.762196	18769.589547	
HLA A*3101	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-3.987889	0.225691	-3.762198	9724.985680	
HLA A*6901	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.386404	0.624086	-3.762318	24344.6714	
HLA A*1101	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.467644	0.705319	-3.762326	29352.453586	
HLA A*1101	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.400078	0.637604	-3.762474	25123.3714	
HLA B*4501	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.643158	0.880566	-3.762592	43970.154144	
HLA A*0250	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.498251	0.735649	-3.762603	31495.6917	
HLA A*3002	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.497603	0.734934	-3.762669	31448.699682	
HLA B*1502	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.574710	0.811904	-3.762806	37558.6904	
HLA B*1503	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.469430	0.706243	-3.763187	29473.385097	
HLA A*3201	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.336571	0.573275	-3.763296	21705.5772	
HLA A*2602	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.548699	0.785066	-3.763633	35375.231701	
HLA A*2603	1:196-204	9	IAMRASEHA	1.101605	-0.216191	-4.649116	0.885414	-3.763702	44577.5588	
HLA A*3101	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.371064	0.607347	-3.763717	23499.798045	
HLA B*7301	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.548018	0.784286	-3.763732	35319.776149	
HLA B*1503	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.424357	0.660487	-3.763871	26567.916540	
HLA B*3801	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.419802	0.655774	-3.764028	26290.6816	
HLA B*3901	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.498963	0.734934	-3.764030	31547.361696	
HLA B*4403	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.608061	0.843953	-3.764108	40556.5852	
HLA A*3002	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.511404	0.747233	-3.764170	32464.1150	
HLA B*1503	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.243215	0.478869	-3.764346	17507.1137	
HLA A*3301	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.607096	0.842742	-3.764354	40466.509270	
HLA A*3001	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.081375	0.316807	-3.764568	12060.768423	
HLA A*0212	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.420401	0.655774	-3.764627	26326.9752	
HLA A*0201	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.324601	0.559811	-3.764790	21115.4681	
HLA A*3001	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.065521	0.300329	-3.765192	11628.4185	
HLA A*2902	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.280759	0.515530	-3.765229	19087.9515	
HLA B*1501	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.396817	0.631559	-3.765258	24935.4284	
HLA A*2601	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.389519	0.624086	-3.765434	24519.9361	
HLA B*1503	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.146465	0.380508	-3.765957	14010.8702	
HLA B*4002	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.646628	0.880566	-3.766062	44322.900958	
HLA B*4403	1:207-215	9	EIRRLAIEC	0.869270	0.013887	-4.649257	0.883157	-3.766100	44592.0307	
HLA B*4403	1:12-20	9	IAKTDFLAP	0.799705	0.096605	-4.662786	0.896310	-3.766476	46002.939782	
HLA B*1517	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.422266	0.655774	-3.766492	26440.3047	
HLA B*0801	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.390633	0.624086	-3.766547	24582.8929	
HLA A*3201	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.126523	0.359849	-3.766674	13382.0510	
HLA A*0201	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.398370	0.631559	-3.766811	25024.7556	
HLA A*2603	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.570049	0.803085	-3.766964	37157.720470	
HLA B*5701	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.427461	0.660487	-3.766975	26758.463244	
HLA B*4403	1:28-36	9	DADGGPALV	0.931987	-0.051421	-4.647606	0.880566	-3.767039	44422.762589	
HLA B*4403	1:61-69	9	LRHIIDVGH	0.992364	-0.149622	-4.609957	0.842742	-3.767216	40734.033436	
HLA B*3901	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.459706	0.692096	-3.767609	28820.764728	
HLA A*0250	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.552813	0.785066	-3.767747	35711.923395	
HLA A*8001	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.392780	0.625007	-3.767773	24704.7475	
HLA B*3801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.530054	0.762047	-3.768007	33888.6118	
HLA B*4601	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.387983	0.619672	-3.768310	24433.336236	
HLA A*0219	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.474707	0.706243	-3.768464	29833.689259	
HLA B*1517	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.471721	0.703256	-3.768464	29629.257373	
HLA A*1101	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.471749	0.703256	-3.768493	29631.180928	
HLA A*3001	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.247531	0.478869	-3.768662	17681.9662	
HLA A*2402	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.553950	0.785066	-3.768885	35805.553534	
HLA A*8001	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.328766	0.559811	-3.768956	21318.9765	
HLA A*6801	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-3.829365	0.060047	-3.769317	6750.944201	
HLA A*6802	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.425105	0.655774	-3.769330	26613.6618	
HLA A*3201	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.329264	0.559811	-3.769454	21343.4412	
HLA B*4402	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.401239	0.631559	-3.769680	25190.6031	
HLA B*5401	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.531821	0.762047	-3.769774	34026.7596	
HLA B*0803	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.502628	0.732654	-3.769974	31814.729984	
HLA A*2301	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.532037	0.762047	-3.769990	34043.6992	
HLA A*3101	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.343958	0.573275	-3.770683	22077.9182	
HLA A*0206	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.476239	0.705319	-3.770920	29939.105878	
HLA A*0211	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.519547	0.748410	-3.771137	33078.5819	
HLA B*0802	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.463293	0.692096	-3.771197	29059.836318	
HLA A*6801	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.585473	0.814245	-3.771228	38501.1261	
HLA A*0219	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.431737	0.660487	-3.771251	27023.228326	
HLA B*5701	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.408990	0.637604	-3.771385	25644.2213	
HLA A*0216	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.463958	0.692096	-3.771862	29104.360962	
HLA B*4801	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.432365	0.660487	-3.771878	27062.289973	
HLA A*6802	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.340432	0.568388	-3.772043	21899.366132	
HLA B*7301	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.585060	0.812772	-3.772288	38464.4850	
HLA A*0250	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.584907	0.812136	-3.772771	38450.961700	
HLA B*5701	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.411081	0.638108	-3.772973	25767.9909	
HLA A*6801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.063331	0.290041	-3.773290	11569.9353	
HLA B*4403	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-3.915689	0.141991	-3.773698	8235.48719	
HLA B*5401	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.526417	0.752698	-3.773719	33605.9964	
HLA B*7301	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.613759	0.839978	-3.773781	41092.151657	
HLA A*0201	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.398020	0.624086	-3.773934	25004.5919	
HLA A*2301	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.509905	0.735649	-3.774256	32352.2579	
HLA B*3801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.526955	0.752698	-3.774257	33647.6559	
HLA B*4001	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.434803	0.660487	-3.774317	27214.684796	
HLA A*0212	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.434848	0.660487	-3.774361	27217.482280	
HLA B*1509	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.412063	0.637604	-3.774458	25826.3268	
HLA B*4001	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.347894	0.573275	-3.774618	22278.8879	
HLA A*0203	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.430426	0.655774	-3.774652	26941.7758	
HLA A*0203	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.343364	0.568388	-3.774975	22047.720863	
HLA A*3101	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.226183	0.451144	-3.775039	16833.8377	
HLA B*0802	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.480402	0.705319	-3.775084	30227.491906	
HLA A*2403	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.406837	0.631559	-3.775279	25517.4568	
HLA B*5801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.348709	0.573275	-3.775434	22320.7498	
HLA B*4402	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.399808	0.624086	-3.775722	25107.7461	
HLA A*0301	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.349237	0.573275	-3.775962	22347.9357	
HLA A*3101	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.280294	0.504252	-3.776042	19067.516305	
HLA A*0212	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.414426	0.638108	-3.776319	25967.2659	
HLA B*1801	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.414537	0.638108	-3.776429	25973.8693	
HLA A*3002	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.567352	0.790864	-3.776488	36927.665611	
HLA B*4403	1:131-139	9	ILTEAADAA	1.112012	-0.238517	-4.650206	0.873495	-3.776712	44689.5974	
HLA B*3801	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.567704	0.790864	-3.776840	36957.643959	
HLA B*1503	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.432799	0.655774	-3.777025	27089.3882	
HLA A*3201	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.589477	0.811904	-3.777572	38857.6878	
HLA B*4601	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.409159	0.631559	-3.777600	25654.2120	
HLA A*6801	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.539776	0.762047	-3.777729	34655.8016	
HLA A*0216	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.438266	0.660487	-3.777780	27432.567060	
HLA B*5301	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.580937	0.803085	-3.777852	38101.017762	
HLA A*0250	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.590670	0.812772	-3.777899	38964.6243	
HLA B*4002	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.562653	0.784286	-3.778366	36530.270198	
HLA A*2501	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.483689	0.705319	-3.778371	30457.134633	
HLA B*0702	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.403027	0.624086	-3.778941	25294.5247	
HLA A*3201	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-3.839171	0.060047	-3.779124	6905.120612	
HLA A*0101	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.352553	0.573275	-3.779277	22519.1782	
HLA B*1509	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.563628	0.784286	-3.779342	36612.376588	
HLA B*2705	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.435182	0.655774	-3.779407	27238.3988	
HLA A*6802	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.411062	0.631559	-3.779503	25766.8757	
HLA B*2705	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.440069	0.660487	-3.7795		
HLA B*5401	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.483088	0.703401	-3.7796		

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HLA A*3201	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.483083	0.703256	-3.779827	30414.653698	
HLA A*2601	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.387318	0.607347	-3.779971	24395.957452	
HLA A*2602	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.483485	0.703401	-3.780083	30442.803040	
HLA B*0702	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.440973	0.660487	-3.780487	27604.065945	
HLA A*0211	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-3.816409	0.035827	-3.780583	6552.536641	
HLA A*6901	1:204-212	9 ADVEIRRLA	0.833844	-0.278617	-4.336015	0.555227	-3.780787	21677.7654	
HLA A*0250	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.592804	0.811904	-3.780899	39156.4963	
HLA B*5301	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.566036	0.785066	-3.780970	36815.961140	
HLA A*2402	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.486720	0.705319	-3.781401	30670.430980	
HLA A*6901	1:125-133	9 DADLRHILT	0.976283	-0.558013	-4.199813	0.418270	-3.781543	15842.0915	
HLA B*1517	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.401556	0.619672	-3.781883	25209.007436	
HLA A*2603	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.627950	0.846009	-3.781941	42457.0457	
HLA B*4601	1:228-236	9 ADFEVTTLA	0.872294	-0.299019	-4.355452	0.573275	-3.782177	22670.0147	
HLA B*1503	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.487502	0.705319	-3.782184	30725.733348	
HLA B*4501	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.420330	0.638108	-3.782223	26322.7028	
HLA B*5301	1:215-223	9 CLRQLAAVA	1.106552	-0.292307	-4.596617	0.814245	-3.782372	39501.8139	
HLA A*6901	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.350772	0.568388	-3.782383	22427.022979	
HLA A*2601	1:228-236	9 ADFEVTTLA	0.872294	-0.299019	-4.355785	0.573275	-3.782510	22687.4366	
HLA A*6801	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.294741	0.511259	-3.783482	19712.472919	
HLA A*2402	1:102-110	9 SQLSQRYVP	0.667890	0.084808	-4.536461	0.752698	-3.783763	34392.2687	
HLA B*5701	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.415474	0.631559	-3.783915	26029.9956	
HLA B*4801	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.421529	0.637604	-3.783924	26395.4286	
HLA A*0101	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.408299	0.624086	-3.784213	25603.4664	
HLA B*1502	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.531562	0.747233	-3.784329	34006.5167	
HLA B*1503	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.295662	0.511259	-3.784403	19754.321056	
HLA B*1509	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.408578	0.624086	-3.784493	25619.9546	
HLA B*4801	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.422621	0.638108	-3.784514	26461.9124	
HLA B*1801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.517233	0.732654	-3.784579	32902.783548	
HLA B*5801	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.353116	0.568388	-3.784728	22548.435494	
HLA A*0216	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.491041	0.706243	-3.784798	30977.087439	
HLA B*5101	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.404483	0.619672	-3.784811	25379.508348	
HLA A*0212	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.392170	0.607347	-3.784823	24670.022966	
HLA A*0216	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.440964	0.655774	-3.785189	27603.4686	
HLA A*8001	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.446135	0.660487	-3.785648	27934.112303	
HLA A*1101	1:122-130	9 MEDDADLRH	1.015184	-0.359410	-4.441525	0.655774	-3.785751	27639.1819	
HLA A*3201	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.570991	0.785066	-3.785925	37238.416647	
HLA A*3301	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.569433	0.783495	-3.785938	37105.0907	
HLA B*4402	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.423956	0.637604	-3.786351	26543.3501	
HLA A*0203	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-3.954146	0.167651	-3.786495	8997.993330	
HLA A*2603	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.577549	0.790864	-3.786685	37804.945771	
HLA A*2602	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.534043	0.747233	-3.786810	34201.3465	
HLA B*4001	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.406577	0.619672	-3.786904	25502.138252	
HLA B*1502	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.570547	0.783495	-3.787052	37200.3609	
HLA A*2402	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.571614	0.784286	-3.787327	37291.840695	
HLA A*3301	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.633410	0.846009	-3.787401	42994.2101	
HLA B*3801	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.523092	0.735649	-3.787444	33349.7249	
HLA A*0202	1:204-212	9 ADVEIRRLA	0.833844	-0.278617	-4.342694	0.555227	-3.787467	22013.7534	
HLA B*0803	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.522481	0.734934	-3.787548	33302.849132	
HLA A*6801	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.571182	0.783495	-3.787686	37254.7381	
HLA B*4501	1:61-69 9	LRHIIDVGH	0.992364	-0.149622	-4.630565	0.842742	-3.787823	42713.459573	
HLA A*3001	1:179-187	9 TETRIVVTG	1.116102	-0.622367	-4.281605	0.493735	-3.787870	19125.1627	
HLA A*2403	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.407596	0.619672	-3.787924	25562.084862	
HLA B*5801	1:172-180	9 RAVLPNATE	0.899712	-0.448568	-4.239117	0.451144	-3.787973	17342.7136	
HLA B*1801	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.523565	0.734934	-3.788631	33386.008724	
HLA B*5701	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.412986	0.624086	-3.788900	25881.2942	
HLA B*5301	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.550957	0.762047	-3.788910	35559.6230	
HLA B*3801	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.536191	0.747233	-3.788957	34370.8786	
HLA B*1501	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.413197	0.624086	-3.789112	25893.8986	
HLA A*3201	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.580638	0.790864	-3.789774	38074.849223	
HLA A*0212	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.421486	0.631559	-3.789928	26392.8583	
HLA A*3301	1:171-179	9 ARAVLPNAT	0.924326	-0.080373	-4.633964	0.843953	-3.790012	43049.1373	
HLA A*2301	1:133-141	9 TEAADAARA	1.018713	-0.271480	-4.537255	0.747233	-3.790021	34455.2139	
HLA A*0211	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.428201	0.638108	-3.790094	26804.1016	
HLA B*5101	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.482286	0.692096	-3.790190	30358.925787	
HLA B*1501	1:172-180	9 RAVLPNATE	0.899712	-0.448568	-4.241741	0.451144	-3.790598	17447.8302	
HLA B*5101	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.494123	0.703401	-3.790722	31197.737960	
HLA A*3001	1:117-125	9 VVPPGMEDD	1.199814	-0.687818	-4.302753	0.511996	-3.790757	20079.4981	
HLA B*4601	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.415368	0.624086	-3.791283	26023.6595	
HLA A*2602	1:186-194	9 TGNYRAWRH	1.189863	-0.377091	-4.604133	0.812772	-3.791361	40191.3914	
HLA A*3002	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.497147	0.705319	-3.791828	31415.711004	
HLA B*0803	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.495126	0.703256	-3.791870	31269.888744	
HLA B*1502	1:239-247	9 TEVATSPLA	1.014741	-0.279092	-4.527805	0.735649	-3.792157	33713.6149	
HLA A*0202	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.583331	0.790864	-3.792467	38311.636371	
HLA B*1503	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.495841	0.703256	-3.792584	31321.357712	
HLA B*1801	1:240-248	9 EVATSPLAT	0.961736	-0.324132	-4.430283	0.637604	-3.792679	26932.8864	
HLA B*0801	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.361086	0.568388	-3.792698	22966.026796	
HLA B*0801	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.304428	0.511259	-3.793169	20157.099351	
HLA A*2603	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.578249	0.785066	-3.793183	37865.942053	
HLA B*4801	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.424811	0.631559	-3.793252	26595.6708	
HLA A*2902	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.417427	0.624086	-3.793341	26147.2799	
HLA A*3002	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.304691	0.511259	-3.793432	20169.316391	
HLA B*0702	1:111-119	9 EKDSRVVVP	0.794349	-0.162790	-4.425013	0.631559	-3.793454	26608.0473	
HLA B*0803	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.462212	0.668648	-3.793565	28987.609399	
HLA A*2603	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.605749	0.811904	-3.793845	40341.2627	
HLA B*4501	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.579774	0.785066	-3.794708	37999.123724	
HLA A*2301	1:150-158	9 LEAKFADQP	0.710397	0.038013	-4.543136	0.748410	-3.794726	34924.9435	
HLA B*5301	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.584024	0.789295	-3.794729	38372.827389	
HLA A*1101	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.498387	0.703401	-3.794986	31505.575800	
HLA B*5801	1:204-212	9 ADVEIRRLA	0.833844	-0.278617	-4.350753	0.555227	-3.795526	22426.0523	
HLA A*0212	1:228-236	9 ADFEVTTLA	0.872294	-0.299019	-4.369126	0.573275	-3.795851	23395.1484	
HLA A*0202	1:103-111	9 QLSQRYVPE	0.770979	-0.642414	-3.924420	0.128565	-3.795855	8402.7217	
HLA B*4801	1:158-166	9 PNAILRRKQ	0.959799	-0.335713	-4.420027	0.624086	-3.795942	26304.3392	
HLA A*0250	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.528863	0.732654	-3.796209	33795.789095	
HLA A*2601	1:231-239	9 EVTTLADGT	0.843460	-0.396688	-4.243454	0.446772	-3.796682	17516.7770	
HLA B*0803	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.488785	0.692096	-3.796689	30816.625175	
HLA B*4601	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.404291	0.607347	-3.796944	25368.252218	
HLA A*0219	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.404328	0.607347	-3.796981	25370.448144	
HLA B*0803	1:217-225	9 RQLAAVAPA	0.688822	-0.063815	-4.422281	0.625007	-3.797273	26441.1630	
HLA A*2402	1:235-243	9 LADGTEVAT	1.137874	-0.354379	-4.581371	0.783495	-3.797876	38139.1694	
HLA B*0801	1:94-102	9 IRHRHFSYS	0.730701	-0.843332	-3.685285	-0.112631	-3.797915	4844.89869	
HLA A*6801	1:152-160	9 AKFADQPNA	1.017259	-0.171250	-4.644110	0.846009	-3.798100	44066.5985	
HLA A*0203	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.309388	0.511259	-3.798129	20388.618478	
HLA A*0216	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.436236	0.638108	-3.798129	27304.6424	
HLA A*2403	1:134-142	9 EAADAARAT	0.999569	-0.361461	-4.436427	0.638108	-3.798319	27316.6100	
HLA A*2402	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.533381	0.734934	-3.798447	34149.209183	
HLA A*2301	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.504794	0.706243	-3.798552	31973.815665	
HLA B*7301	1:157-165	9 QPNAILRRK	0.836914	-0.025010	-4.610531	0.811904	-3.798626	40787.8383	
HLA A*0101	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.367051	0.568388	-3.798663	23283.657896	
HLA A*6801	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.533836	0.734934	-3.798903	34185.068223	
HLA A*0250	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.588314	0.789295	-3.799019	38753.770202	
HLA A*2501	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.491189	0.692096	-3.799093	30987.646943	
HLA A*6802	1:169-177	9 QAARAVLPN	0.840310	-0.476167	-4.163264	0.364143	-3.799121	14563.4385	
HLA B*1517	1:116-124	9 VVVPPGMED	0.939999	-0.610611	-4.128867	0.329388	-3.799480	13454.4970	
HLA A*3201	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.098738	0.298936	-3.799802	12552.715124	
HLA A*0301	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.368231	0.568388	-3.799842	23346.976765	
HLA A*2402	1:130-138	9 HILTEAADA	0.912003	-0.149956	-4.562204	0.762047			
HLA A*6802	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.117073	0.316807	-3.8002		

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HLA B*1503	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.438534	0.638108	-3.800427	27449.490
HLA B*7301	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.591411	0.790864	-3.800547	39031.081119
HLA A*2902	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.461120	0.660487	-3.800633	28914.779857
HLA B*4001	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.408506	0.607347	-3.801159	25615.658398
HLA B*0801	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.408978	0.607347	-3.801631	25643.527700
HLA A*2501	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.427177	0.625007	-3.802170	26740.952
HLA A*8001	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.440468	0.638108	-3.802360	27571.977
HLA A*0211	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.471075	0.668648	-3.802427	29585.210122
HLA B*4002	1:37-45	9	EFAGRACYQ	0.875308	-0.035330	-4.642470	0.839978	-3.802492	43900.512371
HLA A*0250	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.593518	0.790864	-3.802654	39220.946401
HLA B*4001	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.426770	0.624086	-3.802685	26715.937
HLA A*2603	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.564974	0.762047	-3.802927	36726.0461
HLA B*5801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.363132	0.559811	-3.803321	23074.4983
HLA A*0206	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.495530	0.692096	-3.803434	31298.998946
HLA B*5101	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.464057	0.660487	-3.803570	29110.974671
HLA B*3801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.552268	0.748410	-3.803858	35667.1296
HLA B*5101	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.510241	0.706243	-3.803998	32377.295805
HLA A*3002	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.507268	0.703256	-3.804012	32156.477912
HLA A*2602	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.607317	0.803085	-3.804232	40487.092920
HLA A*2301	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.507724	0.703256	-3.804468	32190.244446
HLA B*4801	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.424209	0.619672	-3.804537	26558.863126
HLA B*5301	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.588937	0.784286	-3.804650	38809.368250
HLA A*1101	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.164754	0.359849	-3.804905	14613.4750
HLA B*1503	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.169203	0.364143	-3.805061	14763.9792
HLA A*2301	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.540079	0.734934	-3.805145	34679.995513
HLA A*2501	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.424928	0.619672	-3.805256	26602.865772
HLA A*3201	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.299010	0.493735	-3.805275	19907.1974
HLA B*5101	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.442897	0.637604	-3.805293	27726.6426
HLA A*2403	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.443139	0.637604	-3.805535	27742.0967
HLA A*0219	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.437221	0.631559	-3.805662	27366.6053
HLA B*0802	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.430757	0.625007	-3.805750	26962.3346
HLA B*3901	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.509188	0.703401	-3.805787	32298.920224
HLA B*1502	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.509545	0.703401	-3.806144	32325.490651
HLA A*0101	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.361417	0.555227	-3.806190	22983.5518
HLA B*5401	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.539294	0.732654	-3.806640	34617.388705
HLA A*2902	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.444833	0.638108	-3.806726	27850.5169
HLA A*2902	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.380528	0.573275	-3.807253	24017.5031
HLA B*1501	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.318593	0.511259	-3.807334	20825.387037
HLA B*1501	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.362780	0.555227	-3.807553	23055.7814
HLA A*0202	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.510842	0.703256	-3.807586	32422.167211
HLA B*4601	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.376165	0.568388	-3.807777	23777.427271
HLA A*0201	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.363095	0.555227	-3.807867	23072.5011
HLA B*5101	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.513239	0.705319	-3.807920	32601.570073
HLA A*2603	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.592254	0.784286	-3.807968	39106.959000
HLA B*0803	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.512024	0.703401	-3.808622	32510.513726
HLA B*4402	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.428309	0.619672	-3.808637	26810.772783
HLA B*5301	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.599937	0.790864	-3.809073	39804.929770
HLA B*5701	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.416804	0.607347	-3.809457	26109.821575
HLA B*2705	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.447115	0.637604	-3.809510	27997.2006
HLA A*2402	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.545309	0.735649	-3.809660	35100.1511
HLA A*0203	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.433845	0.624086	-3.809759	27154.6818
HLA B*7301	1:83-91	9	TGISRSCTH	1.134697	-0.322561	-4.621928	0.812136	-3.809792	41872.418085
HLA A*6801	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.594162	0.784286	-3.809875	39279.127098
HLA B*3501	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.256694	0.446772	-3.809921	18058.9938
HLA A*6901	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-3.845773	0.035827	-3.809947	7010.892721
HLA B*0801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.226395	0.416215	-3.810180	16842.0359
HLA A*2902	1:80-88	9	FYITGISRS	1.033042	-0.849138	-3.994096	0.183904	-3.810192	9864.982289
HLA A*6802	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.434329	0.624086	-3.810243	27184.9608
HLA A*0301	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.365475	0.555227	-3.810247	23199.2906
HLA B*1509	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.502506	0.692096	-3.810410	31805.781307
HLA A*0211	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.515959	0.705319	-3.810641	32806.448628
HLA B*2705	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.442463	0.631559	-3.810904	27698.9068
HLA A*2501	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.471408	0.660487	-3.810922	29607.946338
HLA B*1503	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.514326	0.703401	-3.810925	32683.332146
HLA A*2403	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.384454	0.573275	-3.811179	24235.6038
HLA B*1501	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.379698	0.568388	-3.811310	23971.680870
HLA A*3301	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.574140	0.762047	-3.812093	37509.3481
HLA A*2902	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.437303	0.625007	-3.812296	27371.7875
HLA A*6802	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.323583	0.511259	-3.812324	21066.063434
HLA B*1801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.385793	0.573275	-3.812518	24310.4529
HLA B*0802	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.450282	0.637604	-3.812677	28202.1173
HLA B*3801	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.547710	0.734934	-3.812777	35294.754051
HLA B*4403	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.625640	0.812772	-3.812868	42231.8618
HLA A*0211	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.504999	0.692096	-3.812903	31988.868015
HLA B*2705	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.420615	0.607347	-3.813268	26339.939233
HLA A*0203	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.444866	0.631559	-3.813307	27852.6263
HLA B*4403	1:34-42	9	ALVEFAGRA	0.973591	-0.189305	-4.597703	0.784286	-3.813416	39600.667082
HLA A*1101	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.386693	0.573275	-3.813418	24360.8761
HLA B*7301	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.596972	0.783495	-3.813476	39534.0959
HLA B*4501	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.626307	0.812772	-3.813536	42296.7970
HLA B*3501	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.386940	0.573275	-3.813664	24374.7180
HLA B*4002	1:42-50	9	ACYQSWSKP	0.531103	0.253963	-4.598936	0.785066	-3.813870	39713.300446
HLA A*3101	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.369116	0.555227	-3.813889	23394.6421
HLA B*1517	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-3.627436	-0.186575	-3.814011	4240.681742
HLA A*6901	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.329701	0.515530	-3.814171	21364.9286
HLA A*2402	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.434002	0.619672	-3.814330	27164.526182
HLA A*3301	1:15-23	9	TDFLAPPDV	0.718264	0.084821	-4.617591	0.803085	-3.814506	41456.333780
HLA A*0206	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.470438	0.655774	-3.814664	29541.8676
HLA B*0802	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.453127	0.638108	-3.815019	28387.4865
HLA A*0219	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.388377	0.573275	-3.815102	24455.5528
HLA A*2601	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.370463	0.555227	-3.815235	23467.2749
HLA B*1501	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.330782	0.515530	-3.815252	21418.1625
HLA B*4402	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.422804	0.607347	-3.815458	26473.081016
HLA A*8001	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.439725	0.624086	-3.815640	27524.8828
HLA B*3501	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.476164	0.660487	-3.815677	29933.923375
HLA A*6801	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.563090	0.747233	-3.815856	36567.0468
HLA A*2602	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-3.851995	0.035827	-3.816168	7112.049292
HLA A*2301	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.485017	0.668648	-3.816369	30550.371947
HLA B*1801	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.436060	0.619672	-3.816388	27293.566103
HLA A*2603	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.519798	0.703401	-3.816397	33097.735278
HLA A*0101	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.234686	0.418270	-3.816416	17166.6646
HLA A*0201	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.384900	0.568388	-3.816512	24260.527926
HLA B*5801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.332074	0.515530	-3.816544	21481.9858
HLA A*2301	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.549280	0.732654	-3.816626	35422.533189
HLA B*3901	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.385074	0.568388	-3.816686	24270.242131
HLA A*6802	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.328905	0.511996	-3.816909	21325.7822
HLA B*4002	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.628821	0.811904	-3.816917	42542.3455
HLA B*4501	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.629350	0.811904	-3.817446	42594.1606
HLA A*6801	1:171-179	9	ARAVLPNAT	0.924326	-0.080373	-4.661463	0.843953	-3.817510	45863.0386
HLA B*0801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.391667	0.573275	-3.818392	24641.4786
HLA B*0801	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.322681	0.504252	-3.818429	21022.346273
HLA B*1501	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.182666	0.364143	-3.818523	15228.8102
HLA B*1509	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.523919	0.705319	-3.818601	33413.292672
HLA A*0206	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.479187	0.660487	-3.818701	30143.066371
HLA A*2402	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.443804	0.625007	-3.818797	27784.6023
HLA A*2602	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.602458	0.783495		
HLA B*5301	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.554885	0.735649		

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HLA B*0803	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.475290	0.655774	-3.819515	29873.7425
HLA B*1509	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.457894	0.638108	-3.819787	28700.8029
HLA A*2501	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.018832	0.198739	-3.820092	10443.1541
HLA B*4501	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.603588	0.783495	-3.820093	40140.9791
HLA B*1509	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.555675	0.734934	-3.820741	35948.014985	
HLA A*6801	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-3.962792	0.142013	-3.820778	9178.923952	
HLA A*0101	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.380612	0.559811	-3.820802	24022.1811
HLA A*0206	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.152174	0.331331	-3.820844	14196.273568	
HLA A*3002	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.553624	0.732654	-3.820970	35778.638788	
HLA A*0202	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.459196	0.638108	-3.821088	28786.9505
HLA A*3001	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.055225	0.234045	-3.821180	11355.9954
HLA A*2301	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.526532	0.705319	-3.821213	33614.906073	
HLA B*3801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.553913	0.732654	-3.821259	35802.454403	
HLA A*2602	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.573961	0.752698	-3.821263	37493.9292
HLA B*4801	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.428833	0.607347	-3.821487	26843.136959	
HLA A*3001	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.237740	0.416215	-3.821526	17287.8208
HLA A*6801	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.513694	0.692096	-3.821598	32635.803985	
HLA B*4402	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.390116	0.568388	-3.821728	24553.652431	
HLA A*6801	1:15-23 9	TDFLAPPDV	0.718264	0.084821	-4.625220	0.803085	-3.822135	42190.985533	
HLA B*1502	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.570817	0.748410	-3.822408	37223.5119
HLA A*0250	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.575115	0.752698	-3.822417	37593.6551
HLA A*0202	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.555217	0.732654	-3.822563	35910.112399	
HLA A*1101	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.483158	0.660487	-3.822672	30419.919431	
HLA B*5101	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.272766	0.449835	-3.822931	18739.8614
HLA A*3301	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.608122	0.785066	-3.823057	40562.290191	
HLA A*6802	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.317040	0.493735	-3.823305	20751.0497
HLA A*2402	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.571774	0.748410	-3.823364	37305.5618
HLA A*2601	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.392012	0.568388	-3.823624	24661.082626	
HLA A*0216	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.140526	0.316807	-3.823719	13820.559122	
HLA A*2301	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.516295	0.692096	-3.824199	32831.837981	
HLA B*0702	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.274416	0.449835	-3.824580	18811.1659
HLA B*3501	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.456278	0.631559	-3.824719	28594.1770
HLA B*1509	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.485432	0.660487	-3.824946	30579.639478	
HLA B*5301	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.462675	0.637604	-3.825071	29018.5193
HLA B*5301	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.573526	0.748410	-3.825117	37456.4230
HLA B*4002	1:186-194	9	TGNYRAWRH	1.189863	-0.377091	-4.637975	0.812772	-3.825203	43448.5236
HLA A*6901	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.385044	0.559811	-3.825233	24268.5353
HLA B*4001	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.385309	0.559811	-3.825498	24283.3756
HLA A*2403	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.337849	0.511996	-3.825854	21769.5504
HLA A*1101	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.433344	0.607347	-3.825998	27123.409350	
HLA A*3301	1:34-42 9	ALVEFAGRA	0.973591	-0.189305	-4.610446	0.784286	-3.826160	40779.895488	
HLA B*1501	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.186561	0.359849	-3.826713	15366.0209
HLA B*7301	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.561654	0.734934	-3.826721	36446.376177	
HLA A*0203	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.187130	0.359849	-3.827281	15386.1512
HLA A*1101	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.459144	0.631559	-3.827585	28783.5246
HLA B*1503	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.144421	0.316807	-3.827614	13945.081580	
HLA B*1517	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.332284	0.504252	-3.828032	21492.331501	
HLA B*5301	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.580810	0.752698	-3.828112	38089.8887
HLA B*4002	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.617744	0.789295	-3.828449	41470.914164	
HLA B*5101	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.484225	0.655774	-3.828451	30494.7253
HLA A*2402	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.575716	0.747233	-3.828483	37645.7558
HLA B*5301	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.575996	0.747233	-3.828762	37669.9991
HLA B*5701	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.280184	0.451144	-3.829040	19062.6687
HLA A*0212	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.453630	0.624086	-3.829544	28420.3702
HLA B*1509	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.398212	0.568388	-3.829824	25015.686706	
HLA B*0801	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.385236	0.555227	-3.830009	24279.3034
HLA B*1501	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.324100	0.493735	-3.830365	21091.1506
HLA A*3002	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.203614	0.373143	-3.830471	15981.3691
HLA B*1503	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.324387	0.493735	-3.830652	21105.0755
HLA B*4002	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.643191	0.812136	-3.831055	43973.484502	
HLA B*5401	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.536515	0.705319	-3.831196	34396.548350	
HLA B*4801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.404671	0.573275	-3.831396	25390.4947
HLA A*3001	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.212020	0.380508	-3.831513	16293.7272
HLA A*8001	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.438952	0.607347	-3.831606	27475.936193	
HLA B*3801	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.534887	0.703256	-3.831630	34267.835288	
HLA A*0250	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.469785	0.637604	-3.832180	29497.4715
HLA B*0802	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.463831	0.631559	-3.832272	29095.8598
HLA A*0219	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.392186	0.559811	-3.832375	24670.9572
HLA B*0702	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.392303	0.559811	-3.832493	24677.6314
HLA B*5801	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.344318	0.511259	-3.833059	22096.200028	
HLA A*3101	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.401544	0.568388	-3.833156	25208.325555	
HLA A*2402	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.501954	0.668648	-3.833306	31765.371548	
HLA A*0301	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.344982	0.511259	-3.833723	22130.055189	
HLA B*0803	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.471744	0.637604	-3.834140	29630.8603
HLA B*0801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.327876	0.493735	-3.834141	21275.3099
HLA B*2705	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.472261	0.638108	-3.834154	29666.1472
HLA B*5401	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.540448	0.706243	-3.834205	34709.463569	
HLA A*2902	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.441882	0.607347	-3.834536	27661.919106	
HLA A*6901	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.345817	0.511259	-3.834557	22172.597034	
HLA A*6801	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.570289	0.735649	-3.834640	37178.2300
HLA B*7301	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.503500	0.668648	-3.834852	31878.648461	
HLA A*2601	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.394820	0.559811	-3.835009	24821.0284
HLA A*0201	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.060925	0.225691	-3.835234	11506.018322	
HLA B*4403	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.587971	0.752698	-3.835273	38723.1728
HLA B*4403	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.647462	0.812136	-3.835326	44408.105353	
HLA A*2902	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.467165	0.631559	-3.835606	29320.0775
HLA B*0802	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.455413	0.619672	-3.835741	28537.307245	
HLA B*4501	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.625048	0.789295	-3.835754	42174.326678	
HLA B*3801	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.541108	0.705319	-3.835790	34762.268288	
HLA A*0250	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.539367	0.703401	-3.835966	34623.194755	
HLA B*5801	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.340378	0.504252	-3.836126	21896.641419	
HLA A*2403	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.460643	0.624086	-3.836557	28883.0428
HLA B*5701	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.409882	0.573275	-3.836607	25696.9938
HLA B*0801	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.296207	0.459518	-3.836689	19779.130157	
HLA B*1517	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.106406	0.269704	-3.836702	12776.3379
HLA A*0250	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.505358	0.668648	-3.836711	32015.356579	
HLA B*4002	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.620448	0.783495	-3.836953	41729.9501
HLA B*5301	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.456658	0.619672	-3.836986	28619.248005	
HLA B*4002	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.505852	0.668648	-3.837204	32051.749149	
HLA B*5701	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.405705	0.568388	-3.837317	25451.005036	
HLA A*0211	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.405886	0.568388	-3.837498	25461.609152	
HLA B*5801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.349642	0.511996	-3.837646	22368.7402
HLA A*0216	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.469750	0.631559	-3.838191	29495.0779
HLA B*0803	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.499008	0.660487	-3.838521	31550.604549	
HLA A*2301	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.542041	0.703401	-3.838639	34837.008347	
HLA B*4403	1:157-165	9	QPNAILRRK	0.836914	-0.025010	-4.650634	0.811904	-3.838730	44733.6205
HLA A*0202	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.531384	0.692096	-3.839288	33992.537757	
HLA B*4501	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.601419	0.762047	-3.839372	39941.0416
HLA A*2402	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.546202	0.706243	-3.839959	35172.382748	
HLA A*2403	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.408416	0.568388	-3.840028	25610.392980	
HLA A*6901	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.204483	0.364143	-3.840341	16013.3904
HLA A*0206	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.024494	0.183904	-3.840589	10580.201693	
HLA B*4501	1:83-91 9	TGISRSCTH	1.134697	-0.322561	-4.653416	0.812136	-3.841280	45021.072811	
HLA A*8001	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.414586	0.573275	-3.841311	25976.8203
HLA B*1503	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.401123	0.559811	-3.841313	25183.9263
HLA B*2705	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.396561	0.555227		
HLA B*1502	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.497302	0.655774		

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HLA A*8001	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.357118	0.515530	-3.841588	22757.1350
HLA B*4501	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.140855	0.298936	-3.841919	13831.030564	
HLA A*1101	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.353401	0.511259	-3.842142	22563.200455	
HLA A*6801	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.633074	0.790864	-3.842210	42960.962077	
HLA B*4801	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.410627	0.568388	-3.842239	25741.100367	
HLA B*4403	1:215-223	9	CLRQLAAVA	1.106552	-0.292307	-4.656649	0.814245	-3.842404	45357.4604
HLA A*2603	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.626329	0.783495	-3.842833	42298.8565
HLA A*3002	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.591657	0.748410	-3.843248	39053.2585
HLA B*4601	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.403158	0.559811	-3.843347	25302.1889
HLA B*3901	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.463101	0.619672	-3.843428	29046.947917	
HLA A*0250	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.591841	0.748410	-3.843431	39069.7414
HLA B*0802	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.504108	0.660487	-3.843622	31923.346897	
HLA A*0202	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.549073	0.705319	-3.843754	35405.673588	
HLA A*3201	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.592200	0.748410	-3.843790	39102.0933
HLA B*2705	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.467898	0.624086	-3.843812	29369.6082
HLA B*1517	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.403774	0.559811	-3.843963	25338.0775
HLA B*1517	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.475588	0.631559	-3.844029	29894.2745
HLA B*2705	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.417344	0.573275	-3.844069	26142.3295
HLA A*2602	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.579771	0.735649	-3.844123	37998.9181
HLA A*0216	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.413021	0.568388	-3.844633	25883.394591	
HLA A*2603	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.291426	0.446772	-3.844654	19562.5734
HLA A*6801	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.593323	0.748410	-3.844913	39203.3393
HLA A*3201	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.577734	0.732654	-3.845080	37821.106348	
HLA A*0101	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.356713	0.511259	-3.845454	22735.969376	
HLA B*7301	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.552235	0.705319	-3.846917	35664.428409	
HLA A*0212	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.415516	0.568388	-3.847128	26032.530522	
HLA B*5101	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.472139	0.625007	-3.847132	29657.8029
HLA A*0301	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.351634	0.504252	-3.847382	22471.594480	
HLA A*2501	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.471913	0.624086	-3.847828	29642.4041
HLA B*4001	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.403619	0.555227	-3.848391	25329.0320
HLA A*3001	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.295852	0.446772	-3.849080	19762.9793
HLA B*4601	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.404394	0.555227	-3.849167	25374.2914
HLA A*2602	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.581893	0.732654	-3.849239	38185.001957	
HLA A*3001	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.299095	0.449835	-3.849259	19911.0748
HLA B*0803	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.480898	0.631559	-3.849339	30262.0158
HLA B*1502	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.486974	0.637604	-3.849369	30688.3559
HLA B*3801	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.481145	0.631559	-3.849586	30279.2107
HLA A*6901	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.354171	0.504252	-3.849920	22603.273126	
HLA B*4801	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.301139	0.451144	-3.849995	20005.0092
HLA B*3501	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.457403	0.607347	-3.850056	28668.370260	
HLA B*2705	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-3.957299	0.107209	-3.850090	9063.55711
HLA B*0702	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.423648	0.573275	-3.850373	26524.5456
HLA B*4002	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.641339	0.790864	-3.850476	43786.424861	
HLA A*0211	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.507191	0.655774	-3.851417	32150.7376
HLA A*0211	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.557663	0.706243	-3.851420	36112.917718	
HLA B*3801	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.543528	0.692096	-3.851432	34956.510781	
HLA A*1101	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.489821	0.638108	-3.851714	30890.2340
HLA A*6802	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.050583	0.198739	-3.851843	11235.2470
HLA A*8001	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.483529	0.631559	-3.851971	30445.9323
HLA A*0301	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.363995	0.511996	-3.851999	23120.3566
HLA A*2301	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.471702	0.619672	-3.852030	29627.975073	
HLA B*1509	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.555459	0.703401	-3.852057	35930.127757	
HLA B*3901	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.512834	0.660487	-3.852348	32571.248391	
HLA B*5701	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.412295	0.559811	-3.852484	25840.1626
HLA B*0702	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.460013	0.607347	-3.852667	28841.197113	
HLA B*4403	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.477738	0.625007	-3.852731	30042.6195
HLA B*5701	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.408099	0.555227	-3.852872	25591.6956
HLA B*4403	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.638217	0.785066	-3.853151	43472.740739	
HLA B*5101	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.426907	0.573275	-3.853631	26724.3216
HLA A*0206	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.560151	0.706243	-3.853908	36320.405033	
HLA B*1801	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.478008	0.624086	-3.853922	30061.3159
HLA A*3002	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.510006	0.655774	-3.854231	32359.7847
HLA B*1517	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.514766	0.660487	-3.854279	32716.412945	
HLA A*0216	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.478379	0.624086	-3.854293	30087.0222
HLA B*3501	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.478433	0.624086	-3.854348	30090.7661
HLA B*4001	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.422978	0.568388	-3.854590	26483.681154	
HLA B*5101	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.423476	0.568388	-3.855088	26514.072619	
HLA A*0206	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.423580	0.568388	-3.855191	26520.384651	
HLA B*0803	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.474874	0.619672	-3.855201	29845.150644	
HLA A*2902	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.145370	0.290041	-3.855330	13975.5932
HLA B*3501	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.424440	0.568388	-3.856051	26572.947549	
HLA A*2501	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.487657	0.631559	-3.856099	30736.7060
HLA B*1517	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.035687	0.179565	-3.856122	10856.4264
HLA B*5401	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.516662	0.660487	-3.856175	32859.557866	
HLA B*4403	1:45-53 9	QSWSKPNPK	0.511632	0.277663	-4.645545	0.789295	-3.856250	44212.499191	
HLA B*1509	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.476234	0.619672	-3.856562	29938.781945	
HLA A*3201	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.603966	0.747233	-3.856733	40175.9568
HLA B*4501	1:16-24 9	DFLAPPDVP	0.799126	-0.008262	-4.647697	0.790864	-3.856833	44432.136145	
HLA B*1502	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.591801	0.734934	-3.856867	39066.148397	
HLA B*4801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.121363	0.263887	-3.857476	13224.0113
HLA B*0802	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.481701	0.624086	-3.857616	30318.0579
HLA B*3801	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.561081	0.703401	-3.857680	36398.298228	
HLA A*0211	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.518553	0.660487	-3.858067	33002.972006	
HLA B*0802	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.417969	0.559811	-3.858158	26179.9762
HLA B*4801	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.413740	0.555227	-3.858513	25926.2781
HLA B*4402	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.274843	0.416215	-3.858629	18829.6965
HLA A*0250	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.432451	0.573275	-3.859176	27067.7074
HLA A*2403	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.363628	0.504252	-3.859376	23100.852651	
HLA B*1801	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.520308	0.660487	-3.859822	33136.613046	
HLA B*7301	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.520900	0.660487	-3.860414	33181.818735	
HLA A*6801	1:42-50 9	ACYQSWSKP	0.531103	0.253963	-4.645507	0.785066	-3.860442	44208.672401	
HLA B*5701	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.371736	0.511259	-3.860477	23536.185741	
HLA B*5301	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.498853	0.638108	-3.860745	31539.3413
HLA B*2705	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.095326	0.234045	-3.861281	12454.4978
HLA B*4801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.421468	0.559811	-3.861657	26391.7161
HLA B*5401	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.430123	0.568388	-3.861735	26922.980367	
HLA B*5801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.225976	0.364143	-3.861834	16825.8255
HLA A*2402	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.594601	0.732654	-3.861947	39318.883905	
HLA A*3301	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.614701	0.752698	-3.862003	41181.3923
HLA A*2603	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.597813	0.735649	-3.862164	39610.7374
HLA B*1517	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.222137	0.359849	-3.862289	16677.7448
HLA B*1801	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.493851	0.631559	-3.862292	31178.1660
HLA B*7301	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.565881	0.703401	-3.862480	36802.818248	
HLA A*2902	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.431340	0.568388	-3.862952	26998.533055	
HLA A*0219	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.431549	0.568388	-3.863161	27011.535442	
HLA A*2603	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.422990	0.559811	-3.863179	26484.3975
HLA A*6802	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.423007	0.559811	-3.863196	26485.4004
HLA A*2301	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.488249	0.625007	-3.863242	30778.6376
HLA B*4501	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.500915	0.637604	-3.863311	31689.5058
HLA B*7301	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.567937	0.703256	-3.864681	36977.443000	
HLA A*2602	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.571010	0.706243	-3.864767	37240.028327	
HLA B*1501	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.369142	0.504252	-3.864890	23396.034401	
HLA B*3901	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.438224	0.573275	-3.864949	27429.8958
HLA A*0219	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.489347	0.624086	-3.865261	30856.4957
HLA A*3201	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.600942	0.735649	-3.865294	39897.2021
HLA B*0702	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.433720	0.568388	-3.8653		
HLA B*7301	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.571701	0.706243	-3.8654		

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HLA A*2402	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-3.875997	0.010485	-3.865512	7516.178694	
HLA B*0803	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.503686	0.638108	-3.865578	31892.2757	
HLA A*3301	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.571987	0.706243	-3.865744	37323.931906	
HLA B*3801	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.526638	0.660487	-3.866151	33623.090451	
HLA A*2601	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.381985	0.515530	-3.866454	24098.1962	
HLA A*2301	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.050390	0.183904	-3.866486	11230.264124	
HLA B*1517	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.434947	0.568388	-3.866558	27223.667212	
HLA A*1101	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.426371	0.559811	-3.866560	26691.3786	
HLA A*2501	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.439925	0.573275	-3.866650	27537.5428	
HLA B*5801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.360778	0.493735	-3.867043	22949.7566	
HLA A*2403	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.422360	0.555227	-3.867133	26446.0269	
HLA B*5301	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.599833	0.732654	-3.867179	39795.455927	
HLA A*3101	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.227325	0.359849	-3.867476	16878.1556	
HLA A*3002	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.505213	0.637604	-3.867608	32004.6200	
HLA A*2602	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.492824	0.625007	-3.867817	31104.5441	
HLA B*5101	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.475351	0.607347	-3.868004	29877.944816	
HLA B*5101	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.499637	0.631559	-3.868079	31596.3813	
HLA B*2705	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.428269	0.559811	-3.868459	26808.3071	
HLA A*2403	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.347478	0.478869	-3.868609	22257.5649	
HLA B*0702	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.379879	0.511259	-3.868620	23981.668629	
HLA B*1509	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.524401	0.655774	-3.868627	33450.3694	
HLA A*2603	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.601340	0.732654	-3.868686	39933.695730	
HLA B*3501	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.228580	0.359849	-3.868731	16926.9851	
HLA B*4801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.384400	0.515530	-3.868870	24232.5884	
HLA A*0202	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.529525	0.660487	-3.869039	33847.386919	
HLA A*0203	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.315814	0.446772	-3.869041	20692.5322	
HLA A*0219	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.424912	0.555227	-3.869685	26601.8583	
HLA A*3001	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.288057	0.418270	-3.869787	19411.3984	
HLA B*4002	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.602596	0.732654	-3.869942	40049.442876	
HLA B*5701	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.374318	0.504252	-3.870066	23676.536195	
HLA B*5401	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.443365	0.573275	-3.870090	27756.5082	
HLA A*8001	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.425323	0.555227	-3.870096	26627.0550	
HLA A*6802	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.027919	0.157520	-3.870399	10663.9842	
HLA A*0201	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.381797	0.511259	-3.870537	24087.768990	
HLA A*2603	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.509059	0.638108	-3.870951	32289.3113	
HLA B*5401	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.563083	0.692096	-3.870987	36566.453429	
HLA A*2603	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.618601	0.747233	-3.871368	41552.8839	
HLA A*3101	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.365501	0.493735	-3.871766	23200.6712	
HLA A*0101	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.384043	0.511996	-3.872047	24212.6701	
HLA B*1502	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.491821	0.619672	-3.872148	31032.774860	
HLA A*3001	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.245425	0.373143	-3.872282	17596.4645	
HLA B*5701	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.388227	0.515530	-3.872697	24447.0869	
HLA A*6901	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.385246	0.511996	-3.873250	24279.8288	
HLA A*0301	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.367007	0.493735	-3.873272	23281.2647	
HLA B*3501	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.291565	0.418270	-3.873295	19568.8185	
HLA A*3201	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.542109	0.668648	-3.873461	34842.474242	
HLA A*2402	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.565576	0.692096	-3.873480	36776.944456	
HLA A*6901	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.367437	0.493735	-3.873702	23304.3248	
HLA B*1502	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.577170	0.703256	-3.873914	37772.032295	
HLA B*4403	1:16-24	9	DFLAPPDVP	0.799126	-0.008262	-4.664830	0.790864	-3.873966	46219.967713	
HLA A*0216	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.385302	0.511259	-3.874043	24282.981507	
HLA A*2402	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.577497	0.703401	-3.874095	37800.446586	
HLA A*8001	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.443043	0.568388	-3.874655	27735.944048	
HLA B*1502	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.543422	0.668648	-3.874775	34948.001829	
HLA B*1503	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.175213	0.300329	-3.874885	14969.7107	
HLA A*0212	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.430252	0.555227	-3.875025	26930.9923	
HLA A*0101	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.390617	0.515530	-3.875086	24581.9620	
HLA B*3801	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.543876	0.668648	-3.875228	34984.510394	
HLA A*0206	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.322030	0.446772	-3.875258	20990.8670	
HLA B*4402	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.435461	0.559811	-3.875650	27255.9399	
HLA B*4002	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.637822	0.762047	-3.875775	43433.2479	
HLA A*3301	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.611153	0.734934	-3.876220	40846.354613	
HLA B*5301	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.582534	0.706243	-3.876291	38241.439042	
HLA A*3301	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.496061	0.619672	-3.876389	31337.289599	
HLA A*1101	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.500558	0.624086	-3.876473	31663.4581	
HLA B*0803	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.500939	0.624086	-3.876853	31691.2202	
HLA B*4001	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.392543	0.515530	-3.877013	24691.2525	
HLA A*0201	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.389301	0.511996	-3.877305	24507.6027	
HLA B*4501	1:48-56	9	SKPNPKTAT	1.026076	-0.293422	-4.610084	0.732654	-3.877430	40745.934971	
HLA B*4403	1:235-243	9	LADGTEVAT	1.137874	-0.354379	-4.660976	0.783495	-3.877481	45811.7078	
HLA A*0250	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.582870	0.705319	-3.877552	38271.034606	
HLA B*1509	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.451022	0.573275	-3.877747	28250.2180	
HLA A*2301	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.538253	0.660487	-3.877767	34534.524667	
HLA A*3301	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.581775	0.703401	-3.878374	38174.674522	
HLA A*2301	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.534205	0.655774	-3.878431	34214.1157	
HLA B*3501	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.251576	0.373143	-3.878433	17847.4581	
HLA A*3101	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.251621	0.373143	-3.878478	17849.2927	
HLA A*3101	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.338256	0.459518	-3.878738	21789.934333	
HLA A*0202	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.585184	0.706243	-3.878942	38475.515359	
HLA B*4403	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.295197	0.416215	-3.878982	19733.1723	
HLA B*5101	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.383556	0.504252	-3.879305	24185.570811	
HLA B*1503	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.503404	0.624086	-3.879318	31871.5783	
HLA B*1503	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.434641	0.555227	-3.879414	27204.5279	
HLA A*2501	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.391554	0.511996	-3.879558	24635.0806	
HLA B*1517	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.503824	0.624086	-3.879738	31902.4568	
HLA A*3201	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.571973	0.692096	-3.879877	37322.720415	
HLA A*2403	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.439730	0.559811	-3.879919	27525.1806	
HLA A*2601	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.391986	0.511996	-3.879990	24659.6151	
HLA A*2403	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.373738	0.493735	-3.880003	23644.9197	
HLA A*2602	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.628431	0.748410	-3.880022	42504.1578	
HLA A*0212	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.384303	0.504252	-3.880052	24227.214141	
HLA A*3201	1:18-26	9	LAPPDVPWT	1.068922	-0.333988	-4.615408	0.734934	-3.880475	41248.505763	
HLA A*3101	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.359359	0.478869	-3.880490	22874.8890	
HLA B*3801	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.500446	0.619672	-3.880773	31655.237052	
HLA B*4601	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.393037	0.511996	-3.881041	24719.3196	
HLA B*4601	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.392315	0.511259	-3.881056	24678.299003	
HLA B*1517	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.245315	0.364143	-3.881172	17591.9909	
HLA A*0216	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.106914	0.225691	-3.881223	12791.276318	
HLA B*5301	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.331264	0.449835	-3.881428	21441.9290	
HLA A*0301	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.341061	0.459518	-3.881543	21931.139962	
HLA B*0702	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.436824	0.555227	-3.881597	27341.5962	
HLA B*5801	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.360545	0.478869	-3.881677	22937.4685	
HLA A*0201	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.397573	0.515530	-3.882043	24978.9034	
HLA A*1101	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.437703	0.555227	-3.882475	27396.9724	
HLA B*5301	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.574581	0.692096	-3.882485	37547.516764	
HLA A*0101	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.386848	0.504252	-3.882596	24369.575842	
HLA B*1503	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.091628	0.208763	-3.882866	12348.8959	
HLA B*4601	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.398405	0.515530	-3.882875	25026.7863	
HLA A*0301	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.334111	0.451144	-3.882968	21582.9810	
HLA A*3201	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.589604	0.706243	-3.883361	38869.041123	
HLA B*5401	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.521424	0.637604	-3.883820	33221.8736	
HLA A*0203	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.395825	0.511996	-3.883829	24878.5664	
HLA B*0802	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.491177	0.607347	-3.883830	30986.808756	
HLA B*5301	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.540152	0.655774	-3.884378	34685.8120	
HLA B*5101	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.508626	0.624086	-3.884541	32257.1856	
HLA B*1517	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.491893	0.607347	-3.8845		
HLA A*8001	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.395849	0.511259	-3.8845		

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HLA B*5301	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.588114	0.703401	-3.884713	38735.953743		
HLA B*0702	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.363637	0.478869	-3.884769	23101.3525	
HLA B*1509	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.509808	0.625007	-3.884801	32345.0828	
HLA A*2601	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.396540	0.511259	-3.885281	24919.515593		
HLA B*1517	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.458660	0.573275	-3.885385	28751.4650	
HLA B*1502	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.592141	0.706243	-3.885898	39096.805232		
HLA A*0301	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.364904	0.478869	-3.886035	23168.8127	
HLA A*2902	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.441311	0.555227	-3.886084	27625.5785	
HLA B*1501	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.398208	0.511996	-3.886212	25015.4160	
HLA A*2403	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.402035	0.515530	-3.886505	25236.8438	
HLA A*3301	1:133-141	9	TEAADAARA	1.018713	-0.271480	-4.633821	0.747233	-3.886588	43034.9333	
HLA B*3801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.511730	0.625007	-3.886723	32488.5363	
HLA A*0216	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.441962	0.555227	-3.886735	27667.0076	
HLA A*0250	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.525258	0.638108	-3.887151	33516.4861	
HLA B*4403	1:130-138	9	HILTEAADA	0.912003	-0.149956	-4.649466	0.762047	-3.887419	44613.5061	
HLA B*3801	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.511509	0.624086	-3.887424	32472.0191	
HLA A*0201	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.391930	0.504252	-3.887678	24656.413588		
HLA B*0802	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.460991	0.573275	-3.887715	28906.1777	
HLA A*2603	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.640555	0.752698	-3.887857	43707.3784	
HLA A*0250	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.151775	0.263887	-3.887888	14183.2235	
HLA A*0250	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.580290	0.692096	-3.888194	38044.376279		
HLA A*2402	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.072362	0.183904	-3.888458	11813.058489		
HLA A*0250	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.594707	0.706243	-3.888464	39328.457056		
HLA A*6901	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.248332	0.359849	-3.888483	17714.6155	
HLA A*6801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.143674	0.255019	-3.888655	13921.1118	
HLA A*0206	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.520466	0.631559	-3.888907	33148.6260	
HLA B*7301	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.520590	0.631559	-3.889031	33158.1318	
HLA B*3901	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.496386	0.607347	-3.889039	31360.693649		
HLA A*2501	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.496771	0.607347	-3.889424	31388.529887		
HLA A*0212	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.400933	0.511259	-3.889674	25172.893176		
HLA B*1503	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.497302	0.607347	-3.889955	31426.930071		
HLA A*2602	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.593361	0.703256	-3.890104	39206.732852		
HLA A*0216	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.402256	0.511996	-3.890260	25249.6808	
HLA A*3201	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.341484	0.451144	-3.890340	21952.5064	
HLA A*2902	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.402413	0.511996	-3.890417	25258.8345	
HLA A*2602	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.595757	0.705319	-3.890439	39423.677020		
HLA A*0211	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.522058	0.631559	-3.890500	33270.4352	
HLA B*5801	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.189583	0.298936	-3.890647	15473.296942		
HLA B*1801	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.445898	0.555227	-3.890670	27918.8533	
HLA B*5801	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.350929	0.459518	-3.891411	22435.153409		
HLA A*2602	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.583747	0.692096	-3.891651	38348.339262		
HLA A*6801	1:102-110	9	SQLSQRYVP	0.667890	0.084808	-4.644354	0.752698	-3.891656	44091.3986	
HLA B*5301	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.597024	0.705319	-3.891705	39538.801478		
HLA B*1502	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.597176	0.705319	-3.891858	39552.707458		
HLA A*6901	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.343009	0.451144	-3.891865	22029.7175	
HLA A*3301	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.640332	0.748410	-3.891922	43684.9213	
HLA A*0250	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.499480	0.607347	-3.892133	31584.930949		
HLA B*4001	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.371132	0.478869	-3.892264	23503.4851	
HLA A*3301	1:239-247	9	TEVATSPLA	1.014741	-0.279092	-4.627950	0.735649	-3.892301	42457.0457	
HLA B*3801	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.530653	0.638108	-3.892545	33935.3942	
HLA A*6802	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.311115	0.418270	-3.892845	20469.8504	
HLA A*0101	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.386836	0.493735	-3.893101	24368.9166	
HLA B*3901	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.517338	0.624086	-3.893253	32910.7945	
HLA A*2603	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.628201	0.734934	-3.893268	42481.629464		
HLA B*0802	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.461731	0.568388	-3.893342	28955.479169		
HLA B*0801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.409152	0.515530	-3.893622	25653.7956	
HLA B*1503	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.345074	0.451144	-3.893930	22134.7248	
HLA A*0203	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.409528	0.515530	-3.893997	25676.0107	
HLA A*3201	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.398407	0.504252	-3.894156	25026.921792		
HLA A*0203	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.398464	0.504252	-3.894212	25030.171432		
HLA B*5301	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.398856	0.504252	-3.894604	25052.795196		
HLA A*2603	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.601271	0.706243	-3.895028	39927.431152		
HLA A*3201	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.275783	0.380508	-3.895275	18870.4872	
HLA B*4402	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.374375	0.478869	-3.895506	23679.6104	
HLA A*2603	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.564288	0.668648	-3.895641	36668.076275		
HLA B*3501	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.450954	0.555227	-3.895726	28245.7862	
HLA B*1501	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.374661	0.478869	-3.895793	23695.2443	
HLA B*5401	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.092385	0.196360	-3.896024	12370.4262	
HLA A*3301	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.602155	0.705319	-3.896836	40008.730930		
HLA B*5401	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.552708	0.655774	-3.896933	35703.2305	
HLA A*2602	1:75-83 9	HASVSFYIT	1.066949	-0.398301	-4.565590	0.668648	-3.896942	36778.138231		
HLA A*2601	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.390917	0.493735	-3.897182	24598.9901	
HLA A*6802	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.412904	0.515530	-3.897374	25876.3942	
HLA B*0803	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.504844	0.607347	-3.897497	31977.448342		
HLA A*2501	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.465920	0.568388	-3.897532	29236.130247		
HLA B*4001	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.409915	0.511996	-3.897919	25698.9402	
HLA A*2501	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.458047	0.559811	-3.898236	28710.8971	
HLA B*7301	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-3.785664	-0.112631	-3.898295	6104.69677	
HLA A*0201	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.392508	0.493735	-3.898773	24689.2485	
HLA A*2402	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.559474	0.660487	-3.898987	36263.860157		
HLA A*3101	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.197938	0.298936	-3.899002	15773.847168		
HLA B*7301	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.393250	0.493735	-3.899516	24731.4919	
HLA B*4601	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.403875	0.504252	-3.899623	25343.972465		
HLA A*2601	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.404034	0.504252	-3.899783	25353.297529		
HLA A*0101	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.378806	0.478869	-3.899937	23922.4515	
HLA A*2301	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.537767	0.637604	-3.900163	34495.8729	
HLA A*8001	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.412897	0.511996	-3.900901	25875.9742	
HLA A*0212	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.395003	0.493735	-3.901268	24831.5044	
HLA A*0206	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.200217	0.298936	-3.901281	15856.839454		
HLA A*6901	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.380664	0.478869	-3.901795	24025.0403	
HLA A*0219	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.406276	0.504252	-3.902024	25484.485006		
HLA B*1801	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.470889	0.568388	-3.902501	29572.568660		
HLA A*3201	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.606090	0.703401	-3.902689	40372.920189		
HLA B*5801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.349663	0.446772	-3.902890	22369.8293	
HLA A*1101	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.418611	0.515530	-3.903081	26218.6700	
HLA B*1502	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.541345	0.638108	-3.903238	34781.2675	
HLA A*3301	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.635940	0.732654	-3.903286	43245.444978		
HLA B*4601	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.397047	0.493735	-3.903312	24948.6519	
HLA B*1517	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.070596	0.167005	-3.903590	11765.0977	
HLA A*2402	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.541275	0.637604	-3.903671	34775.6231	
HLA A*2603	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.595853	0.692096	-3.903757	39432.422377		
HLA B*2705	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.235541	0.331331	-3.904210	17200.502557		
HLA B*3501	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.383086	0.478869	-3.904218	24159.4167	
HLA B*5701	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.398121	0.493735	-3.904386	25010.4093	
HLA B*2705	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.383467	0.478869	-3.904598	24180.5993	
HLA B*4002	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.639972	0.734934	-3.905039	43648.777681		
HLA B*4001	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.416339	0.511259	-3.905080	26081.868803		
HLA A*0206	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.221973	0.316807	-3.905166	16671.430268		
HLA A*3001	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.234886	0.329388	-3.905498	17174.5604	
HLA A*0211	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.461214	0.555227	-3.905987	28921.0375	
HLA A*0250	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.474723	0.568388	-3.906335	29834.819060		
HLA A*1101	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.474900	0.568388	-3.906511	29846.926745		
HLA B*4001	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.410918	0.504252	-3.906667	25758.373966		
HLA B*4501	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.610148	0.703256	-3.906891	40751.887043		
HLA A*3002	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.358525	0.451144	-3.907381	22830.999	
HLA A*3001	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.162521	0.255019			
HLA A*0101	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.367063	0.459518	-3.9075			

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HLA B*7301	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.599702	0.692096	-3.907606	39783.401568		
HLA A*3002	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.087310	0.179565	-3.907745	12226.7146	
HLA B*3501	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.419050	0.511259	-3.907791	26245.207558		
HLA B*0803	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.481459	0.573275	-3.908184	30301.1688	
HLA A*0206	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.532363	0.624086	-3.908278	34069.3088	
HLA B*5701	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.420420	0.511996	-3.908424	26328.1147	
HLA B*1801	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.515926	0.607347	-3.908580	32803.964013		
HLA B*6802	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.238053	0.329388	-3.908665	17300.2642	
HLA A*2301	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.546984	0.638108	-3.908877	35235.8026	
HLA B*4002	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.601088	0.692096	-3.908992	39910.586474		
HLA B*3501	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.469282	0.559811	-3.909471	29463.3416	
HLA A*0202	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.565258	0.655774	-3.909484	36750.0947	
HLA A*3301	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.612868	0.703256	-3.909612	41007.984762		
HLA B*4501	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.644727	0.734934	-3.909794	44129.341211		
HLA A*3301	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.547466	0.637604	-3.909861	35274.9018	
HLA B*4402	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.414194	0.504252	-3.909942	25953.362110		
HLA A*0250	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.570528	0.660487	-3.910042	37198.751013		
HLA A*2501	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.466030	0.555227	-3.910803	29243.5649	
HLA B*4402	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.422076	0.511259	-3.910817	26428.721129		
HLA A*0212	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.390126	0.478869	-3.911257	24554.1837	
HLA A*2301	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.471070	0.559811	-3.911259	29584.8900	
HLA A*2603	1:150-158	9	LEAKFADQP	0.710397	0.038013	-4.659973	0.748410	-3.911564	45706.0038	
HLA A*2301	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.535751	0.624086	-3.911666	34336.1249	
HLA B*5801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.361549	0.449835	-3.911713	22990.5158	
HLA A*0201	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.392435	0.478869	-3.913566	24685.1087	
HLA B*7301	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.537852	0.624086	-3.913766	34502.5918	
HLA A*2603	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.617398	0.703256	-3.914142	41437.947376		
HLA B*2705	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.408127	0.493735	-3.914392	25593.3570	
HLA A*2301	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.546002	0.631559	-3.914443	35156.2127	
HLA A*3001	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.246243	0.331331	-3.914912	17629.623611		
HLA B*3801	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.552604	0.637604	-3.915000	35694.7329	
HLA B*4501	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.621315	0.706243	-3.915072	41813.336744		
HLA A*3002	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.553356	0.638108	-3.915248	35756.5799	
HLA A*6801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.279639	0.364143	-3.915496	19038.7582	
HLA B*1502	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.179438	0.263887	-3.915551	15116.0313	
HLA A*0216	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.362766	0.446772	-3.915993	23055.0330	
HLA B*0802	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.420272	0.504252	-3.916020	26319.143009		
HLA B*7301	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.471568	0.555227	-3.916341	29618.8402	
HLA B*2705	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.432146	0.515530	-3.916616	27048.6778	
HLA A*0301	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.363449	0.446772	-3.916677	23091.3566	
HLA A*0101	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.363623	0.446772	-3.916851	23100.6027	
HLA A*2902	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.421111	0.504252	-3.916859	26370.023088		
HLA B*5401	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.541047	0.624086	-3.916961	34757.3790	
HLA A*3101	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.429115	0.511996	-3.917119	26860.5688	
HLA A*2902	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.428878	0.511259	-3.917619	26845.896250		
HLA A*0301	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.277491	0.359849	-3.917643	18944.8508	
HLA A*0301	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.367488	0.449835	-3.917653	23307.0986	
HLA A*3002	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.541771	0.624086	-3.917685	34815.3416	
HLA B*3501	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.433401	0.515530	-3.917871	27126.9312	
HLA A*6801	1:8-16 9	RVQLIAKTD	1.320995	-0.615676	-4.623227	0.705319	-3.917909	41997.874055		
HLA B*5101	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.473791	0.555227	-3.918563	29770.8108	
HLA B*5701	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.398071	0.478869	-3.919203	25007.5680	
HLA B*1501	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.379043	0.459518	-3.919525	23935.526288		
HLA B*7301	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.539447	0.619672	-3.919775	34629.563801		
HLA A*3301	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.852662	-0.067515	-3.920177	7122.98470	
HLA A*2403	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.431554	0.511259	-3.920295	27011.827703		
HLA B*5301	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.580824	0.660487	-3.920337	38091.125177		
HLA B*0802	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.475720	0.555227	-3.920492	29903.3325	
HLA B*5401	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.552703	0.631559	-3.921144	35702.8442	
HLA A*6802	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.425448	0.504252	-3.921196	26634.690793		
HLA A*2603	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.120188	0.198739	-3.921449	13188.2894	
HLA B*3901	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.481450	0.559811	-3.921639	30300.5131	
HLA A*0203	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.415526	0.493735	-3.921791	26033.0938	
HLA A*3201	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.541465	0.619672	-3.921793	34790.865167		
HLA B*0802	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.433091	0.511259	-3.921831	27107.566638		
HLA B*4002	1:90-98 9	THELIRHRH	1.009752	-0.303509	-4.628295	0.706243	-3.922052	42490.823295		
HLA A*0201	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.369128	0.446772	-3.922356	23395.2749	
HLA A*6901	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.381898	0.459518	-3.922380	24093.373065		
HLA B*4002	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.625690	0.703256	-3.922433	42236.659949		
HLA B*4403	1:18-26 9	LAPPDVPWT	1.068922	-0.333988	-4.657377	0.734934	-3.922444	45433.591755		
HLA A*0250	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.578242	0.655774	-3.922468	37865.3275	
HLA A*2601	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.401537	0.478869	-3.922668	25207.9164	
HLA A*0216	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.438461	0.515530	-3.922931	27444.8876	
HLA B*4403	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.655601	0.732654	-3.922947	45248.153458		
HLA B*0803	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.491536	0.568388	-3.923148	31012.467559		
HLA B*4801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.417074	0.493735	-3.923339	26126.0705	
HLA A*3002	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.427713	0.504252	-3.923461	26773.957082		
HLA A*1101	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.149261	0.225691	-3.923570	14101.359946		
HLA B*4402	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.439185	0.515530	-3.923655	27490.6556	
HLA B*4801	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.427931	0.504252	-3.923679	26787.430977		
HLA A*0212	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.435748	0.511996	-3.923752	27273.9350	
HLA B*5401	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.479441	0.555227	-3.924214	30160.6831	
HLA A*0203	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.403337	0.478869	-3.924468	25312.5941	
HLA B*3501	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.418268	0.493735	-3.924533	26197.9695	
HLA A*6801	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.580389	0.655774	-3.924615	38053.0215	
HLA A*6802	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.376007	0.451144	-3.924864	23768.8104	
HLA B*1517	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.403776	0.478869	-3.924907	25338.2145	
HLA A*2301	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.532382	0.607347	-3.925035	34070.783415		
HLA B*3901	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.418832	0.493735	-3.925097	26232.0063	
HLA B*3501	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.092526	0.167005	-3.925521	12374.4422	
HLA B*3501	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.122124	0.196360	-3.925764	13247.2107	
HLA A*0219	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.372730	0.446772	-3.925958	23590.1072	
HLA B*5401	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.533425	0.607347	-3.926079	34152.719488		
HLA A*6801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.499466	0.573275	-3.926191	31583.9057	
HLA A*6801	1:48-56 9	SKPNPKTAT	1.026076	-0.293422	-4.659144	0.732654	-3.926490	45618.802843		
HLA A*0219	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.437797	0.511259	-3.926537	27402.901682		
HLA A*0206	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.377706	0.451144	-3.926562	23861.9605	
HLA A*3301	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.125348	0.198739	-3.926608	13345.9022	
HLA A*2602	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.287131	0.359849	-3.927283	19370.0672	
HLA B*0801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.291619	0.364143	-3.927476	19571.2535	
HLA B*0802	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.421423	0.493735	-3.927688	26389.0035	
HLA A*8001	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.431977	0.504252	-3.927725	27038.144093		
HLA B*4001	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.374830	0.446772	-3.928058	23704.4757	
HLA B*1517	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.440148	0.511996	-3.928152	27551.6991	
HLA A*0211	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.552254	0.624086	-3.928168	35665.9719	
HLA B*1503	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.444807	0.515530	-3.929277	27848.8596	
HLA A*0211	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.289264	0.359849	-3.929416	19465.4505	
HLA B*4403	1:19-27 9	APPDVPWTT	1.064970	-0.361714	-4.632931	0.703256	-3.929674	42946.787159		
HLA A*2501	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.376545	0.446772	-3.929773	23798.2749	
HLA A*3301	1:67-75 9	VGHFSVLEH	1.059901	-0.367805	-4.622151	0.692096	-3.930055	41893.943504		
HLA A*0206	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.442143	0.511996	-3.930147	27678.5350	
HLA B*0801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.442192	0.511996	-3.930197	27681.6796	
HLA B*4002	1:25-33 9	WTTDADGGP	0.759468	-0.056067	-4.633706	0.703401	-3.930305	43023.526967		
HLA B*7301	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.568724	0.638108	-3.930616	37044.5184	
HLA B*1517	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.486010	0.555227	-3.930783	30620.3626	
HLA A*8001	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.409701	0.478869			
HLA A*2902	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.260309	0.329388			

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HLA A*2603	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.587055	0.655774	-3.931280	38641.558
HLA A*3002	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.195715	0.263887	-3.931828	15693.326
HLA A*0201	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.391413	0.459518	-3.931895	24627.085582
HLA A*0206	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.443297	0.511259	-3.932038	27752.154008
HLA A*0202	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.116082	0.183904	-3.932177	13064.162422
HLA B*4501	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.624315	0.692096	-3.932219	42103.201290
HLA A*6901	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.382158	0.449835	-3.932323	24107.8454
HLA B*4801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.444455	0.511996	-3.932459	27826.2698
HLA A*3201	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.588246	0.655774	-3.932472	38747.6907
HLA A*6802	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.411778	0.478869	-3.932910	25809.4265
HLA B*3901	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.488268	0.555227	-3.933041	30779.9697
HLA B*4601	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.412208	0.478869	-3.933340	25834.9908
HLA B*4801	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.393403	0.459518	-3.933885	24740.190160
HLA B*4501	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.639234	0.705319	-3.933916	43574.694217
HLA B*4801	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.445197	0.511259	-3.933938	27873.880273
HLA A*0211	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.445202	0.511259	-3.933943	27874.181864
HLA A*3301	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.572356	0.638108	-3.934249	37355.6465
HLA B*1502	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.594784	0.660487	-3.934298	39335.478849
HLA A*2501	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.438659	0.504252	-3.934407	27457.362253
HLA A*3002	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.542043	0.607347	-3.934697	34837.196812
HLA A*0101	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.384790	0.449835	-3.934954	24254.3601
HLA B*4403	1:90-98	9	THELIRHRH	1.009752	-0.303509	-4.641412	0.706243	-3.935169	43793.768747
HLA A*2501	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.450808	0.515530	-3.935278	28236.3138
HLA B*4002	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.640665	0.705319	-3.935347	43718.493136
HLA B*0702	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.447700	0.511996	-3.935704	28034.9400
HLA A*0212	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.451687	0.515530	-3.936157	28293.5021
HLA B*3901	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.440423	0.504252	-3.936171	27569.143679
HLA A*2603	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.561236	0.625007	-3.936229	36411.2966
HLA B*1509	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.430163	0.493735	-3.936428	26925.4565
HLA B*4402	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.448562	0.511996	-3.936566	28090.6567
HLA B*7301	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.574609	0.637604	-3.937005	37549.9543
HLA B*4001	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.388375	0.451144	-3.937231	24455.4205
HLA B*5801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.353542	0.416215	-3.937327	22570.5255
HLA B*1503	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.441983	0.504252	-3.937732	27668.354715
HLA B*0803	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.493303	0.555227	-3.938076	31138.8906
HLA A*2402	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.594023	0.655774	-3.938249	39266.5918
HLA A*3201	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.576487	0.638108	-3.938379	37712.6154
HLA A*0219	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.454346	0.515530	-3.938816	28467.3030
HLA A*3301	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.450108	0.511259	-3.938849	28190.829435
HLA B*4403	1:67-75	9	VGHFSVLEH	1.059901	-0.367805	-4.631267	0.692096	-3.939171	42782.606932
HLA B*1509	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.443734	0.504252	-3.939482	27780.093373
HLA A*3002	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.229717	0.290041	-3.939676	16971.3645
HLA B*4402	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.390992	0.451144	-3.939849	24603.2489
HLA A*2601	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.399507	0.459518	-3.939989	25090.365937
HLA B*7301	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.595856	0.655774	-3.940082	39432.6357
HLA A*0203	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.390236	0.449835	-3.940400	24560.4278
HLA B*3501	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.452749	0.511996	-3.940753	28362.7720
HLA A*2601	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.392045	0.451144	-3.940901	24662.9504
HLA B*0702	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.068096	0.127125	-3.940970	11697.570990
HLA A*2501	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.452293	0.511259	-3.941034	28333.020444
HLA A*0301	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.358053	0.416215	-3.941838	22806.1870
HLA B*5801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.301963	0.359849	-3.942115	20043.0323
HLA B*4001	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.401800	0.459518	-3.942282	25223.194732
HLA A*0203	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.126274	0.183904	-3.942369	13374.379343
HLA B*5801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.361020	0.418270	-3.942750	22962.5482
HLA A*0101	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.394115	0.451144	-3.942971	24780.7774
HLA A*3002	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.603654	0.660487	-3.943167	40147.060021
HLA B*0801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.361610	0.418270	-3.943340	22993.7498
HLA B*5801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.316547	0.373143	-3.943403	20727.4883
HLA A*0301	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.361810	0.418270	-3.943540	23004.3257
HLA B*0801	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.422859	0.478869	-3.943990	26476.3751
HLA B*3801	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.512646	0.568388	-3.944258	32557.154893
HLA B*4403	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.649715	0.705319	-3.944397	44639.097003
HLA A*0201	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.394521	0.449835	-3.944686	24803.9809
HLA B*1801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.504830	0.559811	-3.945019	31976.4103
HLA A*0206	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.438842	0.493735	-3.945107	27468.9509
HLA A*0219	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.457466	0.511996	-3.945471	28672.5580
HLA A*0201	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.396619	0.451144	-3.945476	24924.0996
HLA A*2602	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.144477	0.198739	-3.945738	13946.8922
HLA A*2403	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.395698	0.449835	-3.945863	24871.2996
HLA B*4601	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.397080	0.451144	-3.945936	24950.5416
HLA B*2705	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.450230	0.504252	-3.945978	28198.761032
HLA B*1501	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.392924	0.446772	-3.946151	24712.9015
HLA A*2602	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.577737	0.631559	-3.946178	37821.3109
HLA A*6801	1:19-27	9	APPDVPWTT	1.064970	-0.361714	-4.650120	0.703256	-3.946863	44680.653056
HLA A*3201	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.462715	0.515530	-3.947185	29021.1882
HLA B*0801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.397444	0.449835	-3.947609	24971.4722
HLA A*2402	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.585727	0.638108	-3.947620	38523.6276
HLA A*0211	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.115461	0.167651	-3.947811	13045.517362
HLA A*2402	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.579377	0.631559	-3.947818	37964.3980
HLA A*1101	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.452168	0.504252	-3.947917	28324.897848
HLA A*2301	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.516720	0.568388	-3.948332	32864.002331
HLA B*5701	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.407857	0.459518	-3.948339	25577.439445
HLA B*3801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.508159	0.559811	-3.948348	32222.4775
HLA B*4001	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.398194	0.449835	-3.948358	25014.6040
HLA A*1101	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.407923	0.459518	-3.948405	25581.314130
HLA A*2403	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.238664	0.290041	-3.948623	17324.6153
HLA A*2603	1:8-16	9	RVQLIAKTD	1.320995	-0.615676	-4.654031	0.705319	-3.948713	45084.930517
HLA B*4601	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.408522	0.459518	-3.949004	25616.628461
HLA B*6802	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.248010	0.298936	-3.949074	17701.491180
HLA B*4501	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.580821	0.631559	-3.949263	38090.9191
HLA A*2602	1:11-19	9	LIAKTDFLA	0.807408	-0.187736	-4.568980	0.619672	-3.949308	37066.369234
HLA B*5101	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.509515	0.559811	-3.949704	32323.2173
HLA A*0202	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.581825	0.631559	-3.950266	38179.0117
HLA B*4403	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.653764	0.703401	-3.950362	45057.133980
HLA A*3001	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.010472	0.060047	-3.950425	10244.062520
HLA A*3002	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.518905	0.568388	-3.950517	33029.764238
HLA A*2301	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.524138	0.573275	-3.950863	33430.1077
HLA A*0201	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.310833	0.359849	-3.950984	20456.5660
HLA A*0202	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.575079	0.624086	-3.950994	37590.6045
HLA A*3101	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.215141	0.263887	-3.951254	16411.2083
HLA B*0801	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.402615	0.451144	-3.951472	25270.5885
HLA B*0802	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.467081	0.515530	-3.951550	29314.3678
HLA B*4501	1:25-33	9	WTTDADGGP	0.759468	-0.056067	-4.655446	0.703401	-3.952044	45232.000367
HLA A*8001	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.446029	0.493735	-3.952294	27927.3127
HLA B*5301	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.584115	0.631559	-3.952557	38380.9243
HLA B*4601	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.402547	0.449835	-3.952712	25266.6246
HLA A*3101	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.371287	0.418270	-3.953018	23511.8786
HLA A*3201	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.613818	0.660487	-3.953331	41097.709633
HLA A*0219	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.447178	0.493735	-3.953443	28001.2904
HLA A*2301	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-3.964014	0.010485	-3.953528	9204.781925
HLA B*1509	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.508786	0.555227	-3.953559	32269.0545
HLA A*6901	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.252998	0.298936	-3.954062	17905.968233
HLA A*2402	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.561445	0.607347	-3.954099	36428.832195
HLA A*3201	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.585866	0.631559	-3.954307	38535.9255
HLA B*4402	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.413900	0.459518	-3.9543	
HLA A*3001	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-3.990351	0.035827	-3.9545	

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HLA A*2601	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.404368	0.449835	-3.954533	25372.7815
HLA A*0203	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.406001	0.451144	-3.954857	25468.3595
HLA B*1501	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.335993	0.380508	-3.955486	21676.7095
HLA B*1801	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.460110	0.504252	-3.955858	28847.594957
HLA A*3002	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.467912	0.511996	-3.955916	29370.5616
HLA A*2402	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.580088	0.624086	-3.956003	38026.6802
HLA A*0212	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.402911	0.446772	-3.956139	25287.8204
HLA B*0702	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.415944	0.459518	-3.956426	26058.174769
HLA A*0219	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.406659	0.449835	-3.956823	25506.9674
HLA B*4601	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.403670	0.446772	-3.956898	25332.0468
HLA A*0211	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.220948	0.263887	-3.957062	16632.1535
HLA B*5301	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.582140	0.625007	-3.957132	38206.6986
HLA B*1517	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.451083	0.493735	-3.957348	28254.1918
HLA A*0216	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.451184	0.493735	-3.957449	28260.7652
HLA A*2602	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.469564	0.511996	-3.957568	29482.4750
HLA B*3501	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.257236	0.299515	-3.957721	18081.575979
HLA A*2602	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.613517	0.655774	-3.957743	41069.2607
HLA A*2902	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.317707	0.359849	-3.957859	20782.9563
HLA A*0250	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.589547	0.631559	-3.957989	38863.9947
HLA B*4403	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.597150	0.638108	-3.959043	39550.3537
HLA B*4403	1:75-83	9	HASVSFYIT	1.066949	-0.398301	-4.627717	0.668648	-3.959070	42434.312728
HLA A*3001	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.157888	0.198739	-3.959149	14384.2859
HLA B*4001	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.378075	0.418270	-3.959805	23882.2364
HLA B*3501	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-3.832339	-0.127574	-3.959913	6797.339573
HLA B*0801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.250136	0.290041	-3.960095	17788.3692
HLA B*5301	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.528813	0.568388	-3.960425	33791.949853
HLA B*1501	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.376750	0.416215	-3.960535	23809.4785
HLA A*8001	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.407500	0.446772	-3.960728	25556.4156
HLA A*2601	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.379153	0.418270	-3.960884	23941.6130
HLA B*0702	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.407723	0.446772	-3.960951	25569.5535
HLA A*0206	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.334346	0.373143	-3.961203	21594.6603
HLA B*5101	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.472759	0.511259	-3.961500	29700.190767
HLA A*0212	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.411576	0.449835	-3.961741	25797.4215
HLA B*4601	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.278903	0.316807	-3.962097	19006.547324
HLA A*0219	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.441189	0.478869	-3.962321	27617.8081
HLA A*2501	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.441210	0.478869	-3.962342	27619.1528
HLA A*0206	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.412204	0.449835	-3.962368	25834.7112
HLA A*2902	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.456111	0.493735	-3.962376	28583.1960
HLA B*2705	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.413905	0.451144	-3.962761	25936.0980
HLA B*5101	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.474980	0.511996	-3.962984	29852.4171
HLA B*0702	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.323287	0.359849	-3.963439	21051.7087
HLA A*6802	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.423432	0.459518	-3.963914	26511.347434
HLA A*2603	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.624541	0.660487	-3.964054	42125.073239
HLA B*1501	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.092657	0.128565	-3.964093	12378.1917
HLA B*1509	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.423864	0.459518	-3.964346	26537.750488
HLA B*5801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.344987	0.380508	-3.964479	22130.2946
HLA B*0803	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.281514	0.316807	-3.964707	19121.128018
HLA B*7301	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.443602	0.478869	-3.964733	27771.6785
HLA A*2602	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.625553	0.660487	-3.965067	42223.409280
HLA B*3901	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.480686	0.515530	-3.965156	30247.2851
HLA A*0216	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.469482	0.504252	-3.965230	29476.893156
HLA B*5401	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-3.748312	-0.216975	-3.965287	5601.598599
HLA A*6901	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.294704	0.329388	-3.965316	19710.7667
HLA A*3301	1:122-130	9	MEDDADLRH	1.015184	-0.359410	-4.621096	0.655774	-3.965322	41792.3049
HLA A*6901	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-3.897876	-0.067515	-3.965391	7904.51997
HLA A*6802	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.415331	0.449835	-3.965495	26021.4070
HLA A*2403	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.416684	0.451144	-3.965540	26102.6187
HLA B*4002	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.572979	0.607347	-3.965632	37409.238782
HLA A*2403	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.412610	0.446772	-3.965838	25858.9015
HLA A*1101	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.264802	0.298936	-3.965866	18399.313629
HLA A*6901	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.382114	0.416215	-3.965899	24105.3675
HLA A*2602	1:7-15	9	LRVQLIAKT	0.813183	-0.244795	-4.534567	0.568388	-3.966179	34242.632175
HLA A*0201	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.283024	0.316807	-3.966218	19187.757805
HLA A*0201	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.384957	0.418270	-3.966687	24263.6780
HLA B*3801	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.574038	0.607347	-3.966692	37500.623525
HLA B*0702	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.460955	0.493735	-3.967221	28903.8321
HLA B*4501	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.383556	0.416215	-3.967342	24185.5708
HLA A*2902	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.383573	0.416215	-3.967358	24186.4867
HLA B*1517	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.426935	0.459518	-3.967417	26726.056572
HLA B*5301	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.267034	0.299515	-3.967519	18494.118375
HLA A*0301	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.331731	0.364143	-3.967589	21465.0251
HLA A*3002	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.599267	0.631559	-3.967709	39743.6050
HLA B*3901	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.201904	0.234045	-3.967858	15918.5519
HLA A*0212	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.419146	0.451144	-3.968003	26251.0295
HLA B*1501	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.258059	0.290041	-3.968018	18115.8451
HLA B*4601	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.341181	0.373143	-3.968038	21937.1916
HLA A*8001	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.418277	0.449835	-3.968442	26198.5364
HLA B*5701	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.418465	0.449835	-3.968630	26209.8774
HLA B*1503	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.384950	0.416215	-3.968735	24263.2842
HLA B*1502	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.528552	0.559811	-3.968742	33771.6639
HLA A*0101	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.385008	0.416215	-3.968794	24266.5660
HLA B*1801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.233067	0.264217	-3.968850	17102.7965
HLA B*1509	1:31-39	9	GGPALVEFA	1.099205	-0.491858	-4.576212	0.607347	-3.968865	37688.752495
HLA B*4601	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.333035	0.364143	-3.968893	21529.5704
HLA A*0216	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.329347	0.359849	-3.969498	21347.4828
HLA A*2902	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.448599	0.478869	-3.969731	28093.0883
HLA A*2402	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.529633	0.559811	-3.969822	33855.8110
HLA B*0803	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.474376	0.504252	-3.970124	29810.940967
HLA B*0801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.417044	0.446772	-3.970271	26124.2331
HLA A*1101	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.464137	0.493735	-3.970402	29116.3297
HLA A*2902	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.422172	0.451144	-3.971029	26434.5838
HLA A*0203	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.430614	0.459518	-3.971096	26953.438504
HLA A*3101	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.387346	0.416215	-3.971132	24397.5412
HLA B*3801	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.526659	0.555227	-3.971432	33624.7275
HLA B*3501	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.431613	0.459518	-3.972095	27015.481225
HLA A*2403	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.431902	0.459518	-3.972384	27033.463750
HLA B*4402	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.114489	0.141991	-3.972498	13016.3320
HLA B*2705	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.483891	0.511259	-3.972632	30471.308126
HLA A*1101	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.484688	0.511996	-3.972692	30527.2423
HLA B*5701	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.419647	0.446772	-3.972874	26281.2961
HLA A*0212	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.432428	0.459518	-3.972910	27066.243169
HLA B*5801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.302476	0.329388	-3.973088	20066.6841
HLA A*6901	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.346258	0.373143	-3.973115	22195.1593
HLA B*0801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.237096	0.263887	-3.973210	17262.2139
HLA A*8001	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.433008	0.459518	-3.973491	27102.434411
HLA A*0211	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.489105	0.515530	-3.973575	30839.3066
HLA A*0250	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.597710	0.624086	-3.973624	39601.3097
HLA B*1503	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.433222	0.459518	-3.973704	27115.780222
HLA B*1801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.392066	0.418270	-3.973797	24664.1513
HLA B*4002	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.207881	0.234045	-3.973836	16139.1496
HLA A*2301	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.529704	0.555227	-3.974476	33861.3061
HLA A*0101	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.244293	0.269704	-3.974589	17550.6403
HLA B*5301	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.598819	0.624086	-3.974733	39702.5596
HLA B*1501	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.424614	0.449835	-3.974778	26583.5876
HLA B*1509	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.534687	0.559811	-3.974876	34252.0811
HLA A*0301	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.348053	0.373143		
HLA B*4002	1:50-58	9	PNPKTATNA	1.129060	-0.468573	-4.635440	0.660487	-3.9749	

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HLA B*5101	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.490564	0.515530	-3.975034	30943.0868
HLA B*0803	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.486609	0.511259	-3.975350	30662.633561	
HLA A*0201	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.391970	0.416215	-3.975755	24658.6812
HLA B*3501	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.265868	0.290041	-3.975828	18444.5599
HLA A*0216	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.425972	0.449835	-3.976136	26666.8424
HLA A*8001	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.427677	0.451144	-3.976534	26771.7845
HLA B*1501	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.277045	0.300329	-3.976716	18925.3878
HLA B*4801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.427017	0.449835	-3.977182	26731.1175
HLA A*2902	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.423989	0.446772	-3.977216	26545.3605
HLA B*3801	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.550626	0.573275	-3.977351	35532.5086
HLA A*2601	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.393849	0.416215	-3.977635	24765.6331
HLA B*4402	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.424454	0.446772	-3.977681	26573.8101
HLA B*1501	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.350929	0.373143	-3.977786	22435.1534
HLA A*3101	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.427630	0.449835	-3.977795	26768.8880
HLA B*1517	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.241760	0.263887	-3.977873	17448.5853
HLA B*3801	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.482237	0.504252	-3.977985	30355.476976	
HLA B*3901	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-3.912123	-0.066090	-3.978212	8168.13257
HLA A*2501	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.472007	0.493735	-3.978273	29648.8193
HLA B*0802	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.490437	0.511996	-3.978441	30934.0486
HLA B*7301	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.279514	0.300329	-3.979185	19033.3001
HLA B*5401	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.473100	0.493735	-3.979365	29723.4977
HLA B*0803	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.495039	0.515530	-3.979509	31263.6302
HLA A*0301	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.360454	0.380508	-3.979946	22932.6295
HLA A*3101	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.360792	0.380508	-3.980284	22950.5015
HLA B*1502	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.553964	0.573275	-3.980689	35806.7157
HLA A*0202	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.312045	0.331331	-3.980714	20513.750390	
HLA A*3002	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.554033	0.573275	-3.980757	35812.3338
HLA B*5701	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.354517	0.373143	-3.981373	22621.2556
HLA A*2501	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.271676	0.290041	-3.981636	18692.8798
HLA A*3301	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.642401	0.660487	-3.981915	43893.625501	
HLA A*2603	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.613759	0.631559	-3.982200	41092.1516
HLA B*4601	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.398802	0.416215	-3.982588	25049.6781
HLA B*4501	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.603139	0.619672	-3.983467	40099.523325	
HLA B*4501	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.644135	0.660487	-3.983649	44069.221020	
HLA A*2902	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.401939	0.418270	-3.983669	25231.2468
HLA B*3901	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.435189	0.451144	-3.984045	27238.8409
HLA A*3001	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.306935	0.322700	-3.984235	20273.7896
HLA B*4001	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.364763	0.380508	-3.984255	23161.2935
HLA A*6801	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.615876	0.631559	-3.984317	41292.9364
HLA B*3501	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.301188	0.316807	-3.984382	20007.282141	
HLA B*4801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.431286	0.446772	-3.984514	26995.1739
HLA A*2603	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.274700	0.290041	-3.984659	18823.4837
HLA B*5301	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.592776	0.607347	-3.985429	39153.954493	
HLA A*6801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.501085	0.515530	-3.985555	31701.8517
HLA B*4402	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.435501	0.449835	-3.985666	27258.4467
HLA A*3301	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.127801	0.142013	-3.985787	13421.492170	
HLA A*2902	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.445602	0.459518	-3.986084	27899.829016	
HLA A*1101	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.350393	0.364143	-3.986251	22407.4977
HLA B*4001	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.402552	0.416215	-3.986337	25266.8980
HLA A*0250	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.498423	0.511996	-3.986427	31508.1325
HLA A*0211	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.498507	0.511996	-3.986511	31514.2695
HLA A*2403	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.403024	0.416215	-3.986810	25294.3879
HLA A*2603	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.498103	0.511259	-3.986844	31484.959106	
HLA A*3201	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.594268	0.607347	-3.986921	39288.690570	
HLA A*2601	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.351333	0.364143	-3.987190	22456.0390
HLA A*0203	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.351455	0.364143	-3.987313	22462.3571
HLA A*0202	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.498853	0.511259	-3.987594	31539.341332	
HLA B*1502	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.595123	0.607347	-3.987776	39366.134071	
HLA A*0212	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.347872	0.359849	-3.988024	22277.8032
HLA A*0301	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.317430	0.329388	-3.988043	20769.6934
HLA B*2705	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.500088	0.511996	-3.988093	31629.2175
HLA B*4402	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.369041	0.380508	-3.988533	23390.5925
HLA B*2705	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.352698	0.364143	-3.988555	22526.7326
HLA B*1502	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.613052	0.624086	-3.988966	41025.2926
HLA A*0219	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.440362	0.451144	-3.989218	27565.2661
HLA B*1502	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.621031	0.631559	-3.989472	41785.9748
HLA B*3801	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.468361	0.478869	-3.989492	29400.9255
HLA B*1801	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.449255	0.459518	-3.989737	28135.522896	
HLA A*0203	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.025589	0.035827	-3.989762	10606.908119	
HLA B*4002	1:134-142	9	EAADAARAT	0.999569	-0.361461	-4.628206	0.638108	-3.990098	42482.0891
HLA A*0250	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.501519	0.511259	-3.990260	31733.595731	
HLA B*5701	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.354449	0.364143	-3.990306	22617.7069
HLA B*1801	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.501627	0.511259	-3.990368	31741.493774	
HLA B*3901	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.502048	0.511259	-3.990789	31772.246177	
HLA B*1502	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.506347	0.515530	-3.990817	32088.3566
HLA B*1801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.313723	0.322700	-3.991022	20593.1412
HLA B*0803	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.484817	0.493735	-3.991082	30536.3268
HLA B*5701	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.409535	0.418270	-3.991265	25676.4274
HLA A*3301	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.623035	0.631559	-3.991476	41979.2474
HLA B*5101	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.485315	0.493735	-3.991580	30571.3689
HLA A*2602	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.615765	0.624086	-3.991680	41282.4384
HLA A*2601	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.351690	0.359849	-3.991842	22474.5123
HLA B*3901	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.503862	0.511996	-3.991866	31905.2183
HLA A*3001	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.300206	0.308151	-3.992055	19962.090116	
HLA A*1101	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.471310	0.478869	-3.992441	29601.2197
HLA A*3201	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.471382	0.478869	-3.992514	29606.1844
HLA B*2705	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.452088	0.459518	-3.992571	28319.688352	
HLA A*3301	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.617734	0.625007	-3.992727	41470.0167
HLA B*5401	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.472416	0.478869	-3.993548	29676.7419
HLA A*6801	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.617734	0.624086	-3.993648	41470.0167
HLA A*0250	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.549002	0.555227	-3.993775	35399.9278
HLA A*1101	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.445148	0.451144	-3.994004	27870.7137
HLA A*3201	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.618364	0.624086	-3.994278	41530.1856
HLA A*2603	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.562690	0.568388	-3.994302	36533.432331	
HLA A*3001	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.264132	0.269704	-3.994428	18370.9670
HLA A*0101	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.375058	0.380508	-3.994550	23716.9181
HLA B*4002	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.632174	0.637604	-3.994570	42872.0396
HLA A*0206	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.510229	0.515530	-3.994699	32376.4200
HLA B*4501	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.302882	0.308151	-3.994732	20085.473541	
HLA B*1501	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.249960	0.255019	-3.994941	17781.1532
HLA A*0202	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.441838	0.446772	-3.995065	27659.0759
HLA A*3101	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.441875	0.446772	-3.995103	27661.4701
HLA A*2602	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.368463	0.373143	-3.995320	23359.4842
HLA A*0211	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.499835	0.504252	-3.995583	31610.743007	
HLA B*1801	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.474500	0.478869	-3.995632	29819.4897
HLA A*6901	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.376379	0.380508	-3.995871	23789.1357
HLA A*6801	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.447270	0.451144	-3.996126	28007.1989
HLA A*0101	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.360381	0.364143	-3.996238	22928.7839
HLA A*0212	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.376804	0.380508	-3.996296	23812.4412
HLA B*1517	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.443426	0.446772	-3.996654	27760.4127
HLA A*2403	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.356737	0.359849	-3.996888	22737.1994
HLA A*6802	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.181017	0.183904	-3.997112	15171.084862	
HLA B*4002	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.628878	0.631559	-3.997319	42547.8694
HLA A*2403	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.378167	0.380508	-3.997659	23887.2757
HLA B*4403	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.658289	0.660487	-3.997802	45529.058704	
HLA B*5401	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.448959	0.451144		
HLA A*3301	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.622504	0.624086		

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HLA A*0212	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.414673	0.416215	-3.998458	25982.0205
HLA A*0250	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.358335	0.359849	-3.998486	22820.9973
HLA A*8001	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.414844	0.416215	-3.998630	25992.2833
HLA B*5701	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.415058	0.416215	-3.998844	26005.0825
HLA A*3002	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.477888	0.478869	-3.999020	30053.0230
HLA A*0203	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.417304	0.418270	-3.999035	26139.9254
HLA A*0203	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.379565	0.380508	-3.999057	23964.2900
HLA B*4002	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.567627	0.568388	-3.999238	36951.046635	
HLA A*0219	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.458904	0.459518	-3.999387	28767.645994	
HLA B*5301	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.573280	0.573275	-4.000004	37435.1523
HLA B*1503	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-3.944419	-0.055989	-4.000408	8798.705849	
HLA A*2402	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.573693	0.573275	-4.000418	37470.8128
HLA A*3002	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.555858	0.555227	-4.000631	35963.1872
HLA A*2403	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.330712	0.329388	-4.001324	21414.6867
HLA A*6801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.374574	0.373143	-4.001431	23690.5018
HLA B*4601	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.420265	0.418270	-4.001995	26318.7158
HLA B*0803	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.514101	0.511996	-4.002105	32666.3624
HLA B*1801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.517829	0.515530	-4.002299	32948.0267
HLA A*3101	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.366516	0.364143	-4.002373	23254.9562
HLA B*1501	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.420685	0.418270	-4.002416	26344.2144
HLA B*5401	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.562376	0.559811	-4.002565	36506.9579
HLA A*2402	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.570970	0.568388	-4.002582	37236.603590	
HLA A*0212	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.334130	0.331331	-4.002799	21583.915186	
HLA A*2403	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.319881	0.316807	-4.003074	20887.217987	
HLA A*2603	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.576362	0.573275	-4.003087	37701.8038
HLA B*4403	1:240-248	9	EVATSPLAT	0.961736	-0.324132	-4.641161	0.637604	-4.003557	43768.4257
HLA A*0216	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.454906	0.451144	-4.003762	28503.9798
HLA B*2705	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-3.937920	-0.066090	-4.004010	8668.02436
HLA B*0702	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.420720	0.416215	-4.004506	26346.3523
HLA A*2602	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.612124	0.607347	-4.004777	40937.719007	
HLA B*1501	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.195504	0.190565	-4.004939	15685.687634	
HLA B*4801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.423274	0.418270	-4.005005	26501.7398
HLA B*5701	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.385603	0.380508	-4.005095	24299.8024
HLA A*0211	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.498876	0.493735	-4.005141	31541.0476
HLA B*0802	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.484180	0.478869	-4.005311	30491.5909
HLA A*0212	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.423878	0.418270	-4.005609	26538.6118
HLA A*2603	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.521368	0.515530	-4.005838	33217.5604
HLA B*5401	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.379276	0.373143	-4.006132	23948.3490
HLA A*2603	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.630349	0.624086	-4.006263	42692.2059
HLA A*3001	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.306188	0.299515	-4.006673	20238.941759	
HLA B*5701	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.305657	0.298936	-4.006721	20214.212042	
HLA B*1501	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.336221	0.329388	-4.006834	21688.0880
HLA B*4601	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.388211	0.380508	-4.007703	24446.1612
HLA A*2902	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.457633	0.449835	-4.007798	28683.5733
HLA A*0201	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.388406	0.380508	-4.007898	24457.1405
HLA B*0802	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.459804	0.451144	-4.008660	28827.3139
HLA B*1801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.150657	0.141991	-4.008666	14146.7471
HLA B*1801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.520724	0.511996	-4.008728	33168.3582
HLA B*0801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.389409	0.380508	-4.008901	24513.7023
HLA B*1501	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.234592	0.225691	-4.008901	17162.950272	
HLA A*2403	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.373268	0.364143	-4.009125	23619.3502
HLA A*0202	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.503079	0.493735	-4.009345	31847.7930
HLA A*2301	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.525141	0.515530	-4.009611	33507.4213
HLA A*0216	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.469200	0.459518	-4.009682	29457.763359	
HLA A*0206	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.513967	0.504252	-4.009715	32656.290918	
HLA B*4403	1:111-119	9	EKDSRVVVP	0.794349	-0.162790	-4.641375	0.631559	-4.009816	43789.9782
HLA A*6801	1:50-58 9	PNPKTATNA	1.129060	-0.468573	-4.670377	0.660487	-4.009890	46814.110064	
HLA A*0101	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.370103	0.359849	-4.010255	23447.8588
HLA B*1517	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.426801	0.416215	-4.010586	26717.8164
HLA A*3001	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.274940	0.264217	-4.010722	18833.8735
HLA A*0216	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.429082	0.418270	-4.010813	26858.5345
HLA A*2601	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.391514	0.380508	-4.011006	24632.8151
HLA A*2501	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.462281	0.451144	-4.011137	28992.1575
HLA A*0203	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.427464	0.416215	-4.011249	26758.6080
HLA B*1501	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.342896	0.331331	-4.011565	22023.997765	
HLA A*2902	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.153584	0.142013	-4.011571	14242.428595	
HLA B*3901	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.220972	0.208763	-4.012209	16633.0533
HLA A*0216	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.491581	0.478869	-4.012712	31015.6554
HLA B*4501	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.154749	0.141991	-4.012758	14280.6966
HLA B*1503	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.072837	0.060047	-4.012790	11825.974827	
HLA B*3501	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.238553	0.225691	-4.012863	17320.210899	
HLA A*2301	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.524173	0.511259	-4.012914	33432.820695	
HLA A*2402	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.528740	0.515530	-4.013210	33786.2831
HLA B*4002	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.632989	0.619672	-4.013317	42952.595986	
HLA B*0801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.386674	0.373143	-4.013531	24359.8218
HLA B*7301	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.620995	0.607347	-4.013649	41782.584108	
HLA A*6901	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.212970	0.198739	-4.014230	16329.3776
HLA B*1517	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.050164	0.035827	-4.014338	11224.433207	
HLA B*1517	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.432856	0.418270	-4.014586	27092.9057
HLA B*3501	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.313972	0.298936	-4.015036	20604.953770	
HLA B*2705	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.461916	0.446772	-4.015144	28967.8568
HLA A*6802	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.388298	0.373143	-4.015154	24451.0549
HLA B*0803	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.461989	0.446772	-4.015217	28972.7153
HLA B*4801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.431669	0.416215	-4.015455	27018.9890
HLA A*0211	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.462325	0.446772	-4.015553	28995.1377
HLA B*0803	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.494663	0.478869	-4.015795	31236.5806
HLA A*0202	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.527819	0.511996	-4.015824	33714.7093
HLA B*4002	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.640064	0.624086	-4.015978	43657.9879
HLA B*7301	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.527328	0.511259	-4.016069	33676.610776	
HLA A*0203	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.347461	0.331331	-4.016130	22256.722125	
HLA A*0201	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.183907	0.167651	-4.016256	15272.372362	
HLA A*2602	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.528656	0.511259	-4.017397	33779.703755	
HLA B*4801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.226240	0.208763	-4.017477	16836.0235
HLA A*3301	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.591209	0.573275	-4.017933	39012.9261
HLA B*4801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.318292	0.300329	-4.017963	20810.9711
HLA A*3301	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.578037	0.559811	-4.018227	37847.5095
HLA B*4001	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.160322	0.141991	-4.018331	14465.1310
HLA B*0802	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.478036	0.459518	-4.018518	30063.267568	
HLA B*4402	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.437031	0.418270	-4.018761	27354.6158
HLA A*2902	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.382913	0.364143	-4.018770	24149.7468
HLA B*1503	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.530806	0.511996	-4.018810	33947.3294
HLA A*2501	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.468753	0.449835	-4.018918	29427.4999
HLA B*5101	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.465826	0.446772	-4.019054	29229.8043
HLA A*0201	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.383347	0.364143	-4.019204	24173.9287
HLA A*2402	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.513166	0.493735	-4.019431	32596.1030
HLA B*3901	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.479079	0.459518	-4.019562	30135.566055	
HLA A*0201	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.392715	0.373143	-4.019571	24701.0056
HLA A*2301	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.531792	0.511996	-4.019796	34024.5507
HLA A*0101	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.393152	0.373143	-4.020008	24725.8732
HLA A*2603	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.639852	0.619672	-4.020180	43636.736455	
HLA A*0206	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.499280	0.478869	-4.020412	31570.4102
HLA B*0702	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.439030	0.418270	-4.020760	27480.8418
HLA B*5801	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.352327	0.331331	-4.020996	22507.485919	
HLA B*4402	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.329302	0.308151	-4.021152	21345.288748	
HLA B*3501	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.057396	0.035827	-4.021569	11412.903227	
HLA A*2403	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.440275	0.418270		
HLA B*0801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.381872	0.359849		

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HLA A*3002	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.206015	0.183904	-4.022111	16069.973407
HLA B*2705	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.438386	0.416215	-4.022172	27440.1368
HLA B*4501	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.629585	0.607347	-4.022238	42617.209871
HLA A*2402	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.533616	0.511259	-4.022357	34167.688524
HLA B*4403	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.590793	0.568388	-4.022404	38975.587151
HLA A*6901	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.345138	0.322700	-4.022437	22137.9581
HLA B*2705	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.402972	0.380508	-4.022465	25291.3776
HLA A*2301	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.526887	0.504252	-4.022635	33642.377082
HLA A*2601	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.395797	0.373143	-4.022654	24876.9514
HLA B*5101	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.482615	0.459518	-4.023098	30381.927876
HLA A*6802	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.403790	0.380508	-4.023282	25339.0370
HLA B*0802	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.470111	0.446772	-4.023339	29519.6612
HLA B*1502	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.340284	0.316807	-4.023477	21891.903596
HLA A*6801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.383749	0.359849	-4.023900	24196.3021
HLA B*1509	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.475830	0.451144	-4.024686	29910.9368
HLA A*2602	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.584731	0.559811	-4.024920	38435.3637
HLA B*1509	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.540572	0.515530	-4.025042	34719.4170
HLA A*0219	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.443348	0.418270	-4.025079	27755.4571
HLA A*6802	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.280198	0.255019	-4.025179	19063.2874
HLA B*4001	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.398396	0.373143	-4.025252	25026.2448
HLA A*6802	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.442115	0.416215	-4.025900	27676.7382
HLA B*1801	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.477052	0.451144	-4.025908	29995.1990
HLA A*0202	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.325338	0.298936	-4.026403	21151.367589
HLA A*2301	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.520315	0.493735	-4.026580	33137.1508
HLA A*0219	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.386535	0.359849	-4.026687	24352.0478
HLA A*3101	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.343507	0.316807	-4.026700	22054.997883
HLA B*5401	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.542527	0.515530	-4.026997	34876.0423
HLA A*3101	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.327664	0.300329	-4.027336	21264.9537
HLA B*4501	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.651501	0.624086	-4.027415	44823.0091
HLA B*4601	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.387677	0.359849	-4.027829	24416.1586
HLA A*2902	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.401168	0.373143	-4.028025	25186.5151
HLA B*5401	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.392214	0.364143	-4.028071	24672.5588
HLA A*0203	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.401572	0.373143	-4.028429	25209.9621
HLA A*2602	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.479725	0.451144	-4.028582	30180.4326
HLA B*3901	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.475896	0.446772	-4.029123	29915.4679
HLA B*1502	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.597625	0.568388	-4.029237	39593.597951
HLA A*0203	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.293355	0.263887	-4.029468	19649.6542
HLA B*4403	1:158-166	9	PNAILRRKQ	0.959799	-0.335713	-4.653681	0.624086	-4.029596	45048.6033
HLA A*0219	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.445938	0.416215	-4.029723	27921.4210
HLA B*0802	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.445947	0.416215	-4.029732	27922.0252
HLA A*2301	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.319857	0.290041	-4.029816	20886.0880
HLA B*4801	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.361234	0.331331	-4.029903	22973.855480
HLA B*2705	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.448310	0.418270	-4.030041	28074.4009
HLA A*2402	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.585375	0.555227	-4.030148	38492.3790
HLA B*5401	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.541543	0.511259	-4.030284	34797.076807
HLA B*0702	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.403442	0.373143	-4.030299	25318.7571
HLA B*3501	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.446570	0.416215	-4.030355	27962.0835
HLA B*4403	1:11-19 9	LIAKTDFLA	0.807408	-0.187736	-4.650418	0.619672	-4.030746	44711.361711
HLA B*0802	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.449231	0.418270	-4.030962	28134.0008
HLA B*5801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.353730	0.322700	-4.031029	22580.2959
HLA B*7301	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.265307	0.234045	-4.031262	18420.7268
HLA A*2501	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.257058	0.225691	-4.031367	18074.143238
HLA B*4601	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.360778	0.329388	-4.031391	22949.7566
HLA B*1517	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.481255	0.449835	-4.031419	30286.9106
HLA B*1801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.447643	0.416215	-4.031429	28031.3003
HLA B*5101	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.404789	0.373143	-4.031645	25397.3636
HLA A*0212	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.405059	0.373143	-4.031916	25413.1692
HLA A*3301	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.639335	0.607347	-4.031989	43584.831970
HLA B*3801	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.547804	0.515530	-4.032274	35302.3925
HLA A*3201	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.600776	0.568388	-4.032387	39881.880527
HLA B*5301	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.587743	0.555227	-4.032516	38702.8578
HLA A*0216	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.448783	0.416215	-4.032568	28104.9453
HLA A*1101	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.413096	0.380508	-4.032589	25887.8758
HLA B*5701	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.392456	0.359849	-4.032608	24686.3107
HLA B*4601	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.363945	0.331331	-4.032614	23117.730176
HLA A*2603	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.640602	0.607347	-4.033255	43712.107773
HLA A*8001	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.451795	0.418270	-4.033525	28300.5440
HLA B*4001	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.397912	0.364143	-4.033769	24998.3701
HLA A*6801	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.641128	0.607347	-4.033781	43765.110877
HLA A*6801	1:217-225	9	RQLAAVAPA	0.688822	-0.063815	-4.659306	0.625007	-4.034299	45635.8347
HLA B*4501	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.603431	0.568388	-4.035042	40126.432163
HLA A*3001	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.310478	0.275281	-4.035197	20439.862044
HLA A*3002	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.395189	0.359849	-4.035340	24842.1192
HLA B*5101	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.514333	0.478869	-4.035465	32683.8625
HLA B*4402	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.395621	0.359849	-4.035772	24866.8598
HLA B*5301	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.595687	0.559811	-4.035876	39417.2792
HLA A*8001	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.400078	0.364143	-4.035935	25123.3714
HLA A*3101	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.270201	0.234045	-4.036156	18629.4802
HLA A*2501	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.495932	0.459518	-4.036414	31327.966767
HLA B*4001	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.367951	0.331331	-4.036620	23331.951360
HLA A*6801	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.605045	0.568388	-4.036656	40275.843292
HLA B*5801	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.353528	0.316807	-4.036721	22569.792897
HLA A*0301	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.368057	0.331331	-4.036726	23337.632098
HLA B*4402	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.410059	0.373143	-4.036915	25707.4223
HLA B*4402	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-3.840440	-0.196676	-4.037116	6925.32231
HLA A*6901	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.194766	0.157520	-4.037245	15659.0648
HLA B*5101	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.488599	0.451144	-4.037456	30803.4575
HLA B*1801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.484382	0.446772	-4.037610	30505.7805
HLA B*1509	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.455928	0.418270	-4.037658	28571.1373
HLA A*0202	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.418395	0.380508	-4.037887	26205.6239
HLA B*1503	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.411433	0.373143	-4.038290	25788.9096
HLA B*1509	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.549583	0.511259	-4.038324	35447.262342
HLA B*0803	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.498056	0.459518	-4.038538	31481.552688
HLA B*2705	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.488787	0.449835	-4.038952	30816.7918
HLA B*1801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.398816	0.359849	-4.038968	25050.4912
HLA B*4801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.419492	0.380508	-4.038984	26271.9140
HLA B*4001	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.398941	0.359849	-4.039092	25057.6748
HLA A*1101	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.489311	0.449835	-4.039476	30853.9918
HLA A*0203	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.315052	0.275281	-4.039772	20656.294062
HLA B*3501	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.369236	0.329388	-4.039849	23401.0977
HLA A*0301	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.356866	0.316807	-4.040060	22743.965722
HLA A*6901	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.372039	0.331331	-4.040708	23552.616805
HLA A*2601	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.363562	0.322700	-4.040862	23097.3536
HLA A*2402	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.552982	0.511996	-4.040987	35725.8363
HLA B*5801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.349700	0.308151	-4.041550	22371.765730
HLA B*0802	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.491708	0.449835	-4.041872	31024.7174
HLA A*2601	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.332103	0.290041	-4.042062	21483.3804
HLA A*3201	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.597533	0.555227	-4.042306	39585.2451
HLA B*5401	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.554789	0.511996	-4.042793	35874.7727
HLA A*0219	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.268528	0.225691	-4.042837	18557.860489
HLA A*0101	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.360043	0.316807	-4.043236	22910.928810
HLA A*3201	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.490329	0.446772	-4.043556	30926.3515
HLA B*3801	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.554979	0.511259	-4.043720	35890.496516
HLA B*0803	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.495115	0.451144	-4.043971	31269.0429
HLA B*3901	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.403882	0.359849	-4.044033	25344.3835
HLA B*5401	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.503596	0.459518	-4.0440	
HLA B*5701	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.373562	0.329388	

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HLA B*3901	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.424780	0.380508	-4.044273	26593.8004
HLA A*3301	1:7-15 9	LRVQLIAKT	0.813183	-0.244795	-4.612826	0.568388	-4.044438	41003.991681	
HLA A*2601	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.375942	0.331331	-4.044611	23765.210252	
HLA A*1101	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.460960	0.416215	-4.044746	28904.1448
HLA A*0301	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.308786	0.263887	-4.044899	20360.4011
HLA A*1101	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.492154	0.446772	-4.045382	31056.6235
HLA A*6802	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.368207	0.322700	-4.045507	23345.7137
HLA A*6801	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.605320	0.559811	-4.045509	40301.3442
HLA B*3901	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.495420	0.449835	-4.045585	31291.0417
HLA B*3801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.539656	0.493735	-4.045921	34646.2412
HLA B*4403	1:31-39 9	GGPALVEFA	1.099205	-0.491858	-4.653409	0.607347	-4.046062	45020.342140	
HLA A*0301	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.368771	0.322700	-4.046071	23376.0448
HLA A*2602	1:228-236	9	ADFEVTTLA	0.872294	-0.299019	-4.619917	0.573275	-4.046642	41678.9608
HLA A*2402	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.552120	0.504252	-4.047868	35654.975573	
HLA B*4001	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.346808	0.298936	-4.047873	22223.274304	
HLA A*2603	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.603522	0.555227	-4.048295	40134.8991
HLA B*5101	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.466615	0.418270	-4.048346	29282.9843
HLA A*0216	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.216033	0.167651	-4.048383	16444.980473	
HLA A*3101	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.379715	0.331331	-4.048384	23972.588676	
HLA A*2501	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.466989	0.418270	-4.048719	29308.1836
HLA A*0212	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.412946	0.364143	-4.048803	25878.9141
HLA A*2602	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.527730	0.478869	-4.048861	33707.7791
HLA A*8001	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.409037	0.359849	-4.049188	25646.9961
HLA A*2301	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.528219	0.478869	-4.049350	33745.7303
HLA A*0101	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.379106	0.329388	-4.049719	23939.0227
HLA A*0301	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.348678	0.298936	-4.049743	22319.180113	
HLA A*0203	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.348730	0.298936	-4.049794	22321.836645	
HLA A*0219	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.430370	0.380508	-4.049862	26938.2779
HLA B*4001	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.372791	0.322700	-4.050091	23593.4259
HLA A*2403	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.423319	0.373143	-4.050176	26504.4640
HLA A*0301	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.340234	0.290041	-4.050194	21889.4166
HLA B*3501	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.373428	0.322700	-4.050727	23628.0407
HLA A*2501	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.410681	0.359849	-4.050833	25744.3034
HLA A*0211	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.500765	0.449835	-4.050930	31678.5358
HLA B*4801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.424181	0.373143	-4.051038	26557.1390
HLA B*1801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.415265	0.364143	-4.051122	26017.4657
HLA B*5801	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.350779	0.299515	-4.051264	22427.386965	
HLA A*2602	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.606501	0.555227	-4.051274	40411.1605
HLA A*3001	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.260307	0.208763	-4.051544	18209.8788
HLA B*7301	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.511103	0.459518	-4.051585	32441.642494	
HLA A*1101	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.381122	0.329388	-4.051735	24050.3984
HLA A*2501	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.468528	0.416215	-4.052313	29412.2207
HLA B*3801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.564594	0.511996	-4.052598	36693.8734
HLA A*1101	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.426042	0.373143	-4.052899	26671.1707
HLA B*1503	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.412800	0.359849	-4.052952	25870.2354
HLA A*1101	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.471298	0.418270	-4.053028	29600.4190
HLA A*0301	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.361546	0.308151	-4.053396	22990.391468	
HLA B*1502	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.608964	0.555227	-4.053736	40640.9249
HLA A*0211	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.532944	0.478869	-4.054075	34114.8641
HLA B*3901	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.472470	0.418270	-4.054201	29680.4343
HLA A*3001	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.233920	0.179565	-4.054355	17136.4158
HLA A*0101	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.377091	0.322700	-4.054390	23828.1628
HLA A*0219	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.418923	0.364143	-4.054780	26237.5419
HLA B*3901	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.418965	0.364143	-4.054823	26240.0966
HLA B*1502	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.566922	0.511996	-4.054926	36891.1249
HLA B*5301	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.566760	0.511259	-4.055501	36877.356718	
HLA B*0801	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.354503	0.298936	-4.055567	22620.521353	
HLA B*1509	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.567841	0.511996	-4.055845	36969.2421
HLA B*1509	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.505816	0.449835	-4.055981	32049.1483
HLA B*0803	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.506237	0.449835	-4.056402	32080.1987
HLA B*0802	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.420852	0.364143	-4.056709	26354.3352
HLA A*0206	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.516572	0.459518	-4.057055	32852.803431	
HLA A*0202	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.561363	0.504252	-4.057111	36421.935190	
HLA A*2402	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.536167	0.478869	-4.057298	34369.0193
HLA B*1502	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.568642	0.511259	-4.057383	37037.504886	
HLA A*0206	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.421757	0.364143	-4.057614	26409.2834
HLA A*0201	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.389059	0.331331	-4.057728	24493.950489	
HLA A*0206	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.387207	0.329388	-4.057820	24389.7552
HLA B*4402	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.389273	0.331331	-4.057942	24506.011827	
HLA A*8001	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.387426	0.329388	-4.058038	24402.0292
HLA A*0101	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.357371	0.298936	-4.058436	22770.435214	
HLA A*0203	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.388081	0.329388	-4.058694	24438.8884
HLA A*0101	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.390194	0.331331	-4.058863	24558.036296	
HLA B*5801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.359242	0.300329	-4.058913	22868.7023
HLA A*2601	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.375754	0.316807	-4.058947	23754.927105	
HLA A*3001	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.250087	0.190565	-4.059522	17786.348511	
HLA A*2902	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.323804	0.264217	-4.059587	21076.7788
HLA A*3001	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-3.947313	-0.112631	-4.059944	8857.54494
HLA A*0202	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.575568	0.515530	-4.060038	37632.9274
HLA A*3201	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.572330	0.511996	-4.060335	37353.4236
HLA A*0219	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.377333	0.316807	-4.060526	23841.444017	
HLA A*6901	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.360639	0.299515	-4.061124	22942.432629	
HLA A*3001	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.228843	0.167651	-4.061192	16937.244402	
HLA A*2601	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.391079	0.329388	-4.061692	24608.1742
HLA A*0301	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.362023	0.300329	-4.061694	23015.6535
HLA B*3501	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.442625	0.380508	-4.062117	27709.2482
HLA A*0250	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.577685	0.515530	-4.062155	37816.8098
HLA B*5801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.229202	0.167005	-4.062197	16951.2693
HLA B*7301	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.622313	0.559811	-4.062503	41909.5846
HLA A*0206	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.478774	0.416215	-4.062559	30114.3795
HLA A*2402	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.513871	0.451144	-4.062727	32649.0483
HLA B*4402	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.338068	0.275281	-4.062787	21780.505883	
HLA B*4402	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.427271	0.364143	-4.063128	26746.7402
HLA A*3001	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.230299	0.167005	-4.063294	16994.1495
HLA A*0201	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.392703	0.329388	-4.063315	24700.3374
HLA B*5801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.353488	0.290041	-4.063447	22567.7172
HLA A*6901	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.338731	0.275281	-4.063450	21813.759337	
HLA B*5101	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.480369	0.416215	-4.064155	30225.2026
HLA B*0802	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.444807	0.380508	-4.064300	27848.8596
HLA A*0211	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.515499	0.451144	-4.064355	32771.6811
HLA B*0801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.319392	0.255019	-4.064373	20863.7277
HLA B*5101	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.364126	0.299515	-4.064611	23127.362137	
HLA A*6802	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.397317	0.331331	-4.065987	24964.178281	
HLA A*3101	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.396298	0.329388	-4.066910	24905.6338
HLA A*2601	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.322080	0.255019	-4.067061	20993.2519
HLA A*0219	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.440597	0.373143	-4.067454	27580.1826
HLA B*4801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.432071	0.364143	-4.067928	27043.9956
HLA A*8001	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.441210	0.373143	-4.068067	27619.1528
HLA A*0206	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.448705	0.380508	-4.068197	28099.9282
HLA A*6901	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.323607	0.255019	-4.068588	21067.2031
HLA A*0212	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.236535	0.167651	-4.068884	17239.908967	
HLA B*4001	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.359000	0.290041	-4.068959	22855.9630
HLA B*3901	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.485616	0.416215	-4.069401	30592.5459
HLA B*7301	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.585100	0.515530	-4.069570	38468.0227
HLA B*0801	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.105443	0.035827	-4.069616	12748.030771	
HLA A*3301	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.624933	0.555227		
HLA B*0702	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.359977	0.290041		

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HLA A*6901	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.359991	0.290041	-4.069950	22908.2021
HLA A*0301	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.369626	0.299515	-4.070111	23422.122346	
HLA A*0201	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.369074	0.298936	-4.070139	23392.364161	
HLA A*3001	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.004147	-0.066090	-4.070237	10095.9550
HLA A*3201	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.486499	0.416215	-4.070284	30654.8381
HLA B*0702	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.387285	0.316807	-4.070478	24394.109810	
HLA A*0216	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.451132	0.380508	-4.070624	28257.4019
HLA B*1801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.360715	0.290041	-4.070674	22946.4046
HLA B*1801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.520663	0.449835	-4.070827	33163.6931
HLA B*1509	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.517735	0.446772	-4.070963	32940.8976
HLA A*0301	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.296827	0.225691	-4.071137	19807.399105	
HLA B*4801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.431023	0.359849	-4.071174	26978.8222
HLA A*0202	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.550046	0.478869	-4.071177	35485.0603
HLA A*6901	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.379414	0.308151	-4.071264	23955.994224	
HLA A*2902	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.341113	0.269704	-4.071409	21933.7503
HLA A*6901	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.388276	0.316807	-4.071470	24449.864529	
HLA A*0211	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.531492	0.459518	-4.071974	34000.998020	
HLA A*0216	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.401384	0.329388	-4.071997	25199.0538
HLA B*1501	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.380488	0.308151	-4.072337	24015.294366	
HLA B*4501	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.632158	0.559811	-4.072347	42870.4161
HLA B*1801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.452962	0.380508	-4.072455	28376.7385
HLA A*8001	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.452984	0.380508	-4.072476	28378.1201
HLA A*6901	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.373270	0.300329	-4.072941	23619.4780
HLA A*0201	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.395893	0.322700	-4.073193	24882.4699
HLA B*0702	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.453775	0.380508	-4.073268	28429.9044
HLA A*6801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.491593	0.418270	-4.073323	31016.4943
HLA B*5801	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.348760	0.275281	-4.073480	22323.406563	
HLA B*0803	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.489824	0.416215	-4.073609	30890.4011
HLA B*7301	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.585868	0.511996	-4.073872	38536.1342
HLA A*2403	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.308453	0.234045	-4.074408	20344.7662
HLA B*5301	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.590046	0.515530	-4.074515	38908.5933
HLA A*0216	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.447697	0.373143	-4.074554	28034.7883
HLA A*0212	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.338641	0.263887	-4.074754	21809.2754
HLA B*4402	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.373726	0.298936	-4.074791	23644.280153	
HLA A*0101	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.382995	0.308151	-4.074844	24154.319958	
HLA A*3001	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.258893	0.183904	-4.074988	18150.670279	
HLA B*1503	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.524833	0.449835	-4.074998	33483.6832
HLA B*4001	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.404481	0.329388	-4.075093	25379.3710
HLA B*1502	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.579388	0.504252	-4.075136	37965.425024	
HLA B*0702	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.406736	0.331331	-4.075406	25511.521513	
HLA B*3801	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.526908	0.451144	-4.075764	33644.0151
HLA A*6801	1:204-212	9	ADVEIRRLA	0.833844	-0.278617	-4.631091	0.555227	-4.075864	42765.2517
HLA A*0211	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.405327	0.329388	-4.075939	25428.8470
HLA A*0250	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.580504	0.504252	-4.076252	38063.110133	
HLA A*3201	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.587609	0.511259	-4.076350	38690.925134	
HLA A*2902	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.384658	0.308151	-4.076508	24247.013275	
HLA B*7301	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.580833	0.504252	-4.076581	38091.949461	
HLA B*1503	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.406809	0.329388	-4.077422	25515.8003
HLA A*6801	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.571261	0.493735	-4.077527	37261.5912
HLA B*0702	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.341486	0.263887	-4.077600	21952.6252
HLA A*2602	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.367740	0.290041	-4.077699	23320.5940
HLA B*0802	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.437602	0.359849	-4.077753	27390.5999
HLA A*2403	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.376968	0.298936	-4.078033	23821.460563	
HLA B*5301	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.525026	0.446772	-4.078254	33498.5402
HLA A*0202	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.010806	-0.067515	-4.078321	10251.9350
HLA B*1517	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.458846	0.380508	-4.078338	28763.7555
HLA B*4601	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.377389	0.298936	-4.078453	23844.539727	
HLA B*2705	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.377396	0.298936	-4.078460	23844.926719	
HLA B*4601	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.401443	0.322700	-4.078743	25202.4621
HLA A*0216	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.442890	0.364143	-4.078747	27726.1926
HLA B*0802	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.395687	0.316807	-4.078880	24870.626923	
HLA A*0101	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.379597	0.300329	-4.079269	23966.1051
HLA A*0250	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.526046	0.446772	-4.079273	33577.2835
HLA B*5701	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.396204	0.316807	-4.079397	24900.244959	
HLA A*2301	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.538947	0.459518	-4.079429	34589.682915	
HLA B*0702	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.443602	0.364143	-4.079459	27771.6785
HLA A*2902	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.460213	0.380508	-4.079705	28854.4625
HLA B*5301	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.574074	0.493735	-4.080339	37503.6667
HLA B*5701	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.411720	0.331331	-4.080389	25805.936156	
HLA B*5801	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.306282	0.225691	-4.080591	20243.321850	
HLA A*0211	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.264632	0.183904	-4.080728	18392.148271	
HLA B*0801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.403475	0.322700	-4.080775	25320.6748
HLA A*0206	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.356192	0.275281	-4.080911	22708.679972	
HLA A*0211	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.497199	0.416215	-4.080984	31419.4502
HLA A*2501	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.445409	0.364143	-4.081266	27887.4550
HLA B*4002	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.641217	0.559811	-4.081407	43774.1088
HLA A*2301	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.532579	0.451144	-4.081436	34086.2697
HLA A*2403	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.412925	0.331331	-4.081594	25877.654149	
HLA A*2601	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.380857	0.298936	-4.081921	24035.700484	
HLA B*5101	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.446083	0.364143	-4.081940	27930.7878
HLA A*6901	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.351733	0.269704	-4.082029	22476.7009
HLA A*2602	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.575880	0.493735	-4.082146	37660.0146
HLA B*1517	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.399533	0.316807	-4.082726	25091.859079	
HLA B*0803	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.501994	0.418270	-4.083724	31768.2930
HLA B*4002	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.595076	0.511259	-4.083817	39361.874973	
HLA A*3101	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.391991	0.308151	-4.083840	24659.881932	
HLA B*4001	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.392057	0.308151	-4.083906	24663.617617	
HLA B*1501	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.406654	0.322700	-4.083954	25506.6914
HLA B*2705	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.400846	0.316807	-4.084040	25167.854926	
HLA A*0211	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.457227	0.373143	-4.084084	28656.7406
HLA B*3801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.534215	0.449835	-4.084379	34214.8561
HLA B*4402	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.384985	0.300329	-4.084656	24265.2532
HLA A*0203	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.144708	0.060047	-4.084661	13954.288462	
HLA A*0206	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.502957	0.418270	-4.084688	31838.8350
HLA B*1503	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.531562	0.446772	-4.084790	34006.5167
HLA A*0250	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.213425	0.128565	-4.084861	16346.5246
HLA B*0801	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.416590	0.331331	-4.085259	26096.970876	
HLA B*4001	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.355212	0.269704	-4.085508	22657.5086
HLA A*0202	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.349820	0.263887	-4.085933	22377.9390
HLA A*0216	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.417333	0.331331	-4.086002	26141.622455	
HLA A*0201	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.386472	0.300329	-4.086143	24348.4910
HLA A*0202	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.450333	0.364143	-4.086191	28205.4741
HLA A*0250	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.579997	0.493735	-4.086262	38018.6575
HLA B*5401	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.533390	0.446772	-4.086618	34149.9481
HLA A*0203	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.387069	0.300329	-4.086740	24381.9716
HLA A*2301	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.536590	0.449835	-4.086755	34402.5034
HLA A*0212	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.385701	0.298936	-4.086766	24305.324380	
HLA A*2902	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.403654	0.316807	-4.086847	25331.087581	
HLA A*3002	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.533667	0.446772	-4.086895	34171.7553
HLA A*3002	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.580751	0.493735	-4.087016	38084.7375
HLA A*3301	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.603038	0.515530	-4.087508	40090.1962
HLA A*2501	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.404495	0.316807	-4.087688	25380.194859	
HLA A*0201	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.395910	0.308151	-4.087759	24883.412205	
HLA A*2403	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.352174	0.263887	-4.088287	22499.5727
HLA B*5801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.358050	0.269704	-4.088346	22806.0636
HLA A*3301	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.343371	0.255019		
HLA B*0801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.230532	0.141991		

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HLA A*2501	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.272466	0.183904	-4.088561	18726.889263		
HLA B*2705	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.448905	0.359849	-4.089056	28112.8527	
HLA B*4801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.418641	0.329388	-4.089254	26220.5140	
HLA A*3001	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.285832	0.196360	-4.089472	19312.2049	
HLA B*5301	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.601490	0.511996	-4.089494	39947.5244	
HLA B*5401	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.406318	0.316807	-4.089512	25486.966755		
HLA A*0211	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.508612	0.418270	-4.090343	32256.1388	
HLA B*4801	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.389832	0.298936	-4.090896	24537.584953		
HLA A*2601	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.399354	0.308151	-4.091204	25081.544642		
HLA A*2902	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.390339	0.298936	-4.091404	24566.274765		
HLA B*4402	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.381632	0.290041	-4.091591	24078.6488	
HLA A*0301	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.361434	0.269704	-4.091730	22984.4222	
HLA A*0250	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.542304	0.449835	-4.092469	34858.1227	
HLA B*7301	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.301496	0.208763	-4.092733	20021.4662	
HLA B*5801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.356979	0.264217	-4.092762	22749.8725	
HLA B*3901	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.424468	0.331331	-4.093137	26574.672685		
HLA B*4001	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.410155	0.316807	-4.093348	25713.125024		
HLA B*1501	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.260697	0.167005	-4.093692	18226.2394	
HLA A*6802	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.383765	0.290041	-4.093725	24197.2184	
HLA A*0301	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.369039	0.275281	-4.093758	23390.465986		
HLA B*1801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.302682	0.208763	-4.093920	20076.2395	
HLA A*2601	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.277867	0.183904	-4.093963	18961.256291		
HLA B*0702	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.423488	0.329388	-4.094101	26514.7898	
HLA A*3001	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-3.907687	-0.186575	-4.094262	8085.128942		
HLA A*0101	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.384334	0.290041	-4.094293	24228.9180	
HLA B*4501	1:82-90 9	ITGISRSCT	0.910830	-0.399571	-4.605637	0.511259	-4.094378	40330.788474		
HLA A*2603	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.545629	0.451144	-4.094485	35125.9853	
HLA A*0219	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.425929	0.331331	-4.094599	26664.245778		
HLA A*0201	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.394578	0.299515	-4.095063	24807.201593		
HLA A*3001	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.224045	0.128565	-4.095480	16751.1684	
HLA A*2601	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.395264	0.299515	-4.095749	24846.420191		
HLA B*1509	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.412934	0.316807	-4.096128	25878.214136		
HLA A*0202	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.547433	0.451144	-4.096289	35272.2302	
HLA A*0212	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.425878	0.329388	-4.096490	26661.0724	
HLA A*0301	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.287737	0.190565	-4.097173	19397.121892		
HLA A*2501	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.470713	0.373143	-4.097570	29560.5722	
HLA B*5701	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.420476	0.322700	-4.097776	26331.5333	
HLA A*0301	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.362178	0.264217	-4.097961	23023.8728	
HLA B*4001	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.399439	0.300329	-4.099110	25086.4298	
HLA A*2403	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.421879	0.322700	-4.099178	26416.7138	
HLA B*1503	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.228199	0.128565	-4.099634	16912.1567	
HLA A*0211	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.431326	0.331331	-4.099995	26997.656715		
HLA A*4501	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.579607	0.478869	-4.100738	37984.5309	
HLA B*4402	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.309966	0.208763	-4.101203	20415.7703	
HLA B*5801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.356526	0.255019	-4.101506	22726.1315	
HLA A*0101	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.376931	0.275281	-4.101650	23819.398709		
HLA B*4501	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.561349	0.459518	-4.101831	36420.752978		
HLA B*4501	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.433297	0.331331	-4.101967	27120.474816		
HLA B*0802	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.475221	0.373143	-4.102078	29869.0561	
HLA B*3801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.336132	0.234045	-4.102087	21683.6299	
HLA B*3901	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.286241	0.183904	-4.102336	19330.392526		
HLA A*2301	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.549174	0.446772	-4.102402	35413.9107	
HLA A*0202	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.162846	0.060047	-4.102799	14549.421332		
HLA B*4601	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.410961	0.308151	-4.102810	25760.882387		
HLA B*5401	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.462703	0.359849	-4.102855	29020.4032	
HLA A*0101	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.402498	0.299515	-4.102983	25263.754350		
HLA A*3101	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.425861	0.322700	-4.103161	26660.0628	
HLA B*4601	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.403654	0.300329	-4.103325	25331.0875	
HLA B*5801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.367314	0.263887	-4.103427	23297.7699	
HLA B*4801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.426618	0.322700	-4.103917	26706.5447	
HLA B*4801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.338077	0.234045	-4.104032	21780.9772	
HLA A*3101	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.288444	0.183904	-4.104540	19428.733443		
HLA A*0202	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.564166	0.459518	-4.104648	36657.762474		
HLA A*0101	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.368576	0.263887	-4.104689	23365.5509	
HLA B*5401	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.523048	0.418270	-4.104778	33346.2971	
HLA A*0101	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.330622	0.225691	-4.104932	21410.284817		
HLA B*5701	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.405343	0.300329	-4.105014	25429.8100	
HLA B*4402	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.434477	0.329388	-4.105089	27194.2277	
HLA B*4403	1:149-157	9	KLEAKFADQ	0.547523	0.012288	-4.665048	0.559811	-4.105237	46243.2277	
HLA A*0212	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.428016	0.322700	-4.105315	26792.6484	
HLA A*0250	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.289356	0.183904	-4.105452	19469.557904		
HLA A*2601	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.405855	0.300329	-4.105526	25459.8185	
HLA A*3101	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.375340	0.269704	-4.105636	23732.3198	
HLA B*1502	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.556789	0.451144	-4.105645	36040.3143	
HLA A*0203	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.395750	0.290041	-4.105710	24874.2599	
HLA A*0201	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.381012	0.275281	-4.105731	24044.284027		
HLA A*2602	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.469952	0.364143	-4.105809	29508.8037	
HLA A*8001	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.422736	0.316807	-4.105930	26468.928065		
HLA A*0203	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.428676	0.322700	-4.105976	26833.4090	
HLA A*2403	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.414144	0.308151	-4.105994	25950.413776		
HLA A*3301	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.618075	0.511996	-4.106079	41502.5600	
HLA B*1502	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.599974	0.493735	-4.106240	39808.3753	
HLA A*0219	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.435647	0.329388	-4.106259	27267.5911	
HLA A*0201	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.396497	0.290041	-4.106457	24917.0890	
HLA B*5701	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.414781	0.308151	-4.106630	25988.487060		
HLA A*3101	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.166689	0.060047	-4.106642	14678.763663		
HLA B*0702	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.406161	0.299515	-4.106646	25477.730358		
HLA B*4402	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.340810	0.234045	-4.106765	21918.4486	
HLA B*4601	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.396932	0.290041	-4.106891	24942.0393	
HLA B*1801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.480193	0.373143	-4.107050	30212.9414	
HLA B*5301	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.558342	0.451144	-4.107198	36169.4229	
HLA A*3002	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.557263	0.449835	-4.107428	36079.7206	
HLA A*0202	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.275139	0.167651	-4.107489	18842.536115		
HLA A*3301	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.480642	0.373143	-4.107498	30244.1763	
HLA A*2601	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.377398	0.269704	-4.107694	23845.0557	
HLA B*1501	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.275435	0.167651	-4.107785	18855.384433		
HLA A*3301	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.612051	0.504252	-4.107799	40930.854059		
HLA A*2301	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.524298	0.416215	-4.108083	33442.4080	
HLA B*5101	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.488611	0.380508	-4.108103	30804.2907	
HLA A*0216	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.144294	0.035827	-4.108468	13941.008342		
HLA A*2602	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.612732	0.504252	-4.108480	40995.119559		
HLA A*3201	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.425579	0.316807	-4.108773	26642.761096		
HLA B*4801	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.425854	0.316807	-4.109048	26659.630158		
HLA A*2902	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.440677	0.331331	-4.109346	27585.256155		
HLA B*3501	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.373576	0.264217	-4.109358	23636.0951	
HLA A*2902	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.384644	0.275281	-4.109364	24246.226246		
HLA B*3801	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.556488	0.446772	-4.109715	36015.3662	
HLA A*3001	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.267417	0.157520	-4.109896	18510.4339	
HLA B*7301	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.054502	-0.055989	-4.110490	11337.089346		
HLA B*0801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.418691	0.308151	-4.110540	26223.493045		
HLA B*0801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.440191	0.329388	-4.110803	27554.3821	
HLA A*0301	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.366332	0.255019	-4.111313	23245.1454	
HLA A*6901	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.375848	0.264217	-4.111630	23760.0681	
HLA A*8001	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.337405	0.225691	-4.111715	21747.303122		
HLA A*3201	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.412067	0.300329	-4.111738	25826.6063	
HLA B*0803	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.376198	0.263887			
HLA B*5701	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.402524	0.290041			

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HLA A*0216	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.296686	0.183904	-4.112782	19800.970798
HLA A*0301	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.346956	0.234045	-4.112911	22230.8497
HLA B*4001	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.368003	0.255019	-4.112984	23334.7284
HLA A*3101	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.412556	0.299515	-4.113041	25855.684228
HLA A*3002	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.280813	0.167651	-4.113163	19090.326784
HLA B*4402	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.435922	0.322700	-4.113221	27284.8558
HLA A*3002	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.430172	0.316807	-4.113366	26926.039198
HLA A*3301	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.607169	0.493735	-4.113434	40473.2963
HLA B*0702	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.412370	0.298936	-4.113435	25844.636355
HLA A*0202	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.563527	0.449835	-4.113691	36603.8606
HLA B*4001	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.377871	0.263887	-4.113984	23870.9986
HLA B*3501	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.281669	0.167651	-4.114018	19127.956487
HLA B*3801	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.573557	0.459518	-4.114039	37459.057364
HLA B*2705	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.487211	0.373143	-4.114068	30705.1286
HLA A*1101	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.445623	0.331331	-4.114292	27901.187463
HLA B*5401	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.494868	0.380508	-4.114360	31251.2859
HLA A*0216	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.437099	0.322700	-4.114398	27358.9077
HLA A*0211	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.413623	0.298936	-4.114687	25919.266156
HLA B*3901	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.404890	0.290041	-4.114849	25403.2724
HLA A*2402	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.574398	0.459518	-4.114880	37531.676130
HLA B*2705	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.415448	0.300329	-4.115119	26028.4466
HLA A*0101	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.379565	0.264217	-4.115347	23964.2900
HLA B*3501	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.379271	0.263887	-4.115384	23948.0899
HLA B*1509	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.415951	0.300329	-4.115622	26058.5976
HLA B*1517	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.175744	0.060047	-4.115697	14988.024465
HLA B*2705	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.324582	0.208763	-4.115819	21114.5543
HLA B*3901	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.489032	0.373143	-4.115888	30834.1351
HLA B*1503	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.300340	0.183904	-4.116435	19968.246649
HLA A*3301	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.567627	0.451144	-4.116483	36951.0466
HLA B*4601	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.380516	0.263887	-4.116629	24016.8534
HLA B*0801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.274277	0.157520	-4.116757	18805.1627
HLA B*0803	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.497481	0.380508	-4.116973	31439.8539
HLA B*1801	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.342760	0.225691	-4.117069	22017.088301
HLA A*3201	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.576726	0.459518	-4.117209	37733.431299
HLA A*2501	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.497725	0.380508	-4.117217	31457.5478
HLA A*0211	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.497894	0.380508	-4.117386	31469.8033
HLA A*2601	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.381646	0.264217	-4.117429	24079.4304
HLA A*0203	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.246250	0.128565	-4.117685	17629.9097
HLA A*0212	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.418216	0.300329	-4.117887	26194.8517
HLA B*2705	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.387647	0.269704	-4.117943	24414.4415
HLA A*0250	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.596838	0.478869	-4.117969	39521.9069
HLA B*2705	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.343787	0.225691	-4.118096	22069.200950
HLA A*0201	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.387879	0.269704	-4.118175	24427.5209
HLA A*3201	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.246915	0.128565	-4.118350	17656.9217
HLA A*3201	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.382410	0.263887	-4.118523	24121.8044
HLA A*0212	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.426808	0.308151	-4.118657	26718.250122
HLA B*5301	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.597536	0.478869	-4.118667	39585.4593
HLA B*0801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.419057	0.300329	-4.118728	26245.6335
HLA A*6901	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.382617	0.263887	-4.118730	24133.2908
HLA A*2403	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.419492	0.300329	-4.119163	26271.9140
HLA B*4601	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.374480	0.255019	-4.119461	23685.3758
HLA A*2601	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.394787	0.275281	-4.119506	24819.148644
HLA A*2603	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.624350	0.504252	-4.120099	42106.618033
HLA B*5701	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.345934	0.225691	-4.120243	22178.595410
HLA B*4601	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.390182	0.269704	-4.120478	24557.3720
HLA B*4002	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.262558	0.141991	-4.120567	18304.4997
HLA A*0219	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.443348	0.322700	-4.120648	27755.4571
HLA B*3501	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.452326	0.331331	-4.120995	28335.166424
HLA B*5701	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.420636	0.299515	-4.121121	26341.221730
HLA B*4801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.429449	0.308151	-4.121298	26881.211155
HLA B*4001	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.385570	0.264217	-4.121352	24297.9621
HLA A*0212	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.305267	0.183904	-4.121362	20196.066988
HLA A*2402	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.571431	0.449835	-4.121595	37276.1079
HLA B*5101	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.451137	0.329388	-4.121749	28257.7076
HLA A*3001	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.263892	0.142013	-4.121879	18360.832624
HLA A*8001	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.430156	0.308151	-4.122006	26925.019549
HLA A*0203	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.356063	0.234045	-4.122018	22701.9241
HLA B*0803	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.495399	0.373143	-4.122256	31289.5182
HLA A*0201	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.386397	0.263887	-4.122510	24344.2763
HLA B*5801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.356594	0.234045	-4.122549	22729.6972
HLA A*3002	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.582074	0.459518	-4.122556	38200.911670
HLA A*0250	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.495815	0.373143	-4.122671	31319.4938
HLA A*3101	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.251360	0.128565	-4.122796	17838.5774
HLA B*4001	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.422337	0.299515	-4.122822	26444.596281
HLA A*0250	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.452213	0.329388	-4.122825	28327.8094
HLA B*1501	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.398198	0.275281	-4.122918	25014.874727
HLA A*6801	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.635238	0.511996	-4.123242	43175.5495
HLA A*6802	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.398661	0.275281	-4.123381	25041.548495
HLA B*1801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.280975	0.157520	-4.123455	19097.4541
HLA B*4601	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.349442	0.225691	-4.123751	22358.456525
HLA B*7301	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.575014	0.451144	-4.123870	37584.9109
HLA B*4002	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.602836	0.478869	-4.123967	40071.5486
HLA B*1502	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.570763	0.446772	-4.123991	37218.8805
HLA B*0702	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.358100	0.234045	-4.124055	22808.6547
HLA B*0702	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.291757	0.167651	-4.124107	19577.501403
HLA B*1509	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.540509	0.416215	-4.124294	34714.3460
HLA A*8001	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.455700	0.331331	-4.124369	28556.148270
HLA A*6801	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.628692	0.504252	-4.124440	42529.689198
HLA B*4601	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.424000	0.299515	-4.124485	26546.078639
HLA B*3801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.540836	0.416215	-4.124621	34740.4601
HLA B*1517	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.292361	0.167651	-4.124711	19604.739747
HLA A*0212	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.414755	0.290041	-4.124715	25986.9405
HLA A*6801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.394987	0.269704	-4.125283	24830.5641
HLA A*0219	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.424303	0.298936	-4.125368	26564.610968
HLA B*3501	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.304957	0.179565	-4.125392	20181.6500
HLA B*3901	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.424334	0.298936	-4.125398	26566.479284
HLA B*4402	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.425001	0.299515	-4.125486	26607.327621
HLA B*4501	1:49-57 9	KPNPKTATN	1.176697	-0.672445	-4.629970	0.504252	-4.125719	42655.037568
HLA B*0702	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.426286	0.300329	-4.125958	26686.1808
HLA B*4501	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.506674	0.380508	-4.126166	32112.4953
HLA B*4801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.416609	0.290041	-4.126568	26098.1003
HLA A*3101	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.317291	0.190565	-4.126727	20763.065154
HLA B*5101	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.486750	0.359849	-4.126902	30672.5880
HLA A*8001	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.417311	0.290041	-4.127271	26140.3496
HLA A*0216	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.391439	0.263887	-4.127552	24628.5511
HLA B*1502	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.587207	0.459518	-4.127690	38655.149056
HLA A*0101	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.382854	0.255019	-4.127835	24146.4808
HLA A*6802	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.428387	0.300329	-4.128058	26815.5596
HLA B*0702	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.324624	0.196360	-4.128264	21116.6105
HLA A*3101	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.383469	0.255019	-4.128450	24180.7301
HLA A*8001	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.428796	0.300329	-4.128467	26840.8135
HLA B*4002	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.644105	0.515530	-4.128575	44066.1218
HLA B*1501	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.398351	0.269704	-4.128647	25023.6725
HLA B*7301	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.578505	0.449835	-4.128669	37888.2773
HLA A*0250	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.579846	0.451144	-4.128703	38005.4966
HLA A*3101	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.327498	0.198739	
HLA A*0203	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.436913	0.308151	-4.1287	

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HLA B*4402	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.393051	0.264217	-4.128833	24720.1220
HLA A*2603	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.640900	0.511996	-4.128904	43742.1507
HLA B*0801	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.428420	0.299515	-4.128905	26817.590685
HLA A*6901	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.325353	0.196360	-4.128992	21152.0541
HLA B*1501	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.363238	0.234045	-4.129193	23080.1164
HLA A*2402	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.545711	0.416215	-4.129496	35132.6369
HLA B*7301	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.510450	0.380508	-4.129942	32392.8885
HLA B*0801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.399660	0.269704	-4.129956	25099.1903
HLA A*6802	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.438121	0.308151	-4.129970	27423.367360
HLA B*4501	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.576778	0.446772	-4.130006	37737.9225
HLA B*5701	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.394113	0.263887	-4.130226	24780.6433
HLA B*5301	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.503441	0.373143	-4.130298	31874.3372
HLA A*2301	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.548584	0.418270	-4.130315	35365.8555
HLA B*1801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.460020	0.329388	-4.130633	28841.6652
HLA B*1801	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.462043	0.331331	-4.130712	28976.320575
HLA A*3002	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.364758	0.234045	-4.130713	23161.0429
HLA A*0301	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.259854	0.128565	-4.131289	18190.8757
HLA A*6901	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.273335	0.142013	-4.131322	18764.411650
HLA A*0211	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.495829	0.364143	-4.131686	31320.5104
HLA B*4402	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.448588	0.316807	-4.131781	28092.328429
HLA B*1502	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.610796	0.478869	-4.131928	40812.7803
HLA A*6802	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.274016	0.142013	-4.132003	18793.873638
HLA B*1501	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.431787	0.299515	-4.132272	27026.298546
HLA A*2501	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.463787	0.331331	-4.132456	29092.869282
HLA A*0212	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.432040	0.299515	-4.132525	27042.093762
HLA B*0801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.397797	0.264217	-4.133579	24991.7443
HLA A*0202	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.551930	0.418270	-4.133660	35639.3549
HLA A*0250	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.593238	0.459518	-4.133721	39195.704992
HLA B*1517	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.388873	0.255019	-4.133854	24483.4844
HLA A*8001	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.403698	0.269704	-4.133995	25333.6914
HLA B*4002	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.638567	0.504252	-4.134315	43507.797090
HLA B*1503	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.552590	0.418270	-4.134320	35693.5743
HLA B*7301	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.581164	0.446772	-4.134392	38121.0168
HLA B*4801	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.433948	0.299515	-4.134433	27161.146380
HLA B*5301	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.553194	0.418270	-4.134924	35743.2351
HLA A*0219	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.410303	0.275281	-4.135022	25721.890142
HLA B*1502	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.464520	0.329388	-4.135132	29142.0161
HLA B*1509	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.508645	0.373143	-4.135502	32258.5819
HLA A*0216	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.434733	0.298936	-4.135797	27210.268302
HLA A*2601	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.399979	0.263887	-4.136092	25117.6637
HLA A*8001	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.435405	0.298936	-4.136469	27252.401385
HLA B*0702	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.459198	0.322700	-4.136498	28787.1062
HLA A*2402	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.583434	0.446772	-4.136662	38320.7569
HLA B*0702	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.444838	0.308151	-4.136687	27850.818245
HLA A*3301	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.320609	0.183904	-4.136704	20922.276613
HLA B*4501	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.652464	0.515530	-4.136934	44922.5393
HLA A*2403	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.304127	0.167005	-4.137122	20143.1460
HLA B*1517	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.468634	0.331331	-4.137303	29419.381846
HLA A*6802	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.165256	0.027900	-4.137357	14630.403107
HLA B*5701	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.393060	0.255019	-4.138041	24720.6569
HLA B*1502	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.588086	0.449835	-4.138251	38733.4391
HLA A*3301	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.597787	0.459518	-4.138269	39608.380301
HLA B*5701	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.413672	0.275281	-4.138391	25922.210951
HLA B*1509	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.519058	0.380508	-4.138550	33041.3809
HLA A*2501	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.393643	0.255019	-4.138624	24753.8457
HLA A*0203	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.408484	0.269704	-4.138780	25614.4112
HLA B*4002	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.650951	0.511996	-4.138955	44766.3029
HLA A*3001	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.280992	0.141991	-4.139001	19098.1774
HLA A*3301	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.586347	0.446772	-4.139575	38578.6868
HLA B*3901	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.403677	0.263887	-4.139790	25332.4580
HLA B*1517	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.448249	0.308151	-4.140099	28070.452352
HLA B*5701	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.410169	0.269704	-4.140465	25713.9596
HLA A*6802	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.440083	0.299515	-4.140568	27547.525987
HLA A*0301	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.339438	0.198739	-4.140698	21849.3092
HLA A*0216	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.415998	0.275281	-4.140717	26061.417323
HLA B*5401	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.557169	0.416215	-4.140955	36071.9139
HLA B*0803	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.501585	0.359849	-4.141737	31738.4030
HLA A*2603	1:179-187	9	TETRIVVTG	1.116102	-0.622367	-4.635553	0.493735	-4.141818	43206.8599
HLA A*8001	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.405933	0.263887	-4.142046	25464.3641
HLA A*2501	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.464809	0.322700	-4.142108	29161.4142
HLA B*2705	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.464856	0.322700	-4.142155	29164.5695
HLA A*3301	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.299774	0.157520	-4.142253	19942.2293
HLA B*4601	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.417654	0.275281	-4.142374	26161.004626
HLA B*3901	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.459278	0.316807	-4.142471	28792.401774
HLA A*3201	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.506622	0.364143	-4.142480	32108.6736
HLA A*0219	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.450653	0.308151	-4.142502	28226.233797
HLA A*2902	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.465403	0.322700	-4.142703	29201.3548
HLA A*6901	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.376752	0.234045	-4.142707	23809.6073
HLA A*2902	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.406624	0.263887	-4.142737	25504.8976
HLA B*5801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.351594	0.208763	-4.142831	22469.5279
HLA A*3001	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.269963	0.127125	-4.142838	18619.303919
HLA A*8001	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.465619	0.322700	-4.142919	29215.8922
HLA B*0802	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.474303	0.331331	-4.142972	29805.941895
HLA B*0801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.377025	0.234045	-4.142980	23824.5536
HLA A*2501	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.472456	0.329388	-4.143069	29679.4709
HLA A*2603	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.622071	0.478869	-4.143203	41886.2383
HLA A*2402	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.561664	0.418270	-4.143394	36447.1648
HLA A*0202	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.516857	0.373143	-4.143713	32874.3158
HLA A*3101	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.408057	0.264217	-4.143839	25589.2036
HLA A*2301	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.517016	0.373143	-4.143873	32886.4115
HLA A*3301	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.622807	0.478869	-4.143938	41957.2242
HLA A*1101	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.452100	0.308151	-4.143950	28320.454394
HLA A*2602	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.442933	0.298936	-4.143997	27728.892670
HLA B*4403	1:82-90	9	ITGISRSCT	0.910830	-0.399571	-4.655284	0.511259	-4.144025	45215.119211
HLA B*3901	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.369765	0.225691	-4.144074	23429.599493
HLA B*5301	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.603804	0.459518	-4.144286	40160.962660
HLA A*2501	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.443301	0.298936	-4.144366	27752.454282
HLA A*0201	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.408672	0.264217	-4.144455	25625.4993
HLA A*2603	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.370430	0.225691	-4.144739	23465.497651
HLA B*3501	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.172714	0.027900	-4.144814	14883.790818
HLA B*4403	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.623974	0.478869	-4.145106	42070.1870
HLA A*2402	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.435353	0.290041	-4.145312	27249.1580
HLA B*4001	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.371071	0.225691	-4.145381	23500.179442
HLA A*0201	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.400755	0.255019	-4.145735	25162.5454
HLA B*1501	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.344994	0.198739	-4.146255	22130.6538
HLA B*3501	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.416010	0.269704	-4.146306	26062.1222
HLA B*0802	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.476032	0.329388	-4.146645	29924.8561
HLA B*4402	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.416646	0.269704	-4.146943	26100.3594
HLA B*1517	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.381808	0.234045	-4.147763	24088.4205
HLA B*3501	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.455935	0.308151	-4.147784	28571.601009
HLA A*2602	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.597670	0.449835	-4.147834	39597.6679
HLA B*0801	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.338418	0.190565	-4.147853	21798.069649
HLA B*5101	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.464733	0.316807	-4.147927	29156.366321
HLA B*4402	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.411908	0.263887	-4.148021	25817.1071
HLA B*4601	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.382109	0.234045	-4.148064	24105.1065
HLA B*0803	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.512454	0.364143		
HLA B*3501	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.423702	0.275281	-4.1484	

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HLA B*4501	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.660871	0.511996	-4.148875	45800.5565
HLA B*4801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.418902	0.269704	-4.149198	26236.2641
HLA A*6802	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.419165	0.269704	-4.149461	26252.1656
HLA A*2403	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.404634	0.255019	-4.149614	25388.2970
HLA B*7301	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.565907	0.416215	-4.149692	36805.0084
HLA B*4001	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.383822	0.234045	-4.149777	24200.3603
HLA A*2602	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.566245	0.416215	-4.150031	36833.6915
HLA B*1801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.405721	0.255019	-4.150702	25451.9688
HLA A*2602	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.610232	0.459518	-4.150715	40759.824490
HLA A*0301	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.292732	0.142013	-4.150719	19621.504307
HLA B*2705	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.480153	0.329388	-4.150766	30210.1629
HLA B*4801	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.426190	0.275281	-4.150909	26680.262404
HLA A*6901	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.359866	0.208763	-4.151104	22901.6347
HLA B*0801	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.376910	0.225691	-4.151219	23818.238994
HLA A*1101	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.474068	0.322700	-4.151368	29789.8215
HLA B*1501	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.187266	0.035827	-4.151440	15390.979785
HLA B*5801	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.342071	0.190565	-4.151507	21982.216714
HLA A*0212	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.426871	0.275281	-4.151591	26722.153062
HLA A*0250	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.569873	0.418270	-4.151603	37142.6470
HLA B*1801	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.468434	0.316807	-4.151627	29405.856730
HLA B*4601	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.415862	0.264217	-4.151644	26053.2412
HLA A*2602	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.309195	0.157520	-4.151675	20379.5758
HLA B*4002	1:58-66	9	AGYLRHIID	1.158754	-0.699236	-4.611334	0.459518	-4.151816	40863.373174
HLA B*1509	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.442042	0.290041	-4.152001	27672.0970
HLA B*4403	1:49-57	9	KPNPKTATN	1.176697	-0.672445	-4.656343	0.504252	-4.152092	45325.572462
HLA A*0202	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.568402	0.416215	-4.152188	37017.0729
HLA A*0201	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.386907	0.234045	-4.152862	24372.8719
HLA B*5401	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.482888	0.329388	-4.153500	30400.9999
HLA A*0216	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.453200	0.299515	-4.153685	28392.247763
HLA A*2403	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.379379	0.225691	-4.153688	23954.050314
HLA A*2301	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.534205	0.380508	-4.153698	34214.1157
HLA A*2403	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.418084	0.264217	-4.153867	26186.9170
HLA B*4402	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.409060	0.255019	-4.154041	25648.3836
HLA B*1509	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.514230	0.359849	-4.154381	32676.0836
HLA B*1517	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.444450	0.290041	-4.154410	27825.9688
HLA B*1501	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.418669	0.264217	-4.154452	26222.2162
HLA A*2902	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.453994	0.299515	-4.154479	28444.211690
HLA A*3101	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.363454	0.208763	-4.154692	23091.6064
HLA A*2902	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.455049	0.300329	-4.154720	28513.3878
HLA A*0219	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.455101	0.300329	-4.154772	28516.7816
HLA B*5801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.334365	0.179565	-4.154800	21595.5950
HLA B*5801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.351202	0.196360	-4.154841	22449.2369
HLA B*4403	1:115-123	9	RVVVPPGME	0.970430	-0.454900	-4.670377	0.515530	-4.154847	46814.1100
HLA B*3801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.535535	0.380508	-4.155027	34319.0398
HLA A*2403	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.454779	0.299515	-4.155264	28495.654083
HLA A*0212	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.419485	0.264217	-4.155267	26271.4876
HLA A*3002	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.571701	0.416215	-4.155486	37299.3059
HLA A*0216	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.463674	0.308151	-4.155523	29085.315581
HLA B*5701	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.389630	0.234045	-4.155585	24526.1714
HLA B*5401	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.454748	0.298936	-4.155813	28493.650095
HLA B*0802	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.455528	0.298936	-4.156593	28544.873048
HLA A*2601	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.391004	0.234045	-4.156959	24603.9145
HLA B*3901	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.479716	0.322700	-4.157016	30179.7796
HLA B*7301	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.488682	0.331331	-4.157351	30809.290609
HLA B*1503	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.447641	0.290041	-4.157600	28031.1486
HLA A*0212	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.366407	0.208763	-4.157645	23249.1698
HLA B*3801	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.576036	0.418270	-4.157766	37673.4636
HLA A*0201	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.341691	0.183904	-4.157786	21962.959894
HLA A*0301	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.366896	0.208763	-4.158134	23275.3458
HLA B*4001	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.325919	0.167651	-4.158268	21179.649839
HLA A*2501	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.458620	0.300329	-4.158291	28748.8209
HLA B*4601	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.342292	0.183904	-4.158388	21993.398164
HLA B*2705	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.422353	0.263887	-4.158467	26445.5977
HLA B*0802	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.448931	0.290041	-4.158890	28114.5257
HLA A*2601	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.316718	0.157520	-4.159198	20735.6757
HLA B*0803	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.449525	0.290041	-4.159485	28153.0324
HLA A*6801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.339076	0.179565	-4.159511	21831.1137
HLA A*2402	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.523666	0.364143	-4.159523	33393.7760
HLA A*1101	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.449713	0.290041	-4.159672	28165.2195
HLA B*0802	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.460192	0.300329	-4.159863	28853.0576
HLA A*0203	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.350520	0.190565	-4.159956	22414.044671
HLA A*0250	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.576402	0.416215	-4.160188	37705.2713
HLA B*1801	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.459337	0.298936	-4.160401	28796.296130
HLA A*0219	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.450700	0.290041	-4.160659	28229.2879
HLA B*0803	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.492070	0.331331	-4.160739	31050.575654
HLA A*0101	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.394965	0.234045	-4.160920	24829.3551
HLA A*3201	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.610761	0.449835	-4.160925	40809.4685
HLA B*1501	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.221057	0.060047	-4.161009	16636.293018
HLA A*3101	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.436432	0.275281	-4.161151	27316.905593
HLA B*3501	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.395710	0.234045	-4.161665	24871.9724
HLA A*0212	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.431460	0.269704	-4.161756	27005.9830
HLA B*4501	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.521685	0.359849	-4.161836	33241.8292
HLA A*6802	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.426084	0.264217	-4.161867	26673.7680
HLA B*5701	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.426145	0.264217	-4.161928	26677.5201
HLA B*5101	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.484784	0.322700	-4.162084	30534.0141
HLA A*3002	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.491691	0.329388	-4.162304	31023.5426
HLA B*4403	1:117-125	9	VVPPGMEDD	1.199814	-0.687818	-4.674639	0.511996	-4.162643	47275.7837
HLA B*1502	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.388624	0.225691	-4.162934	24469.448484
HLA B*2705	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.346918	0.183904	-4.163014	22228.925619
HLA A*2402	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.543523	0.380508	-4.163016	34956.1325
HLA A*0203	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.361983	0.198739	-4.163244	23013.5369
HLA A*6802	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.427182	0.263887	-4.163295	26741.2423
HLA B*0801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.330397	0.167005	-4.163392	21399.1682
HLA A*0203	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.462978	0.299515	-4.163463	29038.777746
HLA A*0250	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.494821	0.331331	-4.163490	31247.904814
HLA B*1503	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.418514	0.255019	-4.163495	26212.8552
HLA A*8001	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.427760	0.264217	-4.163542	26776.8541
HLA B*5301	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.360064	0.196360	-4.163704	22912.0443
HLA A*0216	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.464092	0.300329	-4.163763	29113.3370
HLA A*8001	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.439834	0.275281	-4.164553	27531.733435
HLA A*8001	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.464106	0.299515	-4.164591	29114.282089
HLA A*6802	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.200663	0.035827	-4.164836	15873.146745
HLA B*1509	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.529239	0.364143	-4.165096	33825.0547
HLA A*1101	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.429623	0.263887	-4.165736	26891.9747
HLA A*0212	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.421428	0.255019	-4.166409	26389.2890
HLA A*3002	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.465488	0.298936	-4.166552	29207.042510
HLA A*2403	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.441948	0.275281	-4.166667	27666.109565
HLA B*2705	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.456762	0.290041	-4.166721	28626.0612
HLA A*0301	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.363090	0.196360	-4.166730	23072.2515
HLA B*3901	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.496273	0.329388	-4.166885	31352.5511
HLA A*2603	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.585210	0.418270	-4.166941	38477.8050
HLA A*1101	1:60-68	9	YLRHIIDVG	0.914107	-0.597300	-4.483792	0.316807	-4.166986	30464.385364
HLA A*2402	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.526880	0.359849	-4.167031	33641.8310
HLA B*1502	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.540267	0.373143	-4.167124	34695.0079
HLA A*2403	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.436845	0.269704	-4.167141	27342.9275
HLA A*3201	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.457565	0.290041		
HLA A*0212	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.401669	0.234045		

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HLA B*5101	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.498998	0.331331	-4.167668	31549.921815		
HLA A*6901	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.351610	0.183904	-4.167706	22470.378825		
HLA B*5801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.366471	0.198739	-4.167731	23252.5660	
HLA A*2402	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.540901	0.373143	-4.167758	34745.7229	
HLA B*1501	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.347621	0.179565	-4.168056	22264.9112	
HLA B*4001	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.376961	0.208763	-4.168199	23821.0739	
HLA B*5301	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.584491	0.416215	-4.168277	38414.1605	
HLA B*4002	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.476514	0.308151	-4.168363	29958.062044		
HLA B*1502	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.532594	0.364143	-4.168451	34087.3761	
HLA A*8001	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.364845	0.196360	-4.168485	23165.6794	
HLA A*0219	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.432461	0.263887	-4.168574	27068.2932	
HLA A*2501	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.326156	0.157520	-4.168636	21191.2259	
HLA B*0803	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.438621	0.269704	-4.168917	27454.9856	
HLA B*4801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.424311	0.255019	-4.169291	26565.0421	
HLA B*1502	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.459482	0.290041	-4.169442	28805.9564	
HLA B*5801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.353441	0.183904	-4.169536	22565.275646		
HLA B*1801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.469966	0.300329	-4.169637	29509.7616	
HLA B*0801	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.445364	0.275281	-4.170084	27884.588746		
HLA B*1801	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.470048	0.299515	-4.170533	29515.349701		
HLA B*1509	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.277754	0.107209	-4.170546	18956.3331	
HLA B*0702	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.446149	0.275281	-4.170868	27935.019040		
HLA B*0802	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.493836	0.322700	-4.171136	31177.1540	
HLA B*3801	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.544332	0.373143	-4.171188	35021.2465	
HLA A*2301	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.535904	0.364143	-4.171761	34348.2011	
HLA A*0206	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.300439	0.128565	-4.171874	19972.7842	
HLA B*3501	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.472451	0.300329	-4.172123	29679.1498	
HLA B*1503	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.447432	0.275281	-4.172151	28017.655470		
HLA B*1801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.406497	0.234045	-4.172452	25497.4479	
HLA B*5101	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.471505	0.298936	-4.172569	29614.514270		
HLA A*0301	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.339924	0.167005	-4.172919	21873.7908	
HLA A*2902	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.363644	0.190565	-4.173080	23101.727479		
HLA A*2601	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.315240	0.142013	-4.173227	20665.235857		
HLA A*2301	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.533172	0.359849	-4.173323	34132.7709	
HLA B*4501	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.624477	0.451144	-4.173334	42118.9206	
HLA A*0219	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.472870	0.299515	-4.173355	29707.743440		
HLA B*0702	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.352931	0.179565	-4.173366	22538.8007	
HLA B*3901	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.481650	0.308151	-4.173499	30314.449785		
HLA A*3002	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.537751	0.364143	-4.173608	34494.5666	
HLA B*1801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.372666	0.198739	-4.173927	23586.6617	
HLA B*5401	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.505295	0.331331	-4.173964	32010.680533		
HLA A*3101	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.341188	0.167005	-4.174183	21937.5477	
HLA A*3002	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.592454	0.418270	-4.174184	39124.9461	
HLA B*0802	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.482855	0.308151	-4.174704	30398.697514		
HLA B*7301	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.491513	0.316807	-4.174706	31010.789864		
HLA B*0803	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.429801	0.255019	-4.174782	26903.0336	
HLA B*4801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.439115	0.264217	-4.174897	27486.1943	
HLA B*5101	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.371320	0.196360	-4.174960	23513.6594	
HLA B*1501	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.359054	0.183904	-4.175149	22858.807097		
HLA A*2501	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.439328	0.263887	-4.175442	27499.7291	
HLA B*0702	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.401166	0.225691	-4.175475	25186.378861		
HLA B*1517	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.475835	0.300329	-4.175506	29911.2604	
HLA B*5401	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.401485	0.225691	-4.175795	25204.916430		
HLA A*6802	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.410479	0.234045	-4.176434	25732.3287	
HLA B*4403	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.484739	0.308151	-4.176589	30530.875824		
HLA A*0203	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.431864	0.255019	-4.176845	27031.1238	
HLA B*4403	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-3.980291	-0.196676	-4.176967	9556.32114	
HLA A*2501	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.485280	0.308151	-4.177129	30568.888259		
HLA A*0301	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.361725	0.183904	-4.177820	22999.845947		
HLA A*0206	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.478158	0.300329	-4.177829	30071.7259	
HLA B*0802	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.442270	0.263887	-4.178383	27686.6220	
HLA B*4001	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.453771	0.275281	-4.178490	28429.596843		
HLA B*4403	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.477679	0.298936	-4.178744	30038.556610		
HLA B*0702	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.434284	0.255019	-4.179265	27182.1667	
HLA A*0101	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.388222	0.208763	-4.179460	24446.8224	
HLA B*0801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.363431	0.183904	-4.179526	23090.357300		
HLA B*4801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.346712	0.167005	-4.179707	22218.3456	
HLA A*2601	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.347363	0.167651	-4.179712	22251.665631		
HLA A*2501	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.413855	0.234045	-4.179810	25933.1516	
HLA A*0301	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.359404	0.179565	-4.179839	22877.2404	
HLA B*0702	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.449614	0.269704	-4.179910	28158.8206	
HLA B*5801	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.347948	0.167651	-4.180297	22281.660211		
HLA B*5701	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.347461	0.167005	-4.180456	22256.7221	
HLA A*3201	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.598844	0.418270	-4.180575	39704.9223	
HLA B*4002	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.632919	0.451144	-4.181775	42945.6254	
HLA B*1517	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.407671	0.225691	-4.181981	25566.510463		
HLA B*4403	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.641605	0.459518	-4.182087	43813.200451		
HLA B*5401	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.366184	0.183904	-4.182280	23237.224277		
HLA B*3901	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.481990	0.299515	-4.182475	30338.238797		
HLA A*6801	1:129-137	9	RHILTEAAD	1.107553	-0.628684	-4.661728	0.478869	-4.182860	45891.0841	
HLA A*1101	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.483250	0.300329	-4.182921	30426.3382	
HLA B*5701	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.362564	0.179565	-4.182999	23044.3091	
HLA B*4002	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.632879	0.449835	-4.183044	42941.6760	
HLA B*3501	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.366957	0.183904	-4.183053	23278.619961		
HLA B*0803	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.512496	0.329388	-4.183109	32545.8844	
HLA A*0219	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.447368	0.264217	-4.183151	28013.5633	
HLA A*0301	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.351021	0.167651	-4.183370	22439.887405		
HLA A*0201	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.392494	0.208763	-4.183731	24688.4476	
HLA A*0212	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.219816	0.035827	-4.183989	16588.840558		
HLA A*0101	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.383007	0.198739	-4.184267	24154.9733	
HLA A*2501	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.483856	0.299515	-4.184341	30468.835530		
HLA A*2902	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.364002	0.179565	-4.184437	23120.7319	
HLA B*0802	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.484540	0.299515	-4.185025	30516.839716		
HLA A*2402	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.484023	0.298936	-4.185087	30480.540923		
HLA A*3201	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.419149	0.234045	-4.185104	26251.1715	
HLA A*2601	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.375838	0.190565	-4.185274	23759.553971		
HLA A*2403	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.394122	0.208763	-4.185359	24781.1796	
HLA B*5701	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.384545	0.198739	-4.185806	24240.7177	
HLA B*2705	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.494086	0.308151	-4.185935	31195.037656		
HLA B*4001	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.353140	0.167005	-4.186135	22549.6553	
HLA A*0206	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.394923	0.208763	-4.186161	24826.9374	
HLA A*1101	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.485726	0.299515	-4.186211	30600.325529		
HLA A*2902	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.420366	0.234045	-4.186321	26324.8389	
HLA B*1801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.494901	0.308151	-4.186750	31253.652964		
HLA A*0216	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.476988	0.290041	-4.186948	29990.8180	
HLA B*7301	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.605303	0.418270	-4.187033	40299.8180	
HLA B*0803	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.509872	0.322700	-4.187171	32349.8077	
HLA B*3901	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.457128	0.269704	-4.187424	28650.2301	
HLA A*2601	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.396199	0.208763	-4.187436	24899.9755	
HLA A*3101	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.367225	0.179565	-4.187660	23292.9809	
HLA B*4403	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.634660	0.446772	-4.187888	43118.1283	
HLA A*8001	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.443036	0.255019	-4.188017	27735.4939	
HLA B*5801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.345967	0.157520	-4.188447	22180.2752	
HLA B*1517	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.511803	0.322700	-4.189103	32493.9853	
HLA A*3002	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.570258	0.380508	-4.189750	37175.6154	
HLA B*0801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.388598	0.198739	-4.189859	24467.9923	
HLA B*4002	1:231-239	9	EVTTLADGT	0.843460	-0.396688	-4.636986	0.446772			
HLA B*1801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.454144	0.263887			

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HLA B*1502	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.606750	0.416215	-4.190536	40434.3409
HLA A*8001	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.424684	0.234045	-4.190639	26587.9024
HLA A*2601	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.387008	0.196360	-4.190647	24378.5423
HLA B*4501	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.640616	0.449835	-4.190780	43713.5266
HLA A*2603	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.650571	0.459518	-4.191053	44727.086904	
HLA A*2301	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.507861	0.316807	-4.191054	32200.346479	
HLA A*3001	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.298322	0.107209	-4.191113	19875.6675
HLA B*4002	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.466488	0.275281	-4.191208	29274.431055	
HLA A*0219	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.400019	0.208763	-4.191257	25119.9738
HLA A*0101	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.370895	0.179565	-4.191330	23490.6463
HLA B*3901	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.318501	0.127125	-4.191376	20820.993642	
HLA B*4601	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.358445	0.167005	-4.191440	22826.8006
HLA B*5301	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.555750	0.364143	-4.191607	35954.2387
HLA A*2902	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.251933	0.060047	-4.191886	17862.140165	
HLA B*5101	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.467217	0.275281	-4.191936	29323.567389	
HLA A*3301	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.641774	0.449835	-4.191939	43830.2695
HLA A*0101	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.388420	0.196360	-4.192059	24457.9343
HLA A*2403	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.064562	-0.127574	-4.192137	11602.780170	
HLA B*1503	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.417856	0.225691	-4.192166	26173.178877	
HLA B*0801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.401358	0.208763	-4.192596	25197.5542
HLA B*3801	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.552489	0.359849	-4.192640	35685.2720
HLA A*0206	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.515360	0.322700	-4.192660	32761.2226
HLA B*3801	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.557089	0.364143	-4.192947	36065.2796
HLA B*2705	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.492702	0.299515	-4.193187	31095.795215	
HLA B*3901	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.229357	0.035827	-4.193531	16957.322960	
HLA B*1801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.463331	0.269704	-4.193627	29062.3517
HLA B*4001	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.392372	0.198739	-4.193632	24681.5033
HLA B*1502	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.493973	0.300329	-4.193644	31186.9381
HLA A*6801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.377596	0.183904	-4.193691	23855.894106	
HLA A*0219	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.463528	0.269704	-4.193824	29075.5616
HLA B*5101	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.502133	0.308151	-4.193982	31778.434615	
HLA A*2603	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.643882	0.449835	-4.194046	44043.4803
HLA A*6802	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.373813	0.179565	-4.194248	23649.0134
HLA A*3301	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.511115	0.316807	-4.194308	32442.520035	
HLA B*1501	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.403245	0.208763	-4.194482	25307.2541
HLA A*1101	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.362258	0.167651	-4.194608	23028.108139	
HLA A*1101	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.469893	0.275281	-4.194612	29504.813047	
HLA B*0802	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.464463	0.269704	-4.194759	29138.2327
HLA B*4601	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.393631	0.198739	-4.194891	24753.1762
HLA A*2501	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.465436	0.269704	-4.195732	29203.5665
HLA A*2902	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.363398	0.167651	-4.195747	23088.608538	
HLA A*3001	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.206400	0.010485	-4.195915	16084.237365	
HLA B*1503	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.518821	0.322700	-4.196121	33023.3321
HLA B*4601	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.405059	0.208763	-4.196296	25413.1692
HLA A*0203	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.460610	0.264217	-4.196393	28880.8553
HLA A*0202	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.525829	0.329388	-4.196442	33560.5760
HLA A*2301	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.526001	0.329388	-4.196613	33573.8324
HLA A*6801	1:58-66 9	AGYLRHIID	1.158754	-0.699236	-4.656306	0.459518	-4.196788	45321.649331	
HLA B*0803	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.495763	0.298936	-4.196828	31315.766524	
HLA A*8001	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.376482	0.179565	-4.196917	23794.7991
HLA A*1101	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.466655	0.269704	-4.196951	29285.6775
HLA A*6901	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.324229	0.127125	-4.197104	21097.427152	
HLA B*4601	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.257152	0.060047	-4.197105	18078.054826	
HLA B*1509	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.520341	0.322700	-4.197641	33139.1228
HLA A*0201	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.394019	0.196360	-4.197658	24775.2815
HLA A*3101	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.394164	0.196360	-4.197804	24783.5928
HLA A*2602	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.616418	0.418270	-4.198149	41344.5718
HLA A*3201	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.571320	0.373143	-4.198177	37266.6311
HLA B*0801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.394714	0.196360	-4.198354	24814.9866
HLA B*1502	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.616806	0.418270	-4.198537	41381.4938
HLA B*1501	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.340589	0.141991	-4.198598	21907.3052
HLA B*0702	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.463204	0.264217	-4.198987	29053.8629
HLA A*2902	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.454078	0.255019	-4.199059	28449.7519
HLA A*0101	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.383119	0.183904	-4.199215	24161.246577	
HLA B*4001	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.383234	0.183904	-4.199330	24167.652200	
HLA A*6901	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.366513	0.167005	-4.199508	23254.8304
HLA A*0201	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.390450	0.190565	-4.199885	24572.521898	
HLA A*0301	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.357618	0.157520	-4.200098	22783.3733
HLA A*3301	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.464567	0.264217	-4.200349	29145.1694
HLA B*1509	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.531736	0.331331	-4.200405	34020.133332	
HLA B*4501	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.409856	0.208763	-4.201094	25695.4647
HLA A*0216	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.471197	0.269704	-4.201493	29593.5340
HLA B*0702	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.410350	0.208763	-4.201587	25724.6733
HLA B*1509	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.531076	0.329388	-4.201688	33968.4559
HLA B*3901	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.502022	0.300329	-4.201693	31770.3555
HLA B*0803	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.509876	0.308151	-4.201726	32350.157760	
HLA B*0801	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.369800	0.167651	-4.202150	23431.500843	
HLA A*0211	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.502558	0.300329	-4.202229	31809.5669
HLA A*0201	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.401029	0.198739	-4.202290	25178.4772
HLA B*2705	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.457363	0.255019	-4.202344	28665.7338
HLA A*3001	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.296452	0.093967	-4.202484	19790.261590	
HLA B*5301	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.067419	-0.135764	-4.203183	11679.359802	
HLA A*0202	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.493383	0.290041	-4.203342	31144.6186
HLA A*6801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.532777	0.329388	-4.203389	34101.7631
HLA B*3901	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.370749	0.167005	-4.203744	23482.7686
HLA B*1502	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.563623	0.359849	-4.203775	36611.9804
HLA A*0101	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.394935	0.190565	-4.204370	24827.609022	
HLA B*4501	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.569048	0.364143	-4.204905	37072.1849
HLA A*3002	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.536287	0.331331	-4.204956	34378.503179	
HLA A*0219	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.460016	0.255019	-4.204997	28841.3531
HLA B*2705	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.480282	0.275281	-4.205002	30219.153160	
HLA A*0212	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.401528	0.196360	-4.205167	25207.3709
HLA A*0250	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.569417	0.364143	-4.205274	37103.6856
HLA A*2402	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.522122	0.316807	-4.205315	33275.295334	
HLA A*2403	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.373348	0.167651	-4.205697	23623.695137	
HLA B*1517	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.505241	0.299515	-4.205726	32006.697773	
HLA B*5801	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.348269	0.142013	-4.206256	22298.180492	
HLA B*4402	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.432151	0.225691	-4.206460	27048.970489	
HLA B*4403	1:172-180	9	RAVLPNATE	0.899712	-0.448568	-4.657643	0.451144	-4.206499	45461.3745
HLA B*5401	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.496804	0.290041	-4.206763	31390.9072
HLA B*5101	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.507125	0.300329	-4.206796	32145.8679
HLA A*6901	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.266907	0.060047	-4.206860	18488.716403	
HLA B*5701	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.364718	0.157520	-4.207198	23158.9129
HLA A*1101	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.397790	0.190565	-4.207225	24991.338786	
HLA A*6802	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.403593	0.196360	-4.207232	25327.5248
HLA B*5401	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.441370	0.234045	-4.207325	27629.3150
HLA B*0803	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.507677	0.300329	-4.207348	32186.7617
HLA B*1501	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.403807	0.196360	-4.207446	25339.9966
HLA A*2902	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.364979	0.157520	-4.207459	23172.8240
HLA B*1503	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.515609	0.308151	-4.207459	32780.014875	
HLA A*2601	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.387034	0.179565	-4.207469	24379.9931
HLA A*0211	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.530298	0.322700	-4.207598	33907.6839
HLA B*0802	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.433643	0.225691	-4.207952	27142.051053	
HLA B*3501	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.416973	0.208763	-4.208210	26119.9936
HLA B*4402	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.407058	0.198739	-4.208319	25530.4365
HLA B*4001	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.387924	0.179565		
HLA B*4402	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.404854	0.196360		

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HLA B*0802	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.463631	0.255019	-4.208612	29082.4834
HLA B*5701	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.417401	0.208763	-4.208638	26145.7240
HLA B*0802	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.442949	0.234045	-4.208904	27729.9427
HLA B*3901	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.303159	0.093967	-4.209192	20098.299536
HLA A*0206	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.443269	0.234045	-4.209223	27750.3524
HLA B*0802	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.473471	0.264217	-4.209254	29748.9151
HLA A*8001	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.377001	0.167651	-4.209351	23823.264832
HLA B*4801	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.435337	0.225691	-4.209646	27248.126179
HLA A*0250	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.590924	0.380508	-4.210416	38987.3967
HLA B*0702	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.409185	0.198739	-4.210445	25655.7387
HLA A*3001	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.304578	0.093985	-4.210593	20164.079610
HLA B*0803	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.339191	0.128565	-4.210626	21836.9015
HLA B*5801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.352658	0.141991	-4.210667	22524.6610
HLA A*0219	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.378559	0.167651	-4.210908	23908.866506
HLA B*1517	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.486328	0.275281	-4.211047	30642.734247
HLA A*2301	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.542626	0.331331	-4.211295	34883.967592
HLA A*6901	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.401868	0.190565	-4.211304	25227.152228
HLA A*2501	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.486739	0.275281	-4.211458	30671.758398
HLA A*3101	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.353624	0.141991	-4.211633	22574.7995
HLA A*3301	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.571623	0.359849	-4.211775	37292.6476
HLA B*4601	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.379440	0.167651	-4.211789	23957.419859
HLA A*3101	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.144322	-0.067515	-4.211837	13941.9134
HLA B*3801	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.543295	0.331331	-4.211965	34937.793820
HLA B*4001	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.403003	0.190565	-4.212438	25293.156379
HLA A*3101	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.354735	0.142013	-4.212722	22632.639674
HLA B*4403	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.593262	0.380508	-4.212754	39197.8254
HLA B*5401	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.488609	0.275281	-4.213328	30804.124122
HLA B*5701	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.409697	0.196360	-4.213336	25686.0138
HLA B*4001	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.409795	0.196360	-4.213435	25691.8507
HLA A*6901	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.393013	0.179565	-4.213448	24717.9824
HLA A*3301	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.630179	0.416215	-4.213965	42675.5800
HLA B*4601	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.410425	0.196360	-4.214065	25729.1270
HLA B*0702	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.381298	0.167005	-4.214293	24060.1586
HLA B*4601	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.404934	0.190565	-4.214370	25405.883706
HLA B*5101	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.504799	0.290041	-4.214759	31974.1616
HLA B*5301	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.595475	0.380508	-4.214967	39398.0919
HLA B*5701	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.405806	0.190565	-4.215241	25456.926270
HLA A*0211	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.490547	0.275281	-4.215267	30941.915074
HLA B*0803	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.514909	0.299515	-4.215394	32727.211249
HLA A*0216	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.344224	0.128565	-4.215659	22091.4190
HLA B*1509	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.515426	0.299515	-4.215911	32766.185566
HLA A*2301	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.515019	0.298936	-4.216084	32735.533684
HLA A*0216	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.480369	0.264217	-4.216152	30225.2026
HLA B*0802	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.491499	0.275281	-4.216218	31009.783291
HLA A*0216	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.406797	0.190565	-4.216233	25515.110142
HLA B*4403	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.425130	0.208763	-4.216368	26615.2456
HLA A*0203	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.383399	0.167005	-4.216394	24176.8060
HLA A*2603	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.632618	0.416215	-4.216404	42915.8974
HLA A*0201	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.396190	0.179565	-4.216625	24899.4367
HLA A*0206	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.383641	0.167005	-4.216636	24190.2815
HLA B*4403	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.666479	0.449835	-4.216643	46395.8329
HLA A*2501	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.396248	0.179565	-4.216683	24902.8045
HLA B*4002	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.548063	0.331331	-4.216732	35323.406781
HLA B*7301	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.581120	0.364143	-4.216977	38117.0986
HLA B*5101	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.486797	0.269704	-4.217093	30675.9069
HLA A*1101	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.451604	0.234045	-4.217559	28288.1454
HLA B*4501	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.635976	0.418270	-4.217706	43248.9544
HLA A*0211	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.525874	0.308151	-4.217724	33564.025803
HLA A*6801	1:118-126	9	VPPGMEDDA	0.772465	-0.322630	-4.667637	0.449835	-4.217802	46519.7393
HLA A*0101	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.360061	0.142013	-4.218048	22911.920396
HLA B*3901	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.415007	0.196360	-4.218646	26001.9876
HLA A*0211	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.427501	0.208763	-4.218739	26760.9242
HLA A*0206	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.482648	0.263887	-4.218761	30384.2290
HLA B*7301	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.591913	0.373143	-4.218770	39076.2942
HLA A*2301	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.494309	0.275281	-4.219028	31211.074137
HLA B*1509	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.518318	0.298936	-4.219383	32985.122593
HLA A*0101	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.386568	0.167005	-4.219563	24353.8923
HLA B*7301	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.579433	0.359849	-4.219584	37969.3276
HLA B*4601	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.399373	0.179565	-4.219808	25082.6301
HLA A*2501	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.484081	0.264217	-4.219864	30484.6636
HLA A*2301	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.520336	0.300329	-4.220007	33138.7643
HLA B*1503	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.387074	0.167005	-4.220068	24382.2354
HLA A*2602	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.475722	0.255019	-4.220703	29903.4942
HLA B*5801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.349296	0.128565	-4.220731	22350.9584
HLA B*5301	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.314970	0.093967	-4.221003	20652.383243
HLA A*2603	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.594399	0.373143	-4.221256	39300.5950
HLA A*0202	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.412020	0.190565	-4.221456	25823.812073
HLA A*0301	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.363529	0.141991	-4.221538	23095.6043
HLA A*2403	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.348786	0.127125	-4.221661	22324.735041
HLA A*6901	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.350391	0.128565	-4.221826	22407.3765
HLA B*3801	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.551298	0.329388	-4.221910	35587.5281
HLA B*1501	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.363948	0.142013	-4.221934	23117.855240
HLA B*5301	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.581804	0.359849	-4.221955	38177.1528
HLA B*4002	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.640482	0.418270	-4.222212	43700.0490
HLA B*1509	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.486189	0.263887	-4.222302	30632.9551
HLA A*2902	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.418688	0.196360	-4.222328	26223.3511
HLA B*3501	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.364690	0.142013	-4.222677	23157.409591
HLA A*0203	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.155247	-0.067515	-4.222763	14297.0845
HLA A*2601	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.390024	0.167005	-4.223019	24548.4725
HLA A*0201	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.390111	0.167005	-4.223106	24553.3867
HLA A*2602	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.552524	0.329388	-4.223137	35688.1680
HLA A*0203	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.432040	0.208763	-4.223278	27042.0937
HLA B*0803	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.499026	0.275281	-4.223746	31551.970061
HLA A*0216	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.432609	0.208763	-4.223846	27077.5202
HLA A*2602	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.604413	0.380508	-4.223905	40217.2740
HLA A*6801	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.523071	0.298936	-4.224136	33348.101194
HLA B*5401	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.546874	0.322700	-4.224173	35226.8445
HLA B*0702	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.414884	0.190565	-4.224320	25994.673969
HLA B*4601	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.381919	0.157520	-4.224398	24094.5461
HLA A*2301	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.547132	0.322700	-4.224432	35247.8138
HLA A*2602	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.555806	0.331331	-4.224476	35958.907222
HLA A*0206	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.514850	0.290041	-4.224810	32722.7852
HLA B*1503	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.415448	0.190565	-4.224884	26028.446682
HLA B*5101	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.480390	0.255019	-4.225371	30226.6742
HLA A*6801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.548175	0.322700	-4.225475	35332.5805
HLA B*1501	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.384047	0.157520	-4.226527	24212.9320
HLA B*4501	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.490855	0.263887	-4.226968	30963.8512
HLA B*2705	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.491250	0.264217	-4.227032	30992.0058
HLA B*1509	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.496747	0.269704	-4.227044	31386.8318
HLA B*5701	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.411135	0.183904	-4.227230	25771.197352
HLA B*1517	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.491466	0.264217	-4.227248	31007.4347
HLA A*2403	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.321318	0.093985	-4.227333	20956.487085
HLA A*6802	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.437031	0.208763	-4.228268	27354.6158
HLA B*3901	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.492648	0.264217	-4.228430	31091.9262
HLA A*2402	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.558029	0.329388	-4.228642	36143.4076
HLA A*3201	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.560242	0.331331	-4.2289	
HLA A*2902	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.357609	0.128565		

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HLA A*3101	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.386622	0.157520	-4.229102	24356.9228
HLA A*3002	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.529537	0.300329	-4.229208	33848.3024
HLA A*0216	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.428434	0.198739	-4.229694	26818.4611
HLA B*7301	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.552423	0.322700	-4.229723	35679.8669
HLA A*0202	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.552557	0.322700	-4.229857	35690.8710
HLA B*1801	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.505300	0.275281	-4.230019	32011.026883	
HLA B*1503	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.500126	0.269704	-4.230422	31631.9554
HLA A*0212	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.429169	0.198739	-4.230430	26863.9112
HLA A*3002	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.500394	0.269704	-4.230690	31651.4697
HLA A*0216	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.485731	0.255019	-4.230712	30600.6566
HLA B*4801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.427348	0.196360	-4.230988	26751.5156
HLA A*0201	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.359660	0.128565	-4.231095	22890.7345
HLA A*2403	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.427532	0.196360	-4.231171	26762.8064
HLA B*1502	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.415162	0.183904	-4.231257	26011.273407	
HLA A*0301	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.291621	0.060047	-4.231574	19571.359464	
HLA A*3101	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.399371	0.167651	-4.231720	25082.494478	
HLA A*0206	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.540307	0.308151	-4.232156	34698.198937	
HLA A*0203	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.428645	0.196360	-4.232285	26831.5220
HLA B*7301	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.531280	0.298936	-4.232345	33984.447302	
HLA B*4002	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.522524	0.290041	-4.232483	33306.0922
HLA A*0216	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.466535	0.234045	-4.232490	29277.5986
HLA A*1101	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.487693	0.255019	-4.232673	30739.2003
HLA B*0802	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.390245	0.157520	-4.232725	24560.9593
HLA A*8001	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.441591	0.208763	-4.232828	27643.3689
HLA A*0219	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.467078	0.234045	-4.233033	29314.2092
HLA B*3901	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.508502	0.275281	-4.233221	32247.938298	
HLA A*1101	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.497574	0.264217	-4.233357	31446.6581
HLA A*0219	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.417772	0.183904	-4.233867	26168.081990	
HLA B*3501	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.432867	0.198739	-4.234128	27093.6385
HLA A*2601	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.362759	0.128565	-4.234194	23054.6588
HLA B*3901	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.402296	0.167651	-4.234645	25252.003110	
HLA B*5801	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.362197	0.127125	-4.235072	23024.869300	
HLA A*2301	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.499649	0.264217	-4.235432	31597.2360
HLA B*0803	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.362658	0.127125	-4.235532	23049.296398	
HLA A*8001	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.296407	0.060047	-4.236360	19788.227495	
HLA A*3301	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.600884	0.364143	-4.236741	39891.8065
HLA B*5401	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.296907	0.060047	-4.236860	19811.042738	
HLA A*2403	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.435710	0.198739	-4.236971	27271.5743
HLA B*1509	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.462741	0.225691	-4.237050	29022.915326	
HLA B*1509	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.545365	0.308151	-4.237215	35104.708722	
HLA B*0801	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.331438	0.093967	-4.237471	21450.514627	
HLA A*0202	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.471716	0.234045	-4.237671	29628.9367
HLA A*0101	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.395367	0.157520	-4.237847	24852.3352
HLA A*0202	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.538232	0.300329	-4.237903	34532.8432
HLA A*2403	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.417878	0.179565	-4.238313	26174.4532
HLA B*5701	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.406036	0.167651	-4.238386	25470.426325	
HLA A*2301	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.546545	0.308151	-4.238394	35200.174411	
HLA B*1517	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.422384	0.183904	-4.238479	26447.457683	
HLA B*3501	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.367051	0.128565	-4.238487	23283.6578
HLA B*7301	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.567974	0.329388	-4.238587	36980.6438
HLA B*4801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.437555	0.198739	-4.238815	27387.6365
HLA B*5801	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.299003	0.060047	-4.238956	19906.874362	
HLA B*3801	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.561706	0.322700	-4.239006	36450.7141
HLA A*8001	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.381162	0.142013	-4.239149	24052.610391	
HLA B*0702	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.423164	0.183904	-4.239259	26495.002201	
HLA A*0201	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.396871	0.157520	-4.239350	24938.5313
HLA A*3201	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.568783	0.329388	-4.239395	37049.5289
HLA B*4403	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.599300	0.359849	-4.239452	39746.6153
HLA B*1501	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.366579	0.127125	-4.239454	23258.353293	
HLA B*4402	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.430027	0.190565	-4.239462	26917.009366	
HLA A*0212	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.368186	0.128565	-4.239621	23344.5771
HLA A*0211	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.473774	0.234045	-4.239729	29769.6834
HLA A*0301	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.367305	0.127125	-4.240180	23297.265768	
HLA A*0212	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.420220	0.179565	-4.240655	26316.0107
HLA A*0212	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.408221	0.167005	-4.241216	25598.8959
HLA B*3801	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.558097	0.316807	-4.241291	36149.078684	
HLA B*1502	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.622290	0.380508	-4.241782	41907.3174
HLA A*3101	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.114390	-0.127574	-4.241964	13013.374915	
HLA B*5101	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.467861	0.225691	-4.242170	29367.066226	
HLA B*0802	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.451120	0.208763	-4.242358	28256.6376
HLA A*2301	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.542158	0.299515	-4.242643	34846.432839	
HLA A*0101	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.371332	0.128565	-4.242767	23514.2954
HLA B*3901	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.497915	0.255019	-4.242896	31471.3356
HLA B*4801	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.433619	0.190565	-4.243054	27140.582737	
HLA A*3002	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.400903	0.157520	-4.243382	25171.1228
HLA A*2601	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.176003	-0.067515	-4.243518	14996.9463
HLA A*2603	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.411189	0.167651	-4.243538	25774.404196	
HLA B*0702	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.337560	0.093967	-4.243593	21755.069441	
HLA A*0219	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.442634	0.198739	-4.243895	27709.8479
HLA B*4402	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.401518	0.157520	-4.243998	25206.8254
HLA B*5101	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.508131	0.263887	-4.244244	32220.3857
HLA B*4402	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.428279	0.183904	-4.244374	26808.887286	
HLA A*6801	1:126-134	9	ADLRHILTE	1.217599	-0.801384	-4.660633	0.416215	-4.244419	45775.5380
HLA A*2602	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.561436	0.316807	-4.244629	36428.043900	
HLA B*5401	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.499760	0.255019	-4.244740	31605.2711
HLA A*0101	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.386996	0.141991	-4.245005	24377.8829
HLA A*0219	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.441384	0.196360	-4.245024	27630.2119
HLA B*1503	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.544614	0.299515	-4.245098	35043.989268	
HLA B*1517	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.435745	0.190565	-4.245181	27273.787480	
HLA B*3501	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.305330	0.060047	-4.245283	20199.017182	
HLA B*3801	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.535411	0.290041	-4.245370	34309.2011
HLA A*0203	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.425105	0.179565	-4.245540	26613.6618
HLA B*5801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.352952	0.107209	-4.245743	22539.8981
HLA B*4402	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.425535	0.179565	-4.245970	26640.0226
HLA B*4403	1:125-133	9	DADLRHILT	0.976283	-0.558013	-4.664254	0.418270	-4.245984	46158.7472
HLA B*2705	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.444758	0.198739	-4.246019	27845.6959
HLA B*5101	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.510708	0.264217	-4.246491	32412.1709
HLA A*6901	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.274540	0.027900	-4.246641	18816.560348	
HLA A*2403	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.437223	0.190565	-4.246659	27366.753361	
HLA B*4801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.430750	0.183904	-4.246846	26961.897108	
HLA A*1101	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.375507	0.128565	-4.246942	23741.4372
HLA A*0211	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.537285	0.290041	-4.247245	34457.6372
HLA A*2902	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.456104	0.208763	-4.247341	28582.7321
HLA A*0219	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.404876	0.157520	-4.247355	25402.4478
HLA A*0250	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.283438	0.035827	-4.247611	19206.035947	
HLA B*0801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.427189	0.179565	-4.247624	26741.6763
HLA B*4801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.427468	0.179565	-4.247903	26758.8975
HLA A*6901	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.389898	0.141991	-4.247907	24541.3021
HLA A*0202	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.523313	0.275281	-4.248032	33366.688553	
HLA A*8001	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.432642	0.183904	-4.248737	27079.571159	
HLA B*1509	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.524147	0.275281	-4.248867	33430.831208	
HLA A*0211	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.548789	0.299515	-4.249274	35382.504739	
HLA B*0802	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.433229	0.183904	-4.249325	27116.220306	
HLA B*4402	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.416348	0.167005	-4.249343	26082.4332
HLA A*6802	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.377953	0.128565	-4.249388	23875.5186
HLA A*3301	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.578777	0.329388		
HLA B*4001	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.378197	0.128565		

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HLA A*6802	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.033375	-0.216975	-4.250350	10798.787624
HLA B*5301	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.579950	0.329388	-4.250562	38014.5446
HLA A*2601	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.377725	0.127125	-4.250600	23862.993338
HLA A*0201	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.392846	0.141991	-4.250855	24708.4900
HLA A*8001	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.449925	0.198739	-4.251185	28178.9362
HLA B*4601	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.393206	0.141991	-4.251215	24728.9500
HLA A*0250	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.526534	0.275281	-4.251254	33615.087927
HLA A*2601	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.393546	0.141991	-4.251555	24748.3558
HLA B*1503	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.393737	0.141991	-4.251746	24759.2029
HLA A*6802	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.442503	0.190565	-4.251938	27701.454381
HLA A*8001	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.394070	0.141991	-4.252079	24778.2304
HLA A*8001	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.442655	0.190565	-4.252091	27711.197111
HLA B*5401	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.409767	0.157520	-4.252247	25690.1829
HLA B*5401	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.560616	0.308151	-4.252465	36359.330771
HLA A*2402	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.552816	0.300329	-4.252487	35712.1165
HLA B*0702	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.381284	0.128565	-4.252720	24059.3776
HLA A*6901	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.346815	0.093967	-4.252848	22223.634984
HLA B*0803	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.517531	0.264217	-4.253314	32925.3973
HLA A*0206	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.523071	0.269704	-4.253367	33348.1011
HLA B*1801	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.380692	0.127125	-4.253567	24026.600074
HLA A*2501	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.462546	0.208763	-4.253783	29009.8863
HLA B*0802	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.452544	0.198739	-4.253805	28349.4259
HLA A*0101	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.380934	0.127125	-4.253809	24039.991872
HLA B*5301	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.553034	0.298936	-4.254099	35730.088582
HLA B*0803	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.488271	0.234045	-4.254225	30780.1363
HLA A*0201	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.290528	0.035827	-4.254702	19522.187657
HLA A*1101	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.422010	0.167005	-4.255005	26424.7180
HLA A*6801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.451407	0.196360	-4.255047	28275.2933
HLA A*1101	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.315581	0.060047	-4.255534	20681.452729
HLA B*4002	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.619696	0.364143	-4.255553	41657.7712
HLA B*3801	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.554629	0.298936	-4.255694	35861.577796
HLA B*0801	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.397738	0.142013	-4.255724	24988.364555
HLA A*0212	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.413475	0.157520	-4.255954	25910.4337
HLA B*4002	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.616003	0.359849	-4.256154	41305.0013
HLA B*5401	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.525907	0.269704	-4.256203	33566.5679
HLA A*2501	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.284164	0.027900	-4.256264	19238.168677
HLA B*3801	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.531642	0.275281	-4.256361	34012.772322
HLA A*2602	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.435964	0.179565	-4.256399	27287.5129
HLA B*1503	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.455385	0.198739	-4.256645	28535.4547
HLA B*0802	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.453059	0.196360	-4.256698	28383.0333
HLA A*0206	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.556337	0.299515	-4.256822	36002.898726
HLA B*4001	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.414598	0.157520	-4.257077	25977.5229
HLA B*2705	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.424823	0.167651	-4.257172	26596.390225
HLA A*3301	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.637759	0.380508	-4.257251	43426.9042
HLA B*4001	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.399314	0.142013	-4.257301	25079.238045
HLA B*1801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.437181	0.179565	-4.257616	27364.0885
HLA A*2402	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.588991	0.331331	-4.257660	38814.197501
HLA A*0301	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.364986	0.107209	-4.257777	23173.2001
HLA B*4601	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.386470	0.128565	-4.257905	24348.3593
HLA B*2705	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.386526	0.128565	-4.257961	24351.5209
HLA A*0202	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.527744	0.269704	-4.258040	33708.8732
HLA A*6801	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.575018	0.316807	-4.258212	37585.317569
HLA A*2902	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.457250	0.198739	-4.258511	28658.2910
HLA A*0216	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.438076	0.179565	-4.258511	27420.5487
HLA B*4801	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.426338	0.167651	-4.258688	26689.357201
HLA B*0803	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.485273	0.225691	-4.259582	30568.392140
HLA B*5801	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.353685	0.093985	-4.259700	22577.975085
HLA A*0301	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.295751	0.035827	-4.259925	19758.382483
HLA B*1509	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.524493	0.264217	-4.260275	33457.4277
HLA B*5401	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.560804	0.300329	-4.260475	36375.0701
HLA A*6802	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.387908	0.127125	-4.260782	24429.106789
HLA A*2501	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.402867	0.142013	-4.260853	25285.221300
HLA A*3201	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.427901	0.167005	-4.260895	26785.5471
HLA B*3801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.569090	0.308151	-4.260940	37075.795105
HLA A*1101	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.469761	0.208763	-4.260999	29495.8758
HLA A*0203	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.403074	0.141991	-4.261083	25297.2617
HLA A*6802	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.428281	0.167005	-4.261276	26809.0323
HLA A*2603	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.625506	0.364143	-4.261364	42218.8410
HLA B*1517	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.457777	0.196360	-4.261416	28693.0406
HLA A*0212	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.451999	0.190565	-4.261435	28313.867108
HLA A*0203	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.388603	0.127125	-4.261478	24468.257120
HLA B*4001	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.388939	0.127125	-4.261814	24487.193434
HLA B*1509	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.445790	0.183904	-4.261885	27911.906427
HLA B*5301	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.593316	0.331331	-4.261985	39202.703082
HLA A*2501	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.430022	0.167651	-4.262372	26916.718131
HLA A*0211	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.391023	0.128565	-4.262458	24604.9793
HLA B*3801	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.562174	0.299515	-4.262659	36489.976995
HLA B*4403	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.594256	0.331331	-4.262925	39287.627847
HLA B*0803	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.461728	0.198739	-4.262989	28955.3225
HLA A*0211	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.195499	-0.067515	-4.263014	15685.5179
HLA A*6801	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.453681	0.190565	-4.263117	28423.753007
HLA A*1101	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.299045	0.035827	-4.263219	19908.812948
HLA B*0702	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.421047	0.157520	-4.263527	26366.1715
HLA A*3101	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.197627	-0.066090	-4.263717	15762.5870
HLA A*0212	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.405851	0.141991	-4.263860	25459.5430
HLA B*7301	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.572464	0.308151	-4.264314	37364.943843
HLA A*0219	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.455122	0.190565	-4.264557	28518.170090
HLA A*3201	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.406703	0.142013	-4.264690	25509.589383
HLA A*2403	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.393281	0.128565	-4.264716	24733.2313
HLA B*1502	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.596410	0.331331	-4.265080	39483.012835
HLA A*0201	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.407479	0.142013	-4.265465	25555.171395
HLA B*1502	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.301552	0.035827	-4.265726	20024.065939
HLA B*4501	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.566398	0.300329	-4.266069	36846.6461
HLA B*4403	1:169-177	9	QAARAVLPN	0.840310	-0.476167	-4.630257	0.364143	-4.266114	42683.1994
HLA B*4501	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.541637	0.275281	-4.266356	34804.607555
HLA A*0212	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.360341	0.093967	-4.266374	22926.675308
HLA B*5801	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.360381	0.093967	-4.266414	22928.783928
HLA B*5101	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.500833	0.234045	-4.266788	31683.5061
HLA A*0201	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.394369	0.127125	-4.267243	24795.260293
HLA A*8001	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.424940	0.157520	-4.267420	26603.5853
HLA A*3001	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.295340	0.027900	-4.267441	19739.685470
HLA A*2602	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.531661	0.263887	-4.267774	34014.2443
HLA A*2402	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.537793	0.269704	-4.268089	34497.9257
HLA A*3101	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.395250	0.127125	-4.268124	24845.613706
HLA B*1502	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.590931	0.322700	-4.268231	38988.0295
HLA B*5701	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.328388	0.060047	-4.268341	21300.415955
HLA B*3801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.568764	0.300329	-4.268435	37047.9255
HLA A*2603	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.648978	0.380508	-4.268470	44563.3327
HLA B*0802	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.397179	0.128565	-4.268614	24956.2114
HLA A*3002	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.591352	0.322700	-4.268652	39025.8026
HLA A*0219	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.435807	0.167005	-4.268801	27277.6240
HLA A*0203	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.426568	0.157520	-4.269048	26703.5108
HLA A*3201	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.297020	0.027900	-4.269120	19816.187833
HLA B*4402	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.436878	0.167651	-4.269227	27344.998500
HLA A*0250	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.591935	0.322700	-4.269234	39078.1966
HLA A*2301	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.538958	0.269704		
HLA A*0250	1:76-84 9	ASVSFYITG	0.800579	-0.501643	-4.568447	0.298936	-4.2695		

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HLA B*5301	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.559603	0.290041	-4.269563	36274.6518	
HLA A*2902	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.280116	0.010485	-4.269630	19059.678277		
HLA A*2402	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.534262	0.264217	-4.270044	34218.5582	
HLA B*4801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.427750	0.157520	-4.270230	26776.2746	
HLA B*1517	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.479380	0.208763	-4.270617	30156.4411	
HLA A*2501	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.399206	0.128565	-4.270642	25072.9977	
HLA B*1801	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.412883	0.142013	-4.270869	25875.134358		
HLA A*1101	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.467417	0.196360	-4.271056	29337.0546	
HLA A*3002	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.579346	0.308151	-4.271195	37961.728207		
HLA B*1502	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.438873	0.167651	-4.271222	27470.882837		
HLA A*6801	1:112-120	9	KDSRVVVPP	0.498317	-0.117809	-4.651734	0.380508	-4.271226	44847.0218	
HLA B*3501	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.054285	-0.216975	-4.271260	11331.448170		
HLA B*1503	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.535554	0.264217	-4.271337	34320.5251	
HLA B*1503	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.467976	0.196360	-4.271615	29374.8520	
HLA A*0211	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.541341	0.269704	-4.271637	34780.8912	
HLA A*2402	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.594486	0.322700	-4.271786	39308.4624	
HLA B*5301	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.594688	0.322700	-4.271988	39326.7549	
HLA B*4601	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.399138	0.127125	-4.272013	25069.064417		
HLA A*2301	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.535911	0.263887	-4.272024	34348.7586	
HLA A*2902	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.439232	0.167005	-4.272227	27493.6302	
HLA A*6901	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.379590	0.107209	-4.272382	23965.7161	
HLA B*0702	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.308227	0.035827	-4.272400	20334.202941		
HLA B*4601	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.414868	0.142013	-4.272855	25993.689589		
HLA A*2602	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.414964	0.141991	-4.272973	25999.4557	
HLA A*2501	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.414983	0.141991	-4.272992	26000.5810	
HLA B*5101	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.457051	0.183904	-4.273146	28645.115791		
HLA B*7301	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.573096	0.299515	-4.273581	37419.359143		
HLA A*0301	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.367561	0.093967	-4.273594	23311.007702		
HLA B*4801	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.415819	0.142013	-4.273806	26050.704333		
HLA B*4002	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.647009	0.373143	-4.273866	44361.7626	
HLA B*4403	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.574586	0.300329	-4.274257	37547.9230	
HLA B*4501	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.647514	0.373143	-4.274371	44413.3910	
HLA B*1801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.458357	0.183904	-4.274452	28731.407100		
HLA A*0216	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.470941	0.196360	-4.274580	29576.0885	
HLA A*2301	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.500377	0.225691	-4.274687	31650.271153		
HLA A*3201	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.597644	0.322700	-4.274943	39595.3115	
HLA A*0301	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.369098	0.093985	-4.275113	23393.629696		
HLA B*5701	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.417159	0.142013	-4.275145	26131.159227		
HLA A*0250	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.583378	0.308151	-4.275227	38315.781829		
HLA B*0802	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.442883	0.167651	-4.275233	27725.742634		
HLA A*0250	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.565404	0.290041	-4.275363	36762.4233	
HLA B*0702	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.417504	0.141991	-4.275513	26151.9483	
HLA A*3001	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.148161	-0.127574	-4.275736	14065.702885		
HLA A*3101	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.311625	0.035827	-4.275798	20493.895102		
HLA A*0216	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.417903	0.142013	-4.275890	26176.010911		
HLA B*5701	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.418303	0.141991	-4.276312	26200.0955	
HLA B*4801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.404930	0.128565	-4.276365	25405.6088	
HLA A*3001	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.208999	-0.067515	-4.276514	16180.7632	
HLA A*3201	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.584679	0.308151	-4.276529	38430.789496		
HLA A*0212	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.403715	0.127125	-4.276590	25334.650830		
HLA B*1509	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.531691	0.255019	-4.276672	34016.6366	
HLA A*2603	1:221-229	9	AVAPAVFAD	0.951537	-0.591688	-4.637146	0.359849	-4.277297	43365.6295	
HLA A*8001	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.444772	0.167005	-4.277767	27846.5998	
HLA A*2402	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.586427	0.308151	-4.278277	38585.783504		
HLA A*3301	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.601098	0.322700	-4.278397	39911.4501	
HLA B*5401	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.542454	0.263887	-4.278568	34870.1938	
HLA A*0202	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.587299	0.308151	-4.279148	38663.305599		
HLA A*3201	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.504844	0.225691	-4.279153	31977.448342		
HLA B*7301	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.569213	0.290041	-4.279172	37086.2265	
HLA B*1801	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.446866	0.167651	-4.279215	27981.150322		
HLA B*4002	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.596342	0.316807	-4.279536	39476.818958		
HLA B*1503	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.315539	0.035827	-4.279712	20679.438909		
HLA A*0219	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.459508	0.179565	-4.279943	28807.6706	
HLA A*0206	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.460112	0.179565	-4.280547	28847.7510	
HLA A*2402	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.580133	0.299515	-4.280618	38030.589115		
HLA B*5101	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.479378	0.198739	-4.280638	30156.2779	
HLA A*3101	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.375084	0.093967	-4.281117	23718.329542		
HLA B*1502	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.536374	0.255019	-4.281355	34385.3852	
HLA A*0211	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.480214	0.198739	-4.281475	30214.4125	
HLA B*1801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.477952	0.196360	-4.281591	30057.4131	
HLA A*2501	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.477996	0.196360	-4.281636	30060.5028	
HLA A*0101	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.375763	0.093967	-4.281796	23755.441157		
HLA A*2902	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.317942	0.035827	-4.282116	20794.202747		
HLA B*1502	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.410735	0.128565	-4.282171	25747.5069	
HLA A*0101	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.342487	0.060047	-4.282440	22003.275874		
HLA B*1502	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.590689	0.308151	-4.282539	38966.310697		
HLA B*1502	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.582201	0.299515	-4.282686	38212.073086		
HLA B*7301	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.546575	0.263887	-4.282689	35202.6500	
HLA A*2603	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.591688	0.308151	-4.283537	39056.005224		
HLA B*4801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.425673	0.141991	-4.283682	26648.5270	
HLA A*2603	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.606485	0.322700	-4.283785	40409.6302	
HLA B*0802	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.474639	0.190565	-4.284074	29829.009115		
HLA B*4501	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.518194	0.234045	-4.284148	32975.6663	
HLA B*1517	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.441802	0.157520	-4.284282	27656.8315	
HLA A*3101	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.391582	0.107209	-4.284374	24636.6799	
HLA B*5301	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.601499	0.316807	-4.284693	39948.388939		
HLA B*3501	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.475456	0.190565	-4.284892	29885.219338		
HLA B*4001	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.378890	0.093967	-4.284923	23927.111012		
HLA A*2301	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.539966	0.255019	-4.284947	34670.9911	
HLA B*0802	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.412476	0.127125	-4.285351	25850.928868		
HLA B*0802	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.464954	0.179565	-4.285389	29171.1969	
HLA A*3002	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.157888	-0.127574	-4.285463	14384.285928		
HLA A*2601	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.321452	0.035827	-4.285626	20962.950301		
HLA A*2402	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.560961	0.275281	-4.285681	36388.257164		
HLA A*0101	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.392957	0.107209	-4.285748	24714.7733	
HLA A*2501	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.476486	0.190565	-4.285921	29956.117270		
HLA A*3002	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.482620	0.196360	-4.286260	30382.2566	
HLA B*2705	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.477068	0.190565	-4.286504	29996.334942		
HLA B*5101	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.495519	0.208763	-4.286756	31298.1523	
HLA B*5301	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.562047	0.275281	-4.286766	36479.318589		
HLA A*2403	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.444697	0.157520	-4.287177	27841.7795	
HLA A*3301	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.618620	0.331331	-4.287289	41554.682340		
HLA B*0803	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.496200	0.208763	-4.287437	31347.2935	
HLA A*2603	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.445275	0.157520	-4.287755	27878.8569	
HLA A*3002	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.454767	0.167005	-4.287762	28494.8833	
HLA B*4601	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.323682	0.035827	-4.287855	21070.850511		
HLA A*1101	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.467435	0.179565	-4.287870	29338.3243	
HLA A*0206	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.543049	0.255019	-4.288030	34917.9534	
HLA A*3301	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.552097	0.263887	-4.288210	35653.0467	
HLA B*5701	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.416820	0.128565	-4.288256	26110.8103	
HLA B*4403	1:241-249	9	VATSPLATE	1.089931	-0.716788	-4.661742	0.373143	-4.288599	45892.5737	
HLA A*0219	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.430631	0.142013	-4.288617	26954.459229		
HLA B*2705	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.484986	0.196360	-4.288626	30548.2234	
HLA A*6802	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.430746	0.141991	-4.288755	26961.6053	
HLA A*0211	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.553025	0.264217	-4.288807	35729.3154	
HLA B*4501	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.255171	-0.033665			
HLA A*3101	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.299506	0.010485	-4.2890			

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HLA A*3301	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.588058	0.298936	-4.289122	38730.924696	
HLA B*3801	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.558866	0.269704	-4.289162	36213.0842	
HLA A*2603	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.618573	0.329388	-4.289185	41550.1864	
HLA A*0201	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.396495	0.107209	-4.289286	24916.9543	
HLA B*5701	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.416454	0.127125	-4.289328	26088.783621	
HLA B*4801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.397510	0.107209	-4.290301	24975.2551	
HLA B*1801	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.093870	-0.196676	-4.290546	12412.7937	
HLA B*0803	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.487368	0.196360	-4.291008	30716.2601	
HLA B*1509	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.459151	0.167651	-4.291500	28783.991762	
HLA A*2301	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.526555	0.234045	-4.292510	33616.7246	
HLA A*0211	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.547602	0.255019	-4.292583	35285.9718	
HLA B*4402	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.400341	0.107209	-4.293132	25138.5985	
HLA B*5301	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.601584	0.308151	-4.293433	39956.169886	
HLA B*5101	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.420591	0.127125	-4.293466	26338.514310	
HLA A*3201	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.492836	0.198739	-4.294096	31105.3855	
HLA A*0250	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.484751	0.190565	-4.294186	30531.701679	
HLA A*0212	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.226911	-0.067515	-4.294427	16862.0929	
HLA B*0801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.401640	0.107209	-4.294432	25213.9175	
HLA B*0802	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.461696	0.167005	-4.294690	28953.1295	
HLA B*4002	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.593859	0.298936	-4.294923	39251.724713	
HLA A*2602	1:29-37	9	ADGGPALVE	1.188164	-0.880013	-4.603144	0.308151	-4.294993	40099.957196	
HLA B*1503	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.452535	0.157520	-4.295014	28348.8125	
HLA A*0201	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.388993	0.093967	-4.295026	24490.240502	
HLA A*2601	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.389113	0.093985	-4.295128	24496.998398	
HLA A*0250	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.595851	0.300329	-4.295522	39432.2090	
HLA A*0101	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.389759	0.093985	-4.295774	24533.470184	
HLA A*2603	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.594745	0.298936	-4.295809	39331.861405	
HLA A*2601	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.323830	0.027900	-4.295930	21078.033166	
HLA B*1501	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.389942	0.093967	-4.295975	24543.824790	
HLA B*5401	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.560247	0.264217	-4.296030	36328.4619	
HLA A*1101	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.495368	0.198739	-4.296629	31287.3177	
HLA A*2601	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.390877	0.093967	-4.296910	24596.727913	
HLA B*0803	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.480863	0.183904	-4.296958	30259.560271	
HLA B*7301	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.572598	0.275281	-4.297318	37376.467611	
HLA A*3301	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.169772	-0.127574	-4.297346	14783.320841	
HLA B*0802	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.439418	0.141991	-4.297427	27505.3830	
HLA B*1502	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.561988	0.264217	-4.297771	36474.3851	
HLA B*4601	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.405092	0.107209	-4.297883	25415.0940	
HLA A*2601	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.405421	0.107209	-4.298212	25434.3503	
HLA A*2403	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.440444	0.141991	-4.298453	27570.4860	
HLA B*7301	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.497337	0.198739	-4.298598	31429.4804	
HLA A*0201	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.358753	0.060047	-4.298706	22842.983633	
HLA A*8001	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.427557	0.128565	-4.298993	26764.3990	
HLA A*0250	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.466806	0.167651	-4.299155	29295.819007	
HLA A*6901	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.393302	0.093985	-4.299317	24734.435637	
HLA A*0201	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.393455	0.093985	-4.299470	24743.134852	
HLA B*4402	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.426900	0.127125	-4.299774	26723.887885	
HLA A*0216	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.466949	0.167005	-4.299944	29305.4883	
HLA A*0216	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.457506	0.157520	-4.299986	28675.1951	
HLA B*0801	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.360045	0.060047	-4.299998	22911.052756	
HLA A*2902	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.442084	0.141991	-4.300093	27674.7918	
HLA B*4402	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.442324	0.142013	-4.300311	27690.067226	
HLA A*0219	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.428988	0.128565	-4.300424	26852.7230	
HLA A*0206	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.496834	0.196360	-4.300474	31393.1150	
HLA B*3801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.564702	0.264217	-4.300484	36703.0060	
HLA A*0250	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.600014	0.299515	-4.300499	39812.036633	
HLA A*3002	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.311007	0.010485	-4.300521	20464.757104	
HLA B*4402	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.266890	-0.033665	-4.300556	18488.0162	
HLA B*4001	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.360879	0.060047	-4.300832	22955.095956	
HLA B*0702	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.443294	0.142013	-4.301281	27752.003872	
HLA A*2501	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.468394	0.167005	-4.301389	29403.1524	
HLA B*3901	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.500262	0.198739	-4.301523	31641.8822	
HLA B*2705	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.468612	0.167005	-4.301607	29417.9494	
HLA A*3201	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.571452	0.269704	-4.301748	37277.9229	
HLA A*3301	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.430335	0.128565	-4.301770	26936.0920	
HLA A*0219	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.429160	0.127125	-4.302035	26863.329907	
HLA B*3901	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.430626	0.128565	-4.302061	26954.1675	
HLA B*4402	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.430649	0.128565	-4.302085	26955.6258	
HLA B*5401	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.510995	0.208763	-4.302232	32433.5702	
HLA A*0203	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.444389	0.142013	-4.302376	27822.055168	
HLA B*3901	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.493547	0.190565	-4.302983	31156.415156	
HLA B*1502	1:76-84	9	ASVSFYITG	0.800579	-0.501643	-4.602296	0.298936	-4.303360	40021.719606	
HLA A*2403	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.445463	0.142013	-4.303450	27890.925273	
HLA B*0803	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.494149	0.190565	-4.303584	31199.594554	
HLA A*0212	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.445639	0.142013	-4.303626	27902.244080	
HLA A*2402	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.529650	0.225691	-4.303959	33857.093173	
HLA A*2602	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.604645	0.300329	-4.304316	40238.8193	
HLA A*3002	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.559880	0.255019	-4.304861	36297.8157	
HLA A*0206	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.495446	0.190565	-4.304881	31292.903872	
HLA A*1101	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.488879	0.183904	-4.304975	30823.294478	
HLA A*2602	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.627752	0.322700	-4.305052	42437.7563	
HLA B*5101	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.472113	0.167005	-4.305108	29656.0380	
HLA B*0803	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.472141	0.167005	-4.305136	29657.9633	
HLA B*2705	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.484779	0.179565	-4.305214	30533.6838	
HLA A*0206	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.569805	0.264217	-4.305587	37136.8203	
HLA B*1517	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.447648	0.141991	-4.305657	28031.6036	
HLA A*0202	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.504700	0.198739	-4.305961	31966.8974	
HLA A*0202	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.606579	0.299515	-4.307064	40418.375667	
HLA A*6801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.436053	0.128565	-4.307489	27293.1231	
HLA A*0219	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.343437	0.035827	-4.307610	22051.418720	
HLA B*7301	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.367662	0.060047	-4.307615	23316.431062	
HLA A*2501	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.343648	0.035827	-4.307821	22062.157950	
HLA B*4001	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.415232	0.107209	-4.308023	26015.4952	
HLA B*5301	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.608957	0.300329	-4.308628	40640.2653	
HLA A*6801	1:13-21	9	AKTDFLAPP	0.214925	0.116406	-4.639993	0.331331	-4.308662	43650.902949	
HLA A*3002	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.499353	0.190565	-4.308788	31575.705264	
HLA A*3201	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.466432	0.157520	-4.308912	29270.6303	
HLA B*3801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.573035	0.263887	-4.309148	37414.0962	
HLA B*1503	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.477127	0.167651	-4.309476	30000.392138	
HLA B*1517	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.438203	0.128565	-4.309638	27428.5603	
HLA A*2403	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.345781	0.035827	-4.309955	22170.797837	
HLA B*7301	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.565056	0.255019	-4.310037	36733.0007	
HLA B*5101	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.501282	0.190565	-4.310717	31716.261268	
HLA B*1801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.439634	0.128565	-4.311069	27519.0761	
HLA B*5801	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.346897	0.035827	-4.311071	22227.843341	
HLA B*5701	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.405444	0.093967	-4.311477	25435.726354	
HLA B*3501	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.454010	0.141991	-4.312019	28445.2888	
HLA B*4801	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.439150	0.127125	-4.312025	27488.424939	
HLA A*3001	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.278534	-0.033665	-4.312200	18990.4109	
HLA B*1509	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.511730	0.198739	-4.312991	32488.5363	
HLA B*3801	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.568703	0.255019	-4.313684	37042.7148	
HLA B*5101	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.471209	0.157520	-4.313688	29594.3345	
HLA A*3301	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.583552	0.269704	-4.313848	38331.1239	
HLA B*5701	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.421409	0.107209	-4.314200	26388.1469	
HLA A*1101	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.471725	0.157520	-4.314205	29629.5776	
HLA B*1509	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.510678	0.196360			
HLA A*0206	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.456395	0.141991			

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HLA B*5301	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.499113	0.183904	-4.315209	31558.286321	
HLA B*1502	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.549550	0.234045	-4.315505	35444.5777
HLA B*4001	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.409596	0.093985	-4.315611	25680.039301	
HLA B*5101	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.495223	0.179565	-4.315658	31276.8253
HLA B*4002	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.645134	0.329388	-4.315746	44170.6616
HLA B*5301	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.585502	0.269704	-4.315798	38503.6256
HLA B*3901	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.473349	0.157520	-4.315829	29740.5475
HLA B*1501	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.423380	0.107209	-4.316171	26508.1923
HLA A*2603	1:13-21 9	AKTDFLAPP	0.214925	0.116406	-4.647829	0.331331	-4.316498	44445.599068	
HLA A*3301	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.616848	0.300329	-4.316520	41385.5236
HLA A*2402	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.580697	0.263887	-4.316810	38079.9990
HLA A*0212	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.410965	0.093985	-4.316980	25761.161116	
HLA B*4601	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.411064	0.093967	-4.317097	25767.015112	
HLA B*1801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.484596	0.167005	-4.317591	30520.8021
HLA A*3002	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.581879	0.264217	-4.317661	38183.7625
HLA B*5101	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.485620	0.167651	-4.317970	30592.876939	
HLA B*0702	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.425189	0.107209	-4.317981	26618.8455
HLA A*2402	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.573103	0.255019	-4.318084	37419.9664
HLA A*0203	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.425535	0.107209	-4.318326	26640.0226
HLA A*6802	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.412302	0.093967	-4.318335	25840.581991	
HLA B*4501	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.514911	0.196360	-4.318551	32727.3883
HLA A*2403	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.414055	0.093967	-4.320088	25945.079548	
HLA A*0203	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.414786	0.093967	-4.320819	25988.768251	
HLA B*4501	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.650413	0.329388	-4.321026	44710.8779
HLA A*2402	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.555088	0.234045	-4.321042	35899.4291
HLA A*3002	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.596455	0.275281	-4.321174	39487.071419	
HLA A*3201	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.585791	0.264217	-4.321573	38529.2551
HLA B*4501	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.576684	0.255019	-4.321665	37729.7570
HLA A*0219	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.464003	0.141991	-4.322012	29107.3526
HLA B*4601	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.416367	0.093985	-4.322382	26083.562059	
HLA B*4002	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.622746	0.300329	-4.322417	41951.3230
HLA B*7301	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.592280	0.269704	-4.322576	39109.2862
HLA A*0212	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.430133	0.107209	-4.322924	26923.5629
HLA B*4002	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.645630	0.322700	-4.322929	44221.1106
HLA A*3002	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.622619	0.299515	-4.323104	41939.069467	
HLA B*4403	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.598638	0.275281	-4.323357	39686.024559	
HLA B*3801	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.549254	0.225691	-4.323563	35420.425300	
HLA A*0250	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.593316	0.269704	-4.323612	39202.7030
HLA A*3201	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.599636	0.275281	-4.324356	39777.375759	
HLA B*4501	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.614419	0.290041	-4.324378	41154.6665
HLA A*0211	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.515327	0.190565	-4.324763	32758.741432	
HLA B*4403	1:116-124	9	VVVPPGMED	0.939999	-0.610611	-4.654346	0.329388	-4.324959	45117.6255
HLA A*2902	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.197463	-0.127574	-4.325038	15756.618961	
HLA A*3201	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.361088	0.035827	-4.325262	22966.151040	
HLA A*6802	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.432473	0.107209	-4.325264	27069.0253
HLA A*0202	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.580420	0.255019	-4.325401	38055.6978
HLA A*0219	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.419518	0.093967	-4.325550	26273.477521	
HLA B*1501	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.419626	0.093985	-4.325641	26280.016618	
HLA A*3201	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.625276	0.299515	-4.325761	42196.463854	
HLA B*5701	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.420058	0.093985	-4.326073	26306.189286	
HLA A*2602	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.494116	0.167651	-4.326465	31197.231635	
HLA B*4801	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.420542	0.093967	-4.326575	26335.522223	
HLA A*3301	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.337196	0.010485	-4.326711	21736.834748	
HLA B*4501	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.643562	0.316807	-4.326756	44011.087455	
HLA A*8001	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.434014	0.107209	-4.326805	27165.2609
HLA A*0216	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.468876	0.141991	-4.326885	29435.7794
HLA A*3002	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.468991	0.141991	-4.327000	29443.5834
HLA B*1509	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.535958	0.208763	-4.327195	34352.4752
HLA A*0202	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.591519	0.264217	-4.327301	39040.7954
HLA A*0202	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.494339	0.167005	-4.327334	31213.2692
HLA B*3901	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.506902	0.179565	-4.327337	32129.3511
HLA A*3002	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.526544	0.198739	-4.327804	33615.8153
HLA B*5101	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.422276	0.093967	-4.328309	26440.876922	
HLA A*2603	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.645270	0.316807	-4.328464	44184.523433	
HLA B*5401	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.496224	0.167651	-4.328573	31348.989440	
HLA A*2602	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.598433	0.269704	-4.328729	39667.3503
HLA A*0211	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.495796	0.167005	-4.328791	31318.1384
HLA B*2705	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.471871	0.142013	-4.329858	29639.517773	
HLA B*4402	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.424202	0.093967	-4.330235	26558.432088	
HLA B*1502	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.599979	0.269704	-4.330275	39808.8060
HLA A*3301	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.630464	0.299515	-4.330949	42703.524500	
HLA A*1101	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.473029	0.142013	-4.331016	29718.674111	
HLA B*1517	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.473147	0.142013	-4.331133	29726.713935	
HLA A*2301	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.540699	0.208763	-4.331937	34729.5612
HLA B*0803	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.499597	0.167651	-4.331947	31593.475653	
HLA A*2501	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.459426	0.127125	-4.332301	28802.216559	
HLA A*2603	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.596305	0.263887	-4.332418	39473.4020
HLA B*4501	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.655178	0.322700	-4.332478	45204.1131
HLA B*4002	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.596655	0.263887	-4.332768	39505.2333
HLA B*0802	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.474803	0.142013	-4.332790	29840.307268	
HLA A*0250	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.597096	0.264217	-4.332879	39545.4329
HLA B*1801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.360964	0.027900	-4.333064	22959.567034	
HLA B*0803	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.512773	0.179565	-4.333208	32566.6673
HLA A*8001	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.460970	0.127125	-4.333844	28904.770341	
HLA A*2601	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.394035	0.060047	-4.333988	24776.219783	
HLA A*6801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.501376	0.167005	-4.334371	31723.1252
HLA A*0202	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.531034	0.196360	-4.334673	33965.1483
HLA B*1503	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.462250	0.127125	-4.335125	28990.118623	
HLA A*0206	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.395409	0.060047	-4.335362	24854.755404	
HLA B*1509	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.464153	0.128565	-4.335588	29117.4323
HLA A*1101	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.477667	0.141991	-4.335676	30037.7440
HLA B*2705	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.346230	0.010485	-4.335745	22193.718515	
HLA A*2501	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.268483	-0.067515	-4.335998	18555.9530
HLA B*5301	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.600221	0.264217	-4.336004	39830.9944
HLA A*0202	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.545161	0.208763	-4.336398	35088.1902
HLA A*3002	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.269153	-0.067515	-4.336668	18584.5850
HLA A*2902	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.463951	0.127125	-4.336826	29103.888612	
HLA B*5801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.364944	0.027900	-4.337044	23170.943679	
HLA B*5101	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.479056	0.141991	-4.337065	30133.9357
HLA A*3001	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.281173	-0.055989	-4.337162	19106.134638	
HLA A*3301	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.645357	0.308151	-4.337207	44193.368553	
HLA B*1801	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.527890	0.190565	-4.337325	33720.181566	
HLA A*0202	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.373172	0.035827	-4.337345	23614.111963	
HLA B*1502	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.612991	0.275281	-4.337710	41019.522515	
HLA B*4403	1:194-202	9	HFIAMRASE	0.847376	-0.557335	-4.627809	0.290041	-4.337768	42443.2667
HLA A*0250	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.592848	0.255019	-4.337829	39160.5214
HLA A*2301	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.528484	0.190565	-4.337920	33766.366044	
HLA B*3801	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.536818	0.198739	-4.338078	34420.5612
HLA B*1801	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.374525	0.035827	-4.338698	23687.810573	
HLA A*0301	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.366835	0.027900	-4.338935	23272.072275	
HLA B*7301	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.522914	0.183904	-4.339009	33336.015945	
HLA A*0206	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.537753	0.198739	-4.339014	34494.7532
HLA B*5301	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.594075	0.255019	-4.339056	39271.2659
HLA B*5801	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.349970	0.010485	-4.339485	22385.688369	
HLA B*4403	1:237-245	9	DGTEVATSP	0.480538	-0.157838	-4.662734	0.322700	-4.340034	45997.4646
HLA B*4403	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.574170	0.234045		
HLA A*2602	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.639723	0.299515	-4.3402		

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HLA A*0212	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.400644	0.060047	-4.340597	25156.148293		
HLA B*7301	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.566682	0.225691	-4.340992	36870.773726		
HLA B*3901	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.483367	0.141991	-4.341376	30434.5695	
HLA B*1509	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.508396	0.167005	-4.341391	32240.0886	
HLA A*0203	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.435952	0.093985	-4.341967	27286.774810		
HLA B*3801	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.509052	0.167005	-4.342047	32288.7872	
HLA B*2705	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.499687	0.157520	-4.342166	31599.9711	
HLA B*3901	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.484939	0.142013	-4.342926	30544.918388		
HLA A*0101	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.378947	0.035827	-4.343120	23930.217847		
HLA B*0803	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.500753	0.157520	-4.343233	31677.6789	
HLA A*2603	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.643586	0.300329	-4.343257	44013.4684	
HLA A*2602	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.371160	0.027900	-4.343261	23505.011007		
HLA B*5401	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.542015	0.198739	-4.343276	34834.9353	
HLA A*2902	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.276046	-0.067515	-4.343561	18881.9245	
HLA A*2602	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.577678	0.234045	-4.343633	37816.1960	
HLA B*5301	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.607836	0.263887	-4.343949	40535.5276	
HLA B*2705	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.485952	0.141991	-4.343961	30616.2219	
HLA A*3301	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.523661	0.179565	-4.344096	33393.4147	
HLA A*0203	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.311089	-0.033665	-4.344754	20468.6323	
HLA A*2602	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.620093	0.275281	-4.344812	41695.875171		
HLA B*4402	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.438920	0.093985	-4.344935	27473.855287		
HLA B*0803	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.487227	0.141991	-4.345236	30706.2914	
HLA A*2603	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.609577	0.264217	-4.345359	40698.3496	
HLA A*2403	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.452587	0.107209	-4.345378	28352.1867	
HLA B*3801	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.529828	0.183904	-4.345924	33871.016432		
HLA A*6802	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.440578	0.093985	-4.346593	27578.989073		
HLA B*4001	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.382518	0.035827	-4.346691	24127.808063		
HLA A*0211	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.543173	0.196360	-4.346813	34927.9667	
HLA B*0802	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.454114	0.107209	-4.346905	28452.0606	
HLA A*2902	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.281034	-0.066090	-4.347124	19100.0372	
HLA A*2301	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.546242	0.198739	-4.347502	35175.6176	
HLA A*2902	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.441572	0.093967	-4.347605	27642.172632		
HLA B*4801	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.407824	0.060047	-4.347777	25575.502323		
HLA B*4002	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.647664	0.299515	-4.348149	44428.771051		
HLA A*0301	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.358847	0.010485	-4.348361	22847.927289		
HLA B*1503	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.528440	0.179565	-4.348875	33762.8954	
HLA B*4403	1:60-68 9	YLRHIIDVG	0.914107	-0.597300	-4.665932	0.316807	-4.349125	46337.387670		
HLA A*3201	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.604403	0.255019	-4.349384	40216.4038	
HLA B*4801	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.443417	0.093985	-4.349431	27759.812004		
HLA A*2301	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.546197	0.196360	-4.349837	35172.0021	
HLA A*2902	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.457544	0.107209	-4.350335	28677.6773	
HLA A*1101	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.477599	0.127125	-4.350474	30033.031939		
HLA A*3001	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.287914	-0.062772	-4.350685	19404.9937	
HLA A*0101	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.379109	0.027900	-4.351209	23939.152242		
HLA A*2902	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.445291	0.093985	-4.351306	27879.912710		
HLA B*5101	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.493430	0.142013	-4.351417	31147.988659		
HLA A*0212	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.362101	0.010485	-4.351615	23019.762824		
HLA B*7301	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.615895	0.264217	-4.351677	41294.7236	
HLA A*2602	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.616578	0.264217	-4.352361	41359.7842	
HLA B*5101	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.217180	-0.135764	-4.352944	16488.453007		
HLA A*3201	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.532601	0.179565	-4.353036	34087.9294	
HLA A*6801	1:105-113	9	SQRYVPEKD	0.991805	-0.691476	-4.653519	0.300329	-4.353190	45031.7906	
HLA A*0211	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.533021	0.179565	-4.353456	34120.9551	
HLA B*0702	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.413923	0.060047	-4.353876	25937.220578		
HLA B*1517	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.461216	0.107209	-4.354008	28921.1940	
HLA A*1101	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.448118	0.093967	-4.354151	28061.949590		
HLA A*2402	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.512543	0.157520	-4.355023	32549.4060	
HLA A*3002	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.563865	0.208763	-4.355103	36632.3870	
HLA B*1509	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.534734	0.179565	-4.355169	34255.7873	
HLA B*4001	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.158692	-0.196676	-4.355368	14410.9241	
HLA A*8001	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.449537	0.093967	-4.355570	28153.794033		
HLA B*0702	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.449650	0.093985	-4.355665	28161.105810		
HLA A*2603	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.498232	0.142013	-4.356219	31494.328658		
HLA B*0801	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.450418	0.093985	-4.356433	28210.967847		
HLA A*0219	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.463733	0.107209	-4.356524	29089.2495	
HLA B*4501	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.656369	0.299515	-4.356854	45328.269812		
HLA A*0219	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.451153	0.093985	-4.357168	28258.777813		
HLA A*3301	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.632971	0.275281	-4.357690	42950.737076		
HLA A*2603	1:21-29 9	PDVPWTTDA	0.878208	-0.602927	-4.633302	0.275281	-4.358021	42983.512155		
HLA A*6801	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.622306	0.264217	-4.358089	41908.9045	
HLA A*2301	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.537814	0.179565	-4.358249	34499.6055	
HLA B*3501	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.465530	0.107209	-4.358321	29209.8867	
HLA B*5401	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.538315	0.179565	-4.358750	34539.3825	
HLA B*3801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.567596	0.208763	-4.358834	36948.4480	
HLA B*4403	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.628652	0.269704	-4.358948	42525.7780	
HLA B*1503	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.501118	0.142013	-4.359104	31704.252840		
HLA B*7301	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.501573	0.141991	-4.359582	31737.5445	
HLA A*0250	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.593659	0.234045	-4.359614	39233.6793	
HLA B*1509	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.502414	0.141991	-4.360423	31799.0714	
HLA B*1501	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.243518	-0.116983	-4.360501	17519.3358	
HLA B*5301	1:63-71 9	HIIDVGHFS	1.098577	-0.872886	-4.586228	0.225691	-4.360537	38568.044274		
HLA B*4002	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.569314	0.208763	-4.360551	37094.8547	
HLA A*2602	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.557071	0.196360	-4.360710	36063.7188	
HLA B*4002	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.631441	0.269704	-4.361737	42799.7375	
HLA A*6801	1:29-37 9	ADGGPALVE	1.188164	-0.880013	-4.670034	0.308151	-4.361883	46777.148827		
HLA A*0202	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.519603	0.157520	-4.362083	33082.8770	
HLA B*1509	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.519655	0.157520	-4.362135	33086.8147	
HLA B*1517	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.489499	0.127125	-4.362374	30867.348089		
HLA B*3801	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.558764	0.196360	-4.362404	36204.6611	
HLA A*2603	1:20-28 9	PPDVPWTTD	1.438358	-1.138843	-4.661956	0.299515	-4.362441	45915.172219		
HLA A*3201	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.571212	0.208763	-4.362449	37257.3582	
HLA A*3101	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.456522	0.093985	-4.362537	28610.269450		
HLA A*0216	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.489835	0.127125	-4.362710	30891.236746		
HLA A*6901	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.373705	0.010485	-4.363220	23643.128965		
HLA A*3002	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.505481	0.142013	-4.363467	32024.364221		
HLA A*0202	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.505624	0.142013	-4.363610	32034.934109		
HLA A*6801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.391570	0.027900	-4.363671	24636.013597		
HLA B*1509	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.554319	0.190565	-4.363755	35835.977992		
HLA A*2403	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.423819	0.060047	-4.363772	26535.022868		
HLA A*2603	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.633734	0.269704	-4.364030	43026.3200	
HLA B*1501	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.374628	0.010485	-4.364143	23693.449775		
HLA A*2602	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.531553	0.167005	-4.364548	34005.7808	
HLA B*5301	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.598842	0.234045	-4.364797	39704.7075	
HLA A*0202	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.331647	-0.033665	-4.365312	21460.8451	
HLA B*4402	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.425370	0.060047	-4.365323	26629.936224		
HLA A*2301	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.507461	0.141991	-4.365470	32170.7460	
HLA A*0250	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.574412	0.208763	-4.365649	37532.8944	
HLA B*4501	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.565056	0.198739	-4.366317	36733.0007	
HLA B*1501	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.299215	-0.067515	-4.366730	19916.5691	
HLA B*4801	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.403055	0.035827	-4.367228	25296.166888		
HLA A*0202	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.150638	-0.216975	-4.367613	14146.134943		
HLA A*2402	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.547402	0.179565	-4.367838	35269.7496	
HLA A*8001	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.403666	0.035827	-4.367839	25331.772783		
HLA A*2301	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.525797	0.157520	-4.368276	33558.0342	
HLA B*3801	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.535991	0.167651	-4.368340	34355.077193		
HLA B*4801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.302445	-0.066090			
HLA B*4002	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.623817	0.255019			

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HLA B*4403	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.668516	0.299515	-4.369001	46613.957916
HLA B*5101	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.497711	0.128565	-4.369146	31456.5268
HLA A*0101	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.302165	-0.067515	-4.369681	20052.3595
HLA B*2705	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.430182	0.060047	-4.370135	26926.621872
HLA B*1502	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.566734	0.196360	-4.370374	36875.1622
HLA B*1503	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.380890	0.010485	-4.370404	24037.520979
HLA B*0802	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.465074	0.093967	-4.371107	29179.246537
HLA B*5701	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.407408	0.035827	-4.371582	25551.024212
HLA B*3501	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.465607	0.093985	-4.371622	29215.101971
HLA A*8001	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.465638	0.093985	-4.371653	29217.156700
HLA B*5401	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.538726	0.167005	-4.371721	34572.0975
HLA A*3002	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.407561	0.035827	-4.371734	25560.010626
HLA A*0206	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.478999	0.107209	-4.371791	30130.0235
HLA A*2601	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.382281	0.010485	-4.371795	24114.628259
HLA B*0803	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.479204	0.107209	-4.371995	30144.2078
HLA A*2402	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.514019	0.142013	-4.372005	32660.177821
HLA A*0206	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.466505	0.093967	-4.372538	29275.539676
HLA B*2705	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.499715	0.127125	-4.372590	31602.022669
HLA A*2501	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.432740	0.060047	-4.372693	27085.724752
HLA B*5301	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.499964	0.127125	-4.372839	31620.149991
HLA B*1509	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.500396	0.127125	-4.373271	31651.640978
HLA A*0203	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.317362	-0.055989	-4.373351	20766.435204
HLA B*5401	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.564173	0.190565	-4.373608	36658.357422
HLA A*3201	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.541547	0.167651	-4.373897	34797.453306
HLA A*2403	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.401845	0.027900	-4.373945	25225.787504
HLA A*0216	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.468147	0.093967	-4.374180	29386.455078
HLA B*3801	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.564972	0.190565	-4.374407	36725.847473
HLA B*5401	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.516504	0.141991	-4.374513	32847.6496
HLA B*4001	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.402590	0.027900	-4.374690	25269.085202
HLA B*4403	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.600769	0.225691	-4.375078	39881.233263
HLA B*0802	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.435560	0.060047	-4.375513	27262.133666
HLA B*4403	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.639678	0.263887	-4.375792	43619.2707
HLA A*2301	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.542809	0.167005	-4.375804	34898.6907
HLA A*6801	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.543474	0.167651	-4.375823	34952.161502
HLA A*0216	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.483092	0.107209	-4.375884	30415.3118
HLA A*3301	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.566504	0.190565	-4.375939	36855.617365
HLA A*0206	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.308455	-0.067515	-4.375970	20344.8763
HLA B*1801	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.469980	0.093967	-4.376013	29510.719496
HLA A*2603	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.404293	0.027900	-4.376393	25368.389458
HLA B*4402	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.313911	-0.062772	-4.376682	20602.0557
HLA A*2402	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.543864	0.167005	-4.376859	34983.5640
HLA B*2705	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.471321	0.093967	-4.377354	29602.020430
HLA B*1517	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.471364	0.093967	-4.377396	29604.903156
HLA A*0219	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.437714	0.060047	-4.377667	27397.713540
HLA A*0201	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.388366	0.010485	-4.377880	24454.891345
HLA A*0202	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.311977	-0.066090	-4.378066	20510.5323
HLA A*0216	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.310579	-0.067515	-4.378094	20444.6174
HLA A*2402	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.586885	0.208763	-4.378123	38626.5102
HLA A*2403	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.312116	-0.066090	-4.378205	20517.0799
HLA B*3901	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.485423	0.107209	-4.378214	30578.9777
HLA B*5101	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.485620	0.107209	-4.378412	30592.8769
HLA B*4501	1:143-151	9	YSELLAKLE	0.997619	-0.727915	-4.648242	0.269704	-4.378538	44487.9376
HLA B*4403	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.642756	0.264217	-4.378539	43929.4965
HLA B*0803	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.520759	0.142013	-4.378746	33171.049885
HLA A*2603	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.563050	0.183904	-4.379145	36563.684047
HLA A*2301	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.547125	0.167651	-4.379475	35247.241824
HLA B*1502	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.588443	0.208763	-4.379681	38765.3028
HLA B*5301	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.546735	0.167005	-4.379730	35215.6025
HLA A*3301	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.613876	0.234045	-4.379831	41103.2683
HLA B*4002	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.644140	0.264217	-4.379923	44069.6978
HLA A*1101	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.487213	0.107209	-4.380005	30705.2947
HLA A*2402	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.579024	0.198739	-4.380285	37933.6031
HLA A*0201	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.408186	0.027900	-4.380286	25596.818739
HLA B*4501	1:229-237	9	DFEVTTLAD	1.112977	-0.848760	-4.645092	0.264217	-4.380874	44166.3606
HLA A*2402	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.577448	0.196360	-4.381087	37796.1524
HLA A*2402	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.571879	0.190565	-4.381315	37314.644818
HLA B*4403	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.636446	0.255019	-4.381426	43295.7741
HLA A*2603	1:151-159	9	EAKFADQPN	0.870281	-0.615262	-4.636509	0.255019	-4.381490	43302.0986
HLA A*0250	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.580516	0.198739	-4.381777	38064.1397
HLA B*1502	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.561565	0.179565	-4.382000	36438.8844
HLA A*0211	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.539882	0.157520	-4.382361	34664.2394
HLA B*1502	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.581329	0.198739	-4.382589	38135.4557
HLA B*4001	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.393140	0.010485	-4.382654	24725.204431
HLA A*6801	1:197-205	9	AMRASEHAD	0.912420	-0.648533	-4.646868	0.263887	-4.382981	44347.3654
HLA A*0211	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.525108	0.142013	-4.383095	33504.883653
HLA B*2705	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.419595	0.035827	-4.383768	26278.168448
HLA B*5301	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.592604	0.208763	-4.383842	39138.4947
HLA A*0206	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.541468	0.157520	-4.383947	34791.0533
HLA A*0301	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.316516	-0.067515	-4.384031	20726.0306
HLA A*2402	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.526492	0.141991	-4.384501	33611.8147
HLA B*5101	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.444591	0.060047	-4.384544	27835.002404
HLA A*0216	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.478833	0.093985	-4.384848	30118.452758
HLA B*1502	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.492758	0.107209	-4.385549	31099.8328
HLA B*1501	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.413681	0.027900	-4.385782	25922.771902
HLA B*3801	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.565352	0.179565	-4.385788	36758.0481
HLA B*5801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.352649	-0.033665	-4.386314	22524.1736
HLA A*0101	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.396826	0.010485	-4.386341	24935.968064
HLA A*6801	1:20-28	9	PPDVPWTTD	1.438358	-1.138843	-4.685940	0.299515	-4.386425	48522.119214
HLA A*2402	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.515311	0.128565	-4.386746	32757.5009
HLA A*3101	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.354533	-0.033665	-4.388198	22622.1122
HLA B*1502	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.515466	0.127125	-4.388340	32769.199149
HLA B*4601	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.416583	0.027900	-4.388683	26096.547334
HLA A*0206	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.515936	0.127125	-4.388810	32804.673884
HLA A*0301	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.355698	-0.033665	-4.389364	22682.8958
HLA B*1509	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.483475	0.093967	-4.389508	30442.144279
HLA A*2301	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.531614	0.142013	-4.389600	34010.564330
HLA B*7301	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.569356	0.179565	-4.389791	37098.4671
HLA B*2705	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.483861	0.093985	-4.389876	30469.165198
HLA B*7301	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.581796	0.190565	-4.391232	38176.533254
HLA A*6901	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.357613	-0.033665	-4.391279	22783.1268
HLA A*6801	1:21-29	9	PDVPWTTDA	0.878208	-0.602927	-4.666676	0.275281	-4.391396	46416.921450
HLA B*4501	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.617539	0.225691	-4.391849	41451.400042
HLA B*3801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.499755	0.107209	-4.392546	31604.9291
HLA B*0801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.359432	-0.033665	-4.393097	22878.7256
HLA B*4402	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.429200	0.035827	-4.393373	26865.800590
HLA B*0803	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.429439	0.035827	-4.393613	26880.629464
HLA A*0206	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.487629	0.093985	-4.393644	30734.710691
HLA B*3901	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.337800	-0.055989	-4.393789	21767.077390
HLA B*4601	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.404347	0.010485	-4.393862	25371.546178
HLA A*2603	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.573853	0.179565	-4.394288	37484.5998
HLA A*0202	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.574210	0.179565	-4.394645	37515.4362
HLA A*2603	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.629320	0.234045	-4.395274	42591.1651
HLA B*7301	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.591657	0.196360	-4.395297	39053.2585
HLA B*3801	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.523940	0.128565	-4.395376	33414.9195
HLA A*2301	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.524032	0.128565	-4.395467	33421.9703
HLA B*4501	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.332807	-0.062772		
HLA B*4002	1:63-71	9	HIIDVGHFS	1.098577	-0.872886	-4.621359	0.225691	-4.3956	

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HLA A*0211	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.537741	0.141991	-4.395750	34493.8201
HLA B*7301	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.260100	-0.135764	-4.395864	18201.211777	
HLA B*5301	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.553748	0.157520	-4.396228	35788.8988
HLA B*1501	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.362996	-0.033665	-4.396661	23067.2593
HLA B*1509	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.539120	0.142013	-4.397107	34603.533037	
HLA B*0801	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.341813	-0.055989	-4.397802	21969.139256	
HLA B*5301	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.596610	0.198739	-4.397871	39501.1729
HLA A*2602	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.606997	0.208763	-4.398234	40457.3157
HLA B*1502	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.588979	0.190565	-4.398414	38813.147613	
HLA A*2501	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.506103	0.107209	-4.398894	32070.3079
HLA B*3801	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.556415	0.157520	-4.398895	36009.3267
HLA B*4801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.427189	0.027900	-4.399289	26741.676315	
HLA B*4403	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.595752	0.196360	-4.399392	39423.2504
HLA A*0250	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.596354	0.196360	-4.399994	39477.8867
HLA A*2501	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.494144	0.093967	-4.400177	31199.256983	
HLA B*1501	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.334102	-0.066090	-4.400192	21582.5140
HLA A*8001	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.428871	0.027900	-4.400971	26845.460553	
HLA B*3801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.543239	0.141991	-4.401248	34933.2578
HLA B*7301	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.559284	0.157520	-4.401763	36247.9727
HLA B*3501	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.412286	0.010485	-4.401800	25839.603446	
HLA A*0301	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.336454	-0.066090	-4.402543	21699.7068
HLA B*5701	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.413350	0.010485	-4.402865	25903.005698	
HLA A*0206	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.545222	0.142013	-4.403209	35093.125965	
HLA B*5701	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.431138	0.027900	-4.403238	26985.974897	
HLA A*3002	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.337192	-0.066090	-4.403281	21736.5999
HLA A*1101	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.497481	0.093985	-4.403495	31439.853959	
HLA B*1801	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.464548	0.060047	-4.404501	29143.908099	
HLA A*2602	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.546587	0.142013	-4.404574	35203.602300	
HLA A*3301	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.287662	-0.116983	-4.404645	19393.7642
HLA A*3201	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.595212	0.190565	-4.404647	39374.227627	
HLA A*0216	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.465950	0.060047	-4.405903	29238.186454	
HLA A*3002	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.534936	0.128565	-4.406371	34271.7285
HLA A*6802	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.372770	-0.033665	-4.406435	23592.2768
HLA B*0803	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.500422	0.093985	-4.406437	31653.524585	
HLA B*5401	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.548589	0.142013	-4.406575	35366.238168	
HLA B*0802	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.500617	0.093985	-4.406632	31667.740867	
HLA B*4501	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.574386	0.167651	-4.406736	37530.660933	
HLA A*2602	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.597484	0.190565	-4.406919	39580.748218	
HLA A*3301	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.616296	0.208763	-4.407534	41332.9427
HLA B*5801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.342257	-0.066090	-4.408347	21991.6135
HLA A*0203	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.342795	-0.066090	-4.408885	22018.8750
HLA B*4001	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.341705	-0.067515	-4.409220	21963.6728
HLA A*0250	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.577034	0.167005	-4.410029	37760.1822
HLA A*0250	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.589606	0.179565	-4.410041	38869.2514
HLA A*6801	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.446882	0.035827	-4.411055	27982.209967	
HLA A*3201	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.607495	0.196360	-4.411135	40503.7426
HLA A*0101	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.377471	-0.033665	-4.411136	23849.0550
HLA B*4501	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.214469	-0.196676	-4.411145	16385.8360
HLA A*2902	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.439169	0.027900	-4.411269	27489.614639	
HLA B*5301	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.590854	0.179565	-4.411289	38981.0697
HLA B*4402	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.439263	0.027900	-4.411363	27495.563914	
HLA B*4402	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.422187	0.010485	-4.411701	26435.441877	
HLA A*2601	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.378402	-0.033665	-4.412067	23900.2020
HLA B*4402	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.346550	-0.066090	-4.412639	22210.0534
HLA A*6801	1:193-201	9	RHFIAMRAS	1.077019	-0.842974	-4.647046	0.234045	-4.413001	44365.6027
HLA A*0201	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.346611	-0.067515	-4.414126	22213.1776
HLA B*1503	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.346611	-0.067515	-4.414126	22213.1776
HLA A*0219	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.425147	0.010485	-4.414662	26616.253565	
HLA B*1801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.297990	-0.116983	-4.414974	19860.5123
HLA B*4402	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.359411	-0.055989	-4.415399	22877.611696	
HLA B*5801	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.359422	-0.055989	-4.415411	22878.230531	
HLA A*3201	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.599429	0.183904	-4.415525	39758.443440	
HLA B*3901	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.475607	0.060047	-4.415560	29895.568376	
HLA A*0203	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.443532	0.027900	-4.415632	27767.171677	
HLA A*6901	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.229813	-0.186575	-4.416388	16975.129327	
HLA B*5301	1:84-92 9	GISRSCTHE	0.888751	-0.698186	-4.607107	0.190565	-4.416543	40467.603881	
HLA A*2301	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.544127	0.127125	-4.417002	35004.767325	
HLA B*0803	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.511404	0.093967	-4.417436	32464.115002	
HLA B*5101	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.511791	0.093985	-4.417806	32493.106438	
HLA A*2402	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.352003	-0.066090	-4.418092	22490.6888
HLA B*0801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.446797	0.027900	-4.418898	27976.760794	
HLA A*0201	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.385443	-0.033665	-4.419108	24290.8648
HLA B*7301	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.586763	0.167651	-4.419113	38615.645561	
HLA A*2402	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.586853	0.167651	-4.419202	38623.584819	
HLA B*5801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.351789	-0.067515	-4.419304	22479.6194
HLA A*0216	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.447281	0.027900	-4.419382	28007.956515	
HLA B*4801	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.429980	0.010485	-4.419494	26914.097163	
HLA B*5401	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.548145	0.128565	-4.419580	35330.0957
HLA A*0206	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.386247	-0.033665	-4.419912	24335.8490
HLA B*0801	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.430962	0.010485	-4.420476	26975.027783	
HLA A*0212	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.449060	0.027900	-4.421160	28122.892297	
HLA B*7301	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.588243	0.167005	-4.421238	38747.4811
HLA B*0702	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.432289	0.010485	-4.421804	27057.605450	
HLA B*0803	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.432454	0.010485	-4.421968	27067.853896	
HLA A*0301	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.366147	-0.055989	-4.422135	23235.212991	
HLA A*3301	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.618719	0.196360	-4.422358	41564.1252
HLA B*3901	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.516401	0.093985	-4.422416	32839.831701	
HLA B*4002	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.621432	0.198739	-4.422693	41824.6485
HLA B*5301	1:26-34 9	TTDADGGPA	0.518414	-0.350763	-4.591133	0.167651	-4.423483	39006.172919	
HLA B*4002	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.389867	-0.033665	-4.423532	24539.5762
HLA A*6901	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.207129	-0.216975	-4.424104	16111.234318	
HLA A*3101	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.452034	0.027900	-4.424135	28316.164825	
HLA B*1517	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.307757	-0.116983	-4.424741	20312.2136
HLA A*6901	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.307792	-0.116983	-4.424776	20313.8620
HLA A*0211	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.518776	0.093967	-4.424809	33019.937895	
HLA B*7301	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.567509	0.142013	-4.425496	36941.052934	
HLA A*6802	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.436305	0.010485	-4.425819	27308.926561	
HLA A*0219	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.453900	0.027900	-4.426000	28438.057155	
HLA B*1517	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.520031	0.093985	-4.426046	33115.466479	
HLA A*0202	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.520628	0.093967	-4.426660	33161.002112	
HLA A*2501	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.520787	0.093985	-4.426802	33173.203375	
HLA A*2603	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.555503	0.128565	-4.426939	35933.8211
HLA B*1501	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.364302	-0.062772	-4.427074	23136.7477
HLA B*4002	1:80-88 9	FYITGISRS	1.033042	-0.849138	-4.611149	0.183904	-4.427244	40845.912667	
HLA B*0802	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.463091	0.035827	-4.427264	29046.319360	
HLA B*4601	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.393965	-0.033665	-4.427630	24772.1990
HLA A*0250	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.585159	0.157520	-4.427638	38473.2257
HLA A*0211	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.554867	0.127125	-4.427741	35881.177873	
HLA A*0211	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.487991	0.060047	-4.427944	30760.327153	
HLA B*5101	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.463787	0.035827	-4.427960	29092.869282	
HLA A*0250	1:66-74 9	DVGHFSVLE	0.964068	-0.822055	-4.570239	0.142013	-4.428226	37174.006589	
HLA A*8001	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.438863	0.010485	-4.428378	27470.288386	
HLA A*0301	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.365670	-0.062772	-4.428441	23209.7099
HLA B*1502	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.595705	0.167005	-4.428700	39418.9851
HLA B*1502	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.586409	0.157520	-4.428888	38584.1135
HLA A*2301	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.536555	0.107209		
HLA A*0101	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.373820	-0.055989	-4.4298		

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HLA B*5801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.367058	-0.062772	-4.429830	23284.0357
HLA B*4002	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.627447	0.196360	-4.431087	42407.9209
HLA B*7301	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.525183	0.093967	-4.431216	33510.684402
HLA B*1503	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.525453	0.093967	-4.431486	33531.539134
HLA B*3801	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.558696	0.127125	-4.431571	36198.981536
HLA A*0202	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.573677	0.141991	-4.431686	37469.3939
HLA B*4001	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.365858	-0.066090	-4.431947	23219.7570
HLA A*0203	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.442547	0.010485	-4.432062	27704.301902
HLA A*0211	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.539416	0.107209	-4.432208	34627.1284
HLA B*3801	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.574325	0.142013	-4.432312	37525.382349
HLA B*4403	1:180-188	9	ETRIVVTGN	0.840941	-0.642202	-4.631979	0.198739	-4.433240	42852.7935
HLA B*0702	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.461291	0.027900	-4.433392	28926.201192
HLA B*1502	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.575899	0.142013	-4.433886	37661.644616
HLA A*0101	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.371691	-0.062772	-4.434463	23533.7666
HLA B*1801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.542184	0.107209	-4.434975	34848.5065
HLA B*3901	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.445538	0.010485	-4.435053	27895.754069
HLA A*0101	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.369516	-0.066090	-4.435605	23416.1676
HLA B*4501	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.603741	0.167005	-4.436736	40155.0968
HLA A*0201	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.370726	-0.066090	-4.436815	23481.4982
HLA A*3201	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.370768	-0.066090	-4.436858	23483.7849
HLA A*2603	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.645912	0.208763	-4.437149	44249.8277
HLA B*1509	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.497426	0.060047	-4.437379	31435.942222
HLA A*3001	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.302161	-0.135764	-4.437925	20052.142551
HLA A*6901	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.381966	-0.055989	-4.437954	24097.153293
HLA B*1801	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.310579	-0.127574	-4.438153	20444.617425
HLA A*0201	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.382356	-0.055989	-4.438344	24118.803259
HLA A*0250	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.580751	0.141991	-4.438760	38084.7375
HLA B*0801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.374527	-0.066090	-4.440617	23687.9387
HLA A*0101	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.254577	-0.186575	-4.441152	17971.182875
HLA B*4002	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.609652	0.167651	-4.442001	40705.395849
HLA A*2603	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.584249	0.141991	-4.442258	38392.7614
HLA B*5301	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.584578	0.142013	-4.442565	38421.850564
HLA A*3301	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.610686	0.167651	-4.443035	40802.404399
HLA A*3002	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.257431	-0.186575	-4.444006	18089.696806
HLA A*0203	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.331433	-0.112631	-4.444064	21450.2825
HLA A*6901	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.378059	-0.066090	-4.444148	23881.3320
HLA A*0202	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.571355	0.127125	-4.444230	37269.655377
HLA B*7301	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.573301	0.128565	-4.444736	37436.9750
HLA A*2301	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.504874	0.060047	-4.444827	31979.697349
HLA A*2601	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.388873	-0.055989	-4.444862	24483.484470
HLA B*1509	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.455566	0.010485	-4.445080	28547.343948
HLA A*0206	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.248607	-0.196676	-4.445283	17725.8317
HLA A*2403	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.412088	-0.033665	-4.445754	25827.8638
HLA B*1501	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.389825	-0.055989	-4.445813	24537.186719
HLA A*3301	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.506061	0.060047	-4.446014	32067.185145
HLA B*1517	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.379943	-0.066090	-4.446032	23985.1718
HLA A*6901	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.383263	-0.062772	-4.446034	24169.2211
HLA A*2602	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.573327	0.127125	-4.446201	37439.202992
HLA B*1801	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.540215	0.093985	-4.446230	34690.878886
HLA B*5401	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.553755	0.107209	-4.446547	35789.4797
HLA A*0219	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.379438	-0.067515	-4.446953	23957.2902
HLA A*2603	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.379572	-0.067515	-4.447087	23964.6789
HLA A*0216	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.457852	0.010485	-4.447366	28698.008276
HLA A*2602	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.576252	0.128565	-4.447687	37692.2188
HLA A*0202	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.541963	0.093985	-4.447978	34830.789578
HLA A*2301	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.542187	0.093985	-4.448201	34848.695097
HLA A*3301	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.590271	0.141991	-4.448280	38928.8057
HLA B*7301	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.576254	0.127125	-4.449129	37692.422729
HLA A*3002	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.576282	0.127125	-4.449157	37694.869751
HLA B*0702	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.381710	-0.067515	-4.449225	24082.9479
HLA A*2902	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.416550	-0.033665	-4.450215	26094.5708
HLA A*0202	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.322691	-0.127574	-4.450265	21022.801192
HLA A*2301	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.544289	0.093967	-4.450322	35017.836426
HLA B*1503	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.544778	0.093985	-4.450793	35057.262668
HLA A*0201	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.388079	-0.062772	-4.450851	24438.7562
HLA B*5701	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.417347	-0.033665	-4.451012	26142.4710
HLA B*5701	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.384938	-0.066090	-4.451027	24262.6279
HLA A*0203	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.388617	-0.062772	-4.451389	24469.0513
HLA B*1502	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.593927	0.141991	-4.451936	39257.8832
HLA B*4501	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.643038	0.190565	-4.452473	43958.024261
HLA A*2601	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.386787	-0.066090	-4.452876	24366.1483
HLA B*4002	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.644638	0.190565	-4.454073	44120.270219
HLA B*1801	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.464583	0.010485	-4.454098	29146.273175
HLA A*0212	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.420746	-0.033665	-4.454412	26347.9202
HLA B*4403	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.639681	0.183904	-4.455776	43619.506754
HLA B*4501	1:80-88	9	FYITGISRS	1.033042	-0.849138	-4.639756	0.183904	-4.455851	43627.058662
HLA B*1509	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.550722	0.093985	-4.456737	35540.390857
HLA B*4601	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.400931	-0.055989	-4.456920	25172.756994
HLA A*6801	1:148-156	9	AKLEAKFAD	0.884617	-0.675854	-4.665744	0.208763	-4.456981	46317.3375
HLA A*2601	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.340262	-0.116983	-4.457246	21890.8377
HLA A*0211	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.551246	0.093985	-4.457261	35583.292846
HLA B*4002	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.624416	0.167005	-4.457411	42112.9966
HLA A*2601	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.394768	-0.062772	-4.457540	24818.0745
HLA B*5301	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.599657	0.141991	-4.457666	39779.3125
HLA A*2902	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.240715	-0.216975	-4.457690	17406.630166
HLA A*8001	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.391615	-0.066090	-4.457705	24638.5460
HLA A*3101	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.401981	-0.055989	-4.457970	25233.703932
HLA A*8001	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.390743	-0.067515	-4.458259	24589.1443
HLA B*7301	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.341736	-0.116983	-4.458719	21965.2175
HLA A*3101	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.272506	-0.186575	-4.459081	18728.611619
HLA A*2402	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.553069	0.093985	-4.459084	35732.988137
HLA B*0702	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.426153	-0.033665	-4.459818	26677.9531
HLA B*0801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.342953	-0.116983	-4.459936	22026.8574
HLA B*4001	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.426789	-0.033665	-4.460455	26717.0938
HLA A*3301	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.627618	0.167005	-4.460613	42424.6720
HLA B*0702	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.404840	-0.055989	-4.460829	25400.386580
HLA B*1503	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.427184	-0.033665	-4.460849	26741.3869
HLA A*1101	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.393936	-0.067515	-4.461451	24770.5908
HLA A*2603	1:223-231	9	APAVFADFE	0.916367	-0.720007	-4.657974	0.196360	-4.461614	45496.0655
HLA A*3201	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.603856	0.141991	-4.461865	40165.7428
HLA A*0212	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.406109	-0.055989	-4.462098	25474.698241
HLA A*0216	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.428544	-0.033665	-4.462210	26825.2810
HLA A*2403	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.399577	-0.062772	-4.462349	25094.4383
HLA A*3002	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.569706	0.107209	-4.462497	37128.3832
HLA B*4002	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.642096	0.179565	-4.462531	43862.7665
HLA A*6802	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.345772	-0.116983	-4.462755	22170.3180
HLA B*4601	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.396791	-0.066090	-4.462880	24933.9446
HLA B*4601	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.400440	-0.062772	-4.463212	25144.3110
HLA A*2402	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.591204	0.127125	-4.464078	39012.504005
HLA A*2603	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.654917	0.190565	-4.464352	45176.976338
HLA A*1101	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.475029	0.010485	-4.464543	29855.808838
HLA B*4801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.430903	-0.033665	-4.464568	26971.3797
HLA B*0802	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.397263	-0.067515	-4.464778	24961.0722
HLA A*3101	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.402615	-0.062772	-4.465387	25270.5889
HLA B*4001	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.409560	-0.055989	-4.465549	25677.955493
HLA A*0211	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.399566	-0.066090		
HLA B*0801	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.338216	-0.127574	-4.4657	

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HLA B*1501	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.269599	-0.196676	-4.466276	18603.6975
HLA A*3101	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.354202	-0.112631	-4.466833	22604.8628
HLA A*6802	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.410958	-0.055989	-4.466947	25760.743024
HLA B*1517	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.478567	0.010485	-4.468082	30100.046448
HLA B*5701	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.400600	-0.067515	-4.468115	25153.5626
HLA B*5401	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.562329	0.093985	-4.468344	36503.008166
HLA B*5801	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.355797	-0.112631	-4.468428	22688.0503
HLA B*0702	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.332796	-0.135764	-4.468560	21517.693560
HLA B*0803	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.529161	0.060047	-4.469114	33819.016671
HLA A*0301	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.356800	-0.112631	-4.469431	22740.5207
HLA B*3901	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.497941	0.027900	-4.470041	31473.208520
HLA B*1517	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.498164	0.027900	-4.470265	31489.388001
HLA B*1502	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.530373	0.060047	-4.470326	33913.554440
HLA A*0212	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.407704	-0.062772	-4.470476	25568.4469
HLA A*0212	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.404389	-0.066090	-4.470479	25374.0169
HLA B*1517	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.437146	-0.033665	-4.470811	27361.8681
HLA B*0802	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.498759	0.027900	-4.470859	31532.517097
HLA B*0802	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.482122	0.010485	-4.471637	30347.431274
HLA B*3501	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.405583	-0.066090	-4.471672	25443.8463
HLA B*4501	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.651299	0.179565	-4.471734	44802.1600
HLA B*4501	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.600541	0.128565	-4.471976	39860.3107
HLA B*1503	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.275344	-0.196676	-4.472020	18851.4066
HLA B*0801	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.255162	-0.216975	-4.472137	17995.407492
HLA B*3801	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.508340	0.035827	-4.472513	32235.902958
HLA B*7301	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.406593	-0.066090	-4.472683	25503.1040
HLA B*2705	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.500711	0.027900	-4.472811	31674.594368
HLA A*0250	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.600383	0.127125	-4.473258	39845.865454
HLA B*5101	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.501237	0.027900	-4.473338	31713.001388
HLA B*0801	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.337864	-0.135764	-4.473628	21770.257074
HLA B*5801	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.287359	-0.186575	-4.473934	19380.234506
HLA A*2603	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.601175	0.127125	-4.474050	39918.576012
HLA B*1509	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.346686	-0.127574	-4.474260	22217.023460
HLA A*1101	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.408256	-0.066090	-4.474346	25600.9733
HLA B*4601	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.407068	-0.067515	-4.474583	25530.9889
HLA B*3801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.408968	-0.066090	-4.475058	25642.9727
HLA A*3101	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.358252	-0.116983	-4.475236	22816.6766
HLA B*0801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.412551	-0.062772	-4.475323	25855.4044
HLA B*4403	1:232-240	9	VTTLADGTE	0.928517	-0.748952	-4.654952	0.179565	-4.475388	45180.6425
HLA B*5701	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.412800	-0.062772	-4.475572	25870.2354
HLA B*3801	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.570054	0.093967	-4.476087	37158.122511
HLA B*5701	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.420117	-0.055989	-4.476105	26309.747366
HLA A*2902	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.420765	-0.055989	-4.476754	26349.060566
HLA A*2402	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.536874	0.060047	-4.476827	34425.030608
HLA B*5301	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.605538	0.128565	-4.476973	40321.6257
HLA A*8001	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.443353	-0.033665	-4.477018	27755.7575
HLA B*5801	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.349486	-0.127574	-4.477061	22360.754822
HLA B*5801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.360231	-0.116983	-4.477214	22920.8466
HLA B*3801	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.571471	0.093985	-4.477485	37279.536297
HLA A*2602	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.585546	0.107209	-4.478338	38507.5835
HLA A*3002	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.572791	0.093967	-4.478824	37393.051898
HLA B*4403	1:84-92	9	GISRSCTHE	0.888751	-0.698186	-4.669663	0.190565	-4.479098	46737.182558
HLA A*3001	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.262358	-0.216975	-4.479333	18296.084523
HLA B*1501	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.366828	-0.112631	-4.479459	23271.6945
HLA A*2403	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.412058	-0.067515	-4.479573	25826.0474
HLA A*0219	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.446391	-0.033665	-4.480056	27950.5892
HLA B*4403	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.647552	0.167005	-4.480546	44417.2355
HLA A*6802	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.414671	-0.066090	-4.480760	25981.8799
HLA A*0301	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.353257	-0.127574	-4.480832	22555.755755
HLA B*3501	1:119-127	9	PPGMEDDAD	0.692523	-1.179914	-3.993955	-0.487391	-4.481347	9861.7807
HLA B*5101	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.492067	0.010485	-4.481582	31050.407674
HLA B*3501	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.364692	-0.116983	-4.481676	23157.5348
HLA A*0301	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.364850	-0.116983	-4.481833	23165.9301
HLA B*2705	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.448402	-0.033665	-4.482067	28080.3248
HLA A*6802	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.354890	-0.127574	-4.482465	22640.722162
HLA B*1509	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.518311	0.035827	-4.482484	32984.587259
HLA B*4002	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.640038	0.157520	-4.482517	43655.3899
HLA A*0206	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.416567	-0.066090	-4.482656	26095.5590
HLA A*6901	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.356011	-0.127574	-4.483585	22699.222381
HLA A*3301	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.610766	0.127125	-4.483640	40809.910130
HLA A*3002	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.577894	0.093985	-4.483909	37835.022251
HLA B*4801	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.428323	-0.055989	-4.484312	26811.643057
HLA A*6802	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.371710	-0.112631	-4.484341	23534.7851
HLA A*1101	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.450775	-0.033665	-4.484440	28234.1753
HLA B*3501	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.450886	-0.033665	-4.484551	28241.3552
HLA A*2603	1:199-207	9	RASEHADVE	0.702366	-0.535361	-4.652001	0.167005	-4.484996	44874.6887
HLA A*6802	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.422262	-0.062772	-4.485034	26440.0186
HLA A*0216	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.429388	-0.055989	-4.485376	26877.430387
HLA A*0212	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.358071	-0.127574	-4.485646	22807.174108
HLA B*2705	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.418211	-0.067515	-4.485726	26194.5683
HLA A*0101	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.373853	-0.112631	-4.486484	23651.1884
HLA A*0211	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.514587	0.027900	-4.486687	32702.964305
HLA A*6801	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.269987	-0.216975	-4.486962	18620.311230
HLA A*0202	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.594397	0.107209	-4.487188	39300.3824
HLA B*4501	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.644810	0.157520	-4.487289	44137.6977
HLA A*0250	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.594521	0.107209	-4.487313	39311.6524
HLA B*0702	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.421505	-0.066090	-4.487595	26394.0006
HLA A*0216	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.421949	-0.066090	-4.488039	26421.0015
HLA A*0219	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.421996	-0.066090	-4.488086	26423.8603
HLA A*2402	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.595473	0.107209	-4.488264	39397.8788
HLA B*3501	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.421129	-0.067515	-4.488644	26371.1643
HLA B*5401	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.499217	0.010485	-4.488731	31565.799196
HLA A*2402	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.582809	0.093967	-4.488842	38265.651891
HLA B*4403	1:137-145	9	DAARATYSE	0.875934	-0.718414	-4.646494	0.157520	-4.488974	44309.2354
HLA A*6801	1:206-214	9	VEIRRLAIE	0.882366	-0.740375	-4.631439	0.141991	-4.489448	42799.5060
HLA A*3201	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.616912	0.127125	-4.489787	41391.569186
HLA A*2301	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.424651	-0.066090	-4.490741	26585.8888
HLA B*4403	1:26-34	9	TTDADGGPA	0.518414	-0.350763	-4.658578	0.167651	-4.490927	45559.364566
HLA A*1101	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.519549	0.027900	-4.491650	33078.760881
HLA A*2501	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.502203	0.010485	-4.491718	31783.592568
HLA B*4001	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.379095	-0.112631	-4.491725	23938.3752
HLA B*4001	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.364368	-0.127574	-4.491943	23140.252724
HLA A*3001	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.295918	-0.196676	-4.492595	19765.9731
HLA A*6901	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.358140	-0.135764	-4.493904	22810.752533
HLA B*5801	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.358447	-0.135764	-4.494212	22826.924140
HLA A*2403	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.438877	-0.055989	-4.494866	27471.180068
HLA B*4601	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.382567	-0.112631	-4.495198	24130.5493
HLA A*0101	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.368365	-0.127574	-4.495939	23354.177235
HLA B*3801	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.556182	0.060047	-4.496135	35990.046089
HLA B*4403	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.463162	-0.033665	-4.496827	29051.0338
HLA A*6901	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.384320	-0.112631	-4.496951	24228.1316
HLA A*0206	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.525446	0.027900	-4.497547	33530.994932
HLA A*3201	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.604838	0.107209	-4.497629	40256.6737
HLA B*7301	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.591643	0.093985	-4.497658	39051.990946
HLA B*4402	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.430283	-0.067515	-4.497798	26932.8864
HLA B*5301	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.605451	0.107209	-4.498242	40313.5555
HLA B*4001	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.436126	-0.062772		
HLA A*2402	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.535194	0.035827	-4.4993	

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HLA A*0101	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.382504	-0.116983	-4.499487	24127.0249
HLA A*0212	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.364699	-0.135764	-4.500464	23157.910713
HLA A*2601	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.388065	-0.112631	-4.500696	24437.9630
HLA B*1501	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.373209	-0.127574	-4.500784	23616.156047
HLA B*4601	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.383817	-0.116983	-4.500800	24200.0985
HLA A*0301	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.314434	-0.186575	-4.501010	20626.925167
HLA A*0219	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.438520	-0.062772	-4.501292	27448.5997
HLA A*2902	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.388873	-0.112631	-4.501504	24483.4844
HLA A*8001	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.445700	-0.055989	-4.501689	27906.169005
HLA A*0211	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.512430	0.010485	-4.501945	32540.954910
HLA B*4501	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.596112	0.093967	-4.502145	39455.895114
HLA B*3901	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.468544	-0.033665	-4.502210	29413.3345
HLA A*0250	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.596460	0.093967	-4.502492	39487.498663
HLA B*4801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.439862	-0.062772	-4.502634	27533.5208
HLA A*0301	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.367216	-0.135764	-4.502980	23292.476906
HLA B*5401	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.538848	0.035827	-4.503021	34581.824501
HLA A*0201	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.390668	-0.112631	-4.503299	24584.8879
HLA B*1503	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.386580	-0.116983	-4.503563	24354.5510
HLA B*4002	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.437606	-0.066090	-4.503696	27390.8963
HLA B*5401	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.531611	0.027900	-4.503712	34010.380337
HLA A*2301	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.539649	0.035827	-4.503822	34645.678970
HLA A*0250	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.598748	0.093985	-4.504763	39696.116601
HLA B*1509	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.448794	-0.055989	-4.504783	28105.705535
HLA A*0202	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.448849	-0.055989	-4.504837	28109.202874
HLA B*4501	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.646912	0.142013	-4.504899	44351.924076
HLA A*6801	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.632623	0.127125	-4.505498	42916.361748
HLA B*4501	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.612995	0.107209	-4.505787	41019.9663
HLA B*4002	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.648099	0.142013	-4.506086	44473.258934
HLA A*0101	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.370799	-0.135764	-4.506563	23485.436598
HLA B*4801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.439239	-0.067515	-4.506754	27494.0764
HLA A*0219	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.450928	-0.055989	-4.506917	28244.105445
HLA A*0216	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.444427	-0.062772	-4.507199	27824.4635
HLA A*0201	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.390595	-0.116983	-4.507579	24580.7652
HLA B*0802	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.474218	-0.033665	-4.507884	29800.1375
HLA B*3501	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.445148	-0.062772	-4.507920	27870.7137
HLA B*0702	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.396004	-0.112631	-4.508635	24888.7974
HLA A*3301	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.602648	0.093967	-4.508681	40054.209747
HLA B*5701	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.391916	-0.116983	-4.508899	24655.6132
HLA B*4403	1:66-74	9	DVGHFSVLE	0.964068	-0.822055	-4.651130	0.142013	-4.509116	44784.712516
HLA B*3501	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.453263	-0.055989	-4.509252	28396.395237
HLA B*1502	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.603402	0.093967	-4.509435	40123.827293
HLA B*4601	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.381916	-0.127574	-4.509491	24094.415827
HLA A*0201	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.292561	-0.216975	-4.509536	19613.756875
HLA B*4002	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.639544	0.128565	-4.510980	43605.8222
HLA B*0803	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.539001	0.027900	-4.511101	34593.987089
HLA B*5301	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.605430	0.093985	-4.511445	40311.592755
HLA A*3201	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.605980	0.093967	-4.512013	40362.656081
HLA B*4002	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.315623	-0.196676	-4.512300	20683.4667
HLA A*2603	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.619999	0.107209	-4.512790	41686.8533
HLA B*1503	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.540732	0.027900	-4.512833	34732.191704
HLA A*3002	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.540814	0.027900	-4.512915	34738.768732
HLA A*0216	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.326523	-0.186575	-4.513098	21209.117266
HLA B*0803	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.447051	-0.066090	-4.513141	27993.1114
HLA B*1503	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.450676	-0.062772	-4.513448	28227.7608
HLA B*3901	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.386376	-0.127574	-4.513950	24343.091067
HLA B*1517	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.446466	-0.067515	-4.513981	27955.4284
HLA B*4501	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.641215	0.127125	-4.514090	43773.872036
HLA B*1501	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.378984	-0.135764	-4.514748	23932.289293
HLA B*1509	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.542938	0.027900	-4.515039	34909.076171
HLA B*0702	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.452833	-0.062772	-4.515605	28368.2964
HLA A*3301	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.543507	0.027900	-4.515607	34954.808825
HLA A*2602	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.576256	0.060047	-4.516209	37692.626642
HLA B*1517	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.453512	-0.062772	-4.516284	28412.6837
HLA A*0201	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.388847	-0.127574	-4.516422	24482.027532
HLA A*2602	1:32-40	9	GPALVEFAG	0.915277	-0.821310	-4.610542	0.093967	-4.516575	40788.941695
HLA A*2501	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.483163	-0.033665	-4.516828	30420.2485
HLA B*1801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.449896	-0.067515	-4.517411	28177.1069
HLA A*2301	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.545607	0.027900	-4.517708	35124.275169
HLA A*2902	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.455364	-0.062772	-4.518135	28534.0653
HLA B*0702	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.390953	-0.127574	-4.518527	24600.986380
HLA B*4002	1:51-59	9	NPKTATNAG	0.912262	-0.785137	-4.645778	0.127125	-4.518652	44236.184820
HLA A*8001	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.456517	-0.062772	-4.519289	28609.9598
HLA B*3901	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.452049	-0.067515	-4.519564	28317.0839
HLA A*0202	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.323034	-0.196676	-4.519710	21039.4124
HLA B*4402	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.407105	-0.112631	-4.519736	25533.1989
HLA B*4403	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.580030	0.060047	-4.519983	38021.537576
HLA A*1101	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.464503	-0.055989	-4.520492	29140.912612
HLA B*1503	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.384736	-0.135764	-4.520500	24251.342392
HLA A*2403	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.408336	-0.112631	-4.520967	25605.6827
HLA A*2501	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.455505	-0.066090	-4.521594	28543.3288
HLA A*2601	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.394282	-0.127574	-4.521856	24790.297624
HLA A*0203	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.394409	-0.127574	-4.521983	24797.540771
HLA B*0803	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.488585	-0.033665	-4.522251	30802.4576
HLA B*0802	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.409687	-0.112631	-4.522318	25685.4579
HLA B*5801	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.305408	-0.216975	-4.522383	20202.623561
HLA B*4002	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.629963	0.107209	-4.522755	42654.3452
HLA B*4002	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.582816	0.060047	-4.522769	38266.272935
HLA B*5401	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.326936	-0.196676	-4.523613	21229.3209
HLA B*0803	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.456287	-0.067515	-4.523802	28594.7957
HLA A*8001	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.411175	-0.112631	-4.523805	25773.5675
HLA A*3301	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.632285	0.107209	-4.525076	42882.9418
HLA A*0219	1:38-46	9	FAGRACYQS	0.921032	-1.138007	-4.308951	-0.216975	-4.525926	20368.112966
HLA B*5301	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.586063	0.060047	-4.526016	38553.441620
HLA B*5101	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.493350	-0.033665	-4.527015	31142.2599
HLA A*0206	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.537506	0.010485	-4.527021	34475.164454
HLA A*0201	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.391338	-0.135764	-4.527102	24622.822597
HLA B*1502	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.622203	0.093985	-4.528218	41898.929916
HLA A*2602	1:24-32	9	PWTTDADGG	0.796554	-0.702569	-4.622229	0.093985	-4.528244	41901.423344
HLA B*4402	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.400712	-0.127574	-4.528287	25160.095270
HLA A*0212	1:14-22	9	KTDFLAPPD	0.574641	-0.761216	-4.341757	-0.186575	-4.528332	21966.287027
HLA B*4403	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.462452	-0.066090	-4.528542	29003.6094
HLA B*7301	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.564624	0.035827	-4.528797	36696.454193
HLA A*0212	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.416221	-0.112631	-4.528852	26074.8147
HLA A*3101	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.393241	-0.135764	-4.529005	24730.956807
HLA A*1101	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.466261	-0.062772	-4.529032	29259.0730
HLA A*0203	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.333146	-0.196676	-4.529822	21535.0453
HLA B*5701	1:69-77	9	HFSVLEHAS	0.830528	-0.958102	-4.402637	-0.127574	-4.530211	25271.819409
HLA B*5701	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.417671	-0.112631	-4.530302	26161.9953
HLA A*0250	1:78-86	9	VSFYITGIS	0.920166	-0.860119	-4.590734	0.060047	-4.530687	38970.316168
HLA B*0802	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.474773	-0.055989	-4.530761	29838.208716
HLA B*1502	1:43-51	9	CYQSWSKPN	0.429969	-0.419484	-4.541275	0.010485	-4.530790	34775.623114
HLA B*1517	1:40-48	9	GRACYQSWS	0.834688	-0.890677	-4.474982	-0.055989	-4.530971	29852.578680
HLA B*7301	1:22-30	9	DVPWTTDAD	0.963278	-0.935378	-4.559025	0.027900	-4.531126	36226.408468
HLA A*3301	1:71-79	9	SVLEHASVS	0.966932	-0.931105	-4.567185	0.035827	-4.531358	36913.484340
HLA A*0212	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.334844	-0.196676	-4.531521	21619.4414
HLA A*0211	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.498848	-0.033665		
HLA A*0219	1:23-31	9	VPWTTDADG	0.560397	-0.696161	-4.396958	-0.135764	-4.5327	

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HLA A*3201	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.626777	0.093985	-4.532792	42342.586039		
HLA A*0206	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.315966	-0.216975	-4.532941	20699.809908		
HLA A*0212	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.415960	-0.116983	-4.532944	26059.1615	
HLA A*0203	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.418387	-0.116983	-4.535371	26205.1986	
HLA B*0802	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.469364	-0.066090	-4.535454	29468.9208	
HLA A*6801	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.630043	0.093967	-4.536076	42662.191698		
HLA B*4403	1:51-59 9	NPKTATNAG	0.912262	-0.785137	-4.663420	0.127125	-4.536295	46070.183998		
HLA B*1509	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.503982	-0.033665	-4.537647	31914.0223	
HLA B*4601	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.402051	-0.135764	-4.537816	25237.799610		
HLA B*4403	1:103-111	9	QLSQRYVPE	0.770979	-0.642414	-4.666611	0.128565	-4.538046	46409.8908	
HLA B*5701	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.403024	-0.135764	-4.538788	25294.387908		
HLA B*4801	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.426554	-0.112631	-4.539185	26702.6440	
HLA A*2601	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.404173	-0.135764	-4.539937	25361.391174		
HLA B*4001	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.423115	-0.116983	-4.540098	26491.9923	
HLA B*0803	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.484164	-0.055989	-4.540152	30490.436310		
HLA A*0202	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.568414	0.027900	-4.540514	37018.074212		
HLA A*0206	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.484854	-0.055989	-4.540843	30538.970161		
HLA B*4403	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.648461	0.107209	-4.541252	44510.3260	
HLA B*4801	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.413808	-0.127574	-4.541383	25930.345932		
HLA A*1101	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.355031	-0.186575	-4.541606	22648.072383		
HLA B*4002	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.635926	0.093967	-4.541959	43244.041283		
HLA A*2403	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.425006	-0.116983	-4.541989	26607.6155	
HLA B*0802	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.479218	-0.062772	-4.541990	30145.1863	
HLA B*4501	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.486384	-0.055989	-4.542373	30646.713077		
HLA A*2501	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.486473	-0.055989	-4.542462	30653.013946		
HLA A*2603	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.578456	0.035827	-4.542629	37883.973193		
HLA B*5301	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.578547	0.035827	-4.542720	37891.967012		
HLA B*1801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.509392	-0.033665	-4.543058	32314.1256	
HLA B*4501	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.579562	0.035827	-4.543735	37980.626834		
HLA A*0211	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.487834	-0.055989	-4.543822	30749.179706		
HLA B*3901	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.481819	-0.062772	-4.544591	30326.2599	
HLA B*1501	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.327617	-0.216975	-4.544592	21262.653081		
HLA A*2402	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.572972	0.027900	-4.545072	37408.631648		
HLA A*8001	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.358920	-0.186575	-4.545495	22851.759357		
HLA A*2301	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.478046	-0.067515	-4.545561	30063.9181	
HLA A*3201	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.556283	0.010485	-4.545798	35998.419256		
HLA A*0201	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.359441	-0.186575	-4.546016	22879.220702		
HLA B*5101	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.329330	-0.216975	-4.546305	21346.674501		
HLA A*3002	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.433762	-0.112631	-4.546393	27149.5406	
HLA A*6802	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.349782	-0.196676	-4.546459	22376.0021	
HLA A*6901	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.350370	-0.196676	-4.547046	22406.2855	
HLA B*5101	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.481102	-0.066090	-4.547192	30276.2623	
HLA B*4801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.430678	-0.116983	-4.547661	26957.3758	
HLA A*8001	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.420836	-0.127574	-4.548410	26353.337278		
HLA A*0203	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.331583	-0.216975	-4.548558	21457.710618		
HLA A*6801	1:106-114	9	QRYVPEKDS	0.883994	-0.776785	-4.655916	0.107209	-4.548707	45280.9668	
HLA B*1509	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.436547	-0.112631	-4.549177	27324.1478	
HLA B*4001	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.363553	-0.186575	-4.550128	23096.853860		
HLA B*5801	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.353915	-0.196676	-4.550592	22589.9484	
HLA B*4501	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.610794	0.060047	-4.550747	40812.559541		
HLA A*3301	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.644793	0.093985	-4.550808	44136.026293		
HLA B*3901	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.438452	-0.112631	-4.551083	27444.2937	
HLA B*2705	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.488693	-0.062772	-4.551465	30810.1239	
HLA A*2603	1:78-86 9	VSFYITGIS	0.920166	-0.860119	-4.611560	0.060047	-4.551513	40884.601053		
HLA B*3801	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.579520	0.027900	-4.551620	37976.928536		
HLA B*4402	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.435066	-0.116983	-4.552050	27231.1793	
HLA B*3801	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.563214	0.010485	-4.552729	36577.533053		
HLA B*1801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.489972	-0.062772	-4.552743	30900.9311	
HLA B*1501	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.366184	-0.186575	-4.552759	23237.224277		
HLA B*5101	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.497943	-0.055989	-4.553932	31473.378787		
HLA B*1801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.488759	-0.066090	-4.554849	30814.7913	
HLA A*2403	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.419182	-0.135764	-4.554946	26253.159847		
HLA A*2501	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.438252	-0.116983	-4.555236	27431.6766	
HLA A*0250	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.584165	0.027900	-4.556265	38385.284975		
HLA A*3002	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.500363	-0.055989	-4.556352	31649.243823		
HLA A*0206	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.443757	-0.112631	-4.556388	27781.5962	
HLA A*1101	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.444074	-0.112631	-4.556705	27801.8935	
HLA A*6802	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.420972	-0.135764	-4.556736	26361.607556		
HLA B*2705	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.429183	-0.127574	-4.556758	26864.783223		
HLA B*4001	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.421298	-0.135764	-4.557063	26381.438270		
HLA B*7301	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.568712	0.010485	-4.558227	37043.516438		
HLA A*0219	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.430659	-0.127574	-4.558233	26956.209134		
HLA A*0211	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.495617	-0.062772	-4.558389	31305.2645	
HLA A*0219	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.446243	-0.112631	-4.558874	27941.0647	
HLA B*4801	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.423455	-0.135764	-4.559219	26512.781707		
HLA A*2501	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.431653	-0.127574	-4.559227	27017.965902		
HLA B*4002	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.653430	0.093985	-4.559445	45022.534189		
HLA B*3901	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.363454	-0.196676	-4.560131	23091.6064	
HLA B*4402	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.425288	-0.135764	-4.561052	26624.894426		
HLA A*2603	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.655570	0.093985	-4.561585	45244.971332		
HLA A*2902	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.426242	-0.135764	-4.562006	26683.438013		
HLA A*2501	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.500041	-0.062772	-4.562813	31625.7955	
HLA A*0206	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.376886	-0.186575	-4.563461	23816.950489		
HLA B*1502	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.591620	0.027900	-4.563720	39049.878334		
HLA A*6801	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.436354	-0.127574	-4.563928	27312.029241		
HLA B*0702	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.447171	-0.116983	-4.564154	28000.8359	
HLA B*4501	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.658611	0.093985	-4.564626	45562.815292		
HLA A*2403	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.378317	-0.186575	-4.564892	23895.547753		
HLA A*0301	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.368226	-0.196676	-4.564902	23346.7241	
HLA A*0202	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.575488	0.010485	-4.565003	37626.006057		
HLA B*4002	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.600982	0.035827	-4.565156	39900.871624		
HLA A*2601	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.379344	-0.186575	-4.565919	23952.106562		
HLA A*0219	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.448966	-0.116983	-4.565949	28116.8072	
HLA B*4403	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.660088	0.093967	-4.566121	45718.121454		
HLA B*1517	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.453710	-0.112631	-4.566340	28425.5982	
HLA A*8001	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.431655	-0.135764	-4.567419	27018.112066		
HLA B*5101	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.500044	-0.067515	-4.567559	31625.9666	
HLA A*0211	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.351216	-0.216975	-4.568191	22449.965643		
HLA B*3801	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.512649	-0.055989	-4.568638	32557.331025		
HLA B*0802	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.441229	-0.127574	-4.568804	27620.348253		
HLA B*0802	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.451915	-0.116983	-4.568898	28308.3533	
HLA B*0801	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.372295	-0.196676	-4.568972	23566.5093	
HLA A*0216	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.452692	-0.116983	-4.569676	28359.0897	
HLA B*1517	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.434063	-0.135764	-4.569827	27168.347335		
HLA B*5101	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.507158	-0.062772	-4.569930	32148.3026	
HLA B*2705	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.453212	-0.116983	-4.570195	28393.0157	
HLA B*5701	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.353462	-0.216975	-4.570437	22566.374353		
HLA B*4601	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.354052	-0.216975	-4.571026	22597.037645		
HLA A*2902	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.385192	-0.186575	-4.571767	24276.807985		
HLA B*0803	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.459419	-0.112631	-4.572050	28801.7491	
HLA A*0101	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.355238	-0.216975	-4.572213	22658.857023		
HLA B*4601	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.375700	-0.196676	-4.572376	23751.9715	
HLA B*5301	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.601903	0.027900	-4.574004	39985.578252		
HLA B*5101	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.461677	-0.112631	-4.574307	28951.8765	
HLA A*2601	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.377960	-0.196676	-4.574636	23875.9064	
HLA A*0203	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.439220	-0.135764	-4.5749			
HLA A*0101	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.378439	-0.196676			

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HLA A*0250	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.585720	0.010485	-4.575235	38523.002445
HLA B*3501	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.463093	-0.112631	-4.575724	29046.4764
HLA B*4002	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.513041	-0.062772	-4.575813	32586.7582
HLA A*0216	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.449241	-0.127574	-4.576815	28134.609650
HLA A*1101	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.449300	-0.127574	-4.576874	28138.415035
HLA A*0211	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.464447	-0.112631	-4.577078	29137.1292
HLA A*0301	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.360527	-0.216975	-4.577502	22936.475833
HLA A*2402	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.510156	-0.067515	-4.577671	32370.9907
HLA B*4403	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.515421	-0.062772	-4.578193	32765.8310
HLA A*2603	1:32-40 9	GPALVEFAG	0.915277	-0.821310	-4.672169	0.093967	-4.578202	47007.746157
HLA B*3801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.544910	-0.033665	-4.578575	35067.8850
HLA A*0206	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.516239	-0.062772	-4.579011	32827.5754
HLA A*0216	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.466535	-0.112631	-4.579166	29277.5986
HLA B*4403	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.674037	0.093985	-4.580052	47210.355365
HLA B*1503	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.453181	-0.127574	-4.580755	28391.018998
HLA A*0216	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.445364	-0.135764	-4.581128	27884.588746
HLA B*1509	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.514218	-0.067515	-4.581733	32675.1997
HLA B*5701	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.395226	-0.186575	-4.581801	24844.269622
HLA A*0201	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.385387	-0.196676	-4.582063	24287.7112
HLA B*1502	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.514557	-0.067515	-4.582072	32700.6644
HLA A*3101	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.365150	-0.216975	-4.582125	23181.977302
HLA A*0202	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.519620	-0.062772	-4.582392	33084.1298
HLA A*2301	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.548807	-0.033665	-4.582473	35384.0360
HLA A*0216	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.366450	-0.216975	-4.583425	23251.433941
HLA A*8001	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.467132	-0.116983	-4.584116	29317.8570
HLA B*5401	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.457988	-0.127574	-4.585563	28707.014366
HLA B*1801	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.450355	-0.135764	-4.586119	28206.847456
HLA B*5401	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.552489	-0.033665	-4.586154	35685.2720
HLA B*1801	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.530589	-0.055989	-4.586578	33930.437750
HLA A*2602	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.597872	0.010485	-4.587386	39616.095022
HLA A*2902	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.471147	-0.116983	-4.588131	29590.1721
HLA A*6801	1:24-32 9	PWTTDADGG	0.796554	-0.702569	-4.682211	0.093985	-4.588226	48107.316040
HLA B*5301	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.598769	0.010485	-4.588284	39698.049412
HLA A*2403	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.371334	-0.216975	-4.588309	23514.422694
HLA A*2301	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.532678	-0.055989	-4.588667	34094.015547
HLA B*3901	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.453552	-0.135764	-4.589316	28415.296951
HLA B*1517	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.461947	-0.127574	-4.589521	28969.894182
HLA A*2602	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.472851	-0.116983	-4.589834	29706.4577
HLA A*6802	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.405129	-0.186575	-4.591704	25417.294038
HLA B*0803	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.530110	-0.062772	-4.592882	33893.0121
HLA A*0203	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.407166	-0.186575	-4.593741	25536.790673
HLA B*3801	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.481168	-0.112631	-4.593799	30280.8488
HLA B*4601	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.408416	-0.186575	-4.594991	25610.392980
HLA B*4801	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.409276	-0.186575	-4.595851	25661.152291
HLA A*2501	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.483992	-0.112631	-4.596623	30478.3973
HLA B*4501	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.607272	0.010485	-4.596787	40482.931551
HLA B*4403	1:71-79 9	SVLEHASVS	0.966932	-0.931105	-4.633532	0.035827	-4.597705	43006.306728
HLA B*5101	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.481307	-0.116983	-4.598290	30290.5155
HLA A*0212	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.383253	-0.216975	-4.600228	24168.698177
HLA A*3002	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.566905	-0.033665	-4.600571	36889.7279
HLA A*3101	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.405186	-0.196676	-4.601862	25420.5943
HLA A*2301	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.489276	-0.112631	-4.601907	30851.4882
HLA B*1509	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.539167	-0.062772	-4.601939	34607.2772
HLA B*5401	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.535923	-0.066090	-4.602012	34349.6877
HLA A*2301	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.540232	-0.062772	-4.603004	34692.1926
HLA A*2601	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.387118	-0.216975	-4.604093	24384.741780
HLA B*4801	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.408170	-0.196676	-4.604846	25595.8494
HLA B*0802	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.469982	-0.135764	-4.605746	29510.879146
HLA B*1502	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.572643	-0.033665	-4.606308	37380.3096
HLA A*0250	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.572901	-0.033665	-4.606567	37402.5608
HLA A*2301	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.479491	-0.127574	-4.607065	30164.109827
HLA B*5401	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.539633	-0.067515	-4.607148	34644.3669
HLA B*3901	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.490371	-0.116983	-4.607354	30929.3631
HLA A*0206	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.471664	-0.135764	-4.607429	29625.410639
HLA B*4501	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.480513	-0.127574	-4.608087	30235.178670
HLA A*2402	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.481744	-0.127574	-4.609318	30321.010408
HLA A*6801	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.620420	0.010485	-4.609934	41727.241201
HLA A*2402	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.497405	-0.112631	-4.610036	31434.4116
HLA B*0801	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.423721	-0.186575	-4.610296	26528.994389
HLA B*1503	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.393770	-0.216975	-4.610744	24761.078276
HLA B*5401	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.554935	-0.055989	-4.610924	35886.807597
HLA B*2705	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.424409	-0.186575	-4.610984	26571.078777
HLA B*0803	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.484772	-0.127574	-4.612347	30533.188273
HLA B*5701	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.415841	-0.196676	-4.612517	26051.9727
HLA B*3801	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.545490	-0.067515	-4.613005	35114.7755
HLA A*2403	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.416390	-0.196676	-4.613067	26084.9731
HLA A*1101	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.496224	-0.116983	-4.613207	31348.9894
HLA B*1502	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.547896	-0.066090	-4.613985	35309.8415
HLA A*0219	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.417838	-0.196676	-4.614514	26172.0461
HLA A*2501	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.478905	-0.135764	-4.614670	30123.504244
HLA B*4402	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.428197	-0.186575	-4.614772	26803.811608
HLA B*1801	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.502184	-0.112631	-4.614815	31782.2170
HLA A*1101	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.479279	-0.135764	-4.615043	30149.426797
HLA B*4501	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.549059	-0.066090	-4.615148	35404.5243
HLA A*0211	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.429519	-0.186575	-4.616094	26885.574240
HLA B*0803	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.499421	-0.116983	-4.616404	31580.6594
HLA B*3501	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.420100	-0.196676	-4.616777	26308.7510
HLA B*5401	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.504162	-0.112631	-4.616793	31927.3192
HLA B*5101	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.489983	-0.127574	-4.617558	30901.766984
HLA A*3002	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.554815	-0.062772	-4.617587	35876.9076
HLA B*1502	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.490766	-0.127574	-4.618340	30957.486478
HLA A*0219	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.432219	-0.186575	-4.618794	27053.214447
HLA B*0803	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.483788	-0.135764	-4.619552	30464.055748
HLA B*7301	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.586286	-0.033665	-4.619952	38573.2608
HLA B*3801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.558154	-0.062772	-4.620925	36153.7724
HLA B*4001	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.404051	-0.216975	-4.621026	25354.257657
HLA B*4002	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.632075	0.010485	-4.621590	42862.299575
HLA A*2402	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.588702	-0.033665	-4.622367	38788.3784
HLA B*2705	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.486703	-0.135764	-4.622468	30669.269537
HLA B*4002	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.650540	0.027900	-4.622640	44723.941423
HLA A*0216	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.426315	-0.196676	-4.622991	26687.9133
HLA B*1509	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.487357	-0.135764	-4.623121	30715.429262
HLA B*0702	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.427417	-0.196676	-4.624093	26755.7129
HLA B*1509	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.509620	-0.116983	-4.626604	32331.0872
HLA B*5401	1:119-127	9	PPGMEDDAD	0.692523	-1.179914	-4.139515	-0.487391	-4.626907	13788.4463
HLA B*5401	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.564641	-0.062772	-4.627412	36697.8438
HLA A*3201	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.560169	-0.067515	-4.627685	36321.9769
HLA A*2602	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.572399	-0.055989	-4.628387	37359.284346
HLA A*2902	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.431737	-0.196676	-4.628414	27023.2283
HLA A*6801	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.594829	-0.033665	-4.628494	39339.5222
HLA A*8001	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.431991	-0.196676	-4.628667	27039.0217
HLA A*2402	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.573275	-0.055989	-4.629264	37434.747334
HLA A*0250	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.573646	-0.055989	-4.629635	37466.758831
HLA A*3201	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.596831	-0.033665	-4.630496	39521.2659
HLA B*4501	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.658582	0.027900	-4.630683	45559.857511
HLA B*5401	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.514768	-0.116983	
HLA A*0206	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.504583	-0.127574	-4.6321	

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HLA B*0702	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.446010	-0.186575	-4.632585	27926.104067
HLA B*5301	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.599819	-0.033665	-4.633485	39794.1642
HLA A*0250	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.568308	-0.066090	-4.634398	37009.0634
HLA A*2402	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.571710	-0.062772	-4.634482	37300.1131
HLA A*3002	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.499179	-0.135764	-4.634943	31563.067035
HLA A*0211	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.508204	-0.127574	-4.635778	32225.789770
HLA B*1502	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.580157	-0.055989	-4.636145	38032.646583
HLA A*0250	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.419316	-0.216975	-4.636290	26261.256617
HLA B*3901	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.450113	-0.186575	-4.636688	28191.134455
HLA B*4402	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.420070	-0.216975	-4.637045	26306.900864
HLA A*0250	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.575190	-0.062772	-4.637962	37600.1637
HLA A*2602	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.575591	-0.062772	-4.638363	37634.9634
HLA A*3002	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.521426	-0.116983	-4.638410	33222.0533
HLA B*1801	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.452488	-0.186575	-4.639063	28345.745416
HLA B*7301	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.571656	-0.067515	-4.639171	37295.4722
HLA B*0802	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.422299	-0.216975	-4.639274	26442.307383
HLA B*3501	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.452723	-0.186575	-4.639298	28361.084299
HLA B*4801	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.422567	-0.216975	-4.639542	26458.620107
HLA A*3201	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.576837	-0.062772	-4.639609	37743.0268
HLA A*2602	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.606130	-0.033665	-4.639795	40376.6333
HLA B*4403	1:22-30 9	DVPWTTDAD	0.963278	-0.935378	-4.667872	0.027900	-4.639973	46544.912783
HLA B*4501	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.573181	-0.067515	-4.640696	37426.6474
HLA A*2602	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.528299	-0.112631	-4.640929	33751.9380
HLA B*5101	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.446802	-0.196676	-4.643479	27977.0634
HLA A*0202	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.531029	-0.112631	-4.643660	33964.7808
HLA A*2501	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.448466	-0.196676	-4.645142	28084.4267
HLA B*5301	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.582985	-0.062772	-4.645757	38281.1810
HLA B*7301	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.449511	-0.196676	-4.646188	28152.1186
HLA A*8001	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.431310	-0.216975	-4.648284	26996.634354
HLA B*2705	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.451865	-0.196676	-4.648542	28305.1374
HLA A*2501	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.432137	-0.216975	-4.649111	27048.092511
HLA A*0211	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.532565	-0.116983	-4.649549	34085.1633
HLA B*4403	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.660314	0.010485	-4.649829	45741.871297
HLA A*2301	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.534149	-0.116983	-4.651132	34209.6737
HLA B*1502	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.538632	-0.112631	-4.651263	34564.6170
HLA A*2603	1:43-51 9	CYQSWSKPN	0.429969	-0.419484	-4.662724	0.010485	-4.652239	45996.469596
HLA B*5301	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.587247	-0.066090	-4.653337	38658.7042
HLA A*6801	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.588864	-0.066090	-4.654953	38802.8602
HLA B*2705	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.439838	-0.216975	-4.656813	27532.031324
HLA B*1517	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.439841	-0.216975	-4.656815	27532.180270
HLA B*5301	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.589794	-0.067515	-4.657309	38886.0773
HLA B*5301	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.601793	-0.055989	-4.657782	39975.412620
HLA B*4403	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.601979	-0.055989	-4.657967	39992.501013
HLA A*0211	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.522655	-0.135764	-4.658419	33316.183990
HLA A*0206	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.542438	-0.116983	-4.659421	34868.8733
HLA B*0802	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.473631	-0.186575	-4.660206	29759.860957
HLA A*3301	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.627045	-0.033665	-4.660711	42368.7079
HLA A*2501	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.475767	-0.186575	-4.662342	29906.568156
HLA A*0250	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.550905	-0.112631	-4.663536	35555.3910
HLA B*7301	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.603050	-0.062772	-4.665822	40091.2806
HLA A*2301	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.530723	-0.135764	-4.666488	33940.902278
HLA B*4002	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.554768	-0.112631	-4.667399	35873.0260
HLA A*6801	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.612065	-0.055989	-4.668054	40932.182669
HLA A*2602	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.602347	-0.066090	-4.668437	40026.4831
HLA B*1517	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.472212	-0.196676	-4.668888	29662.7771
HLA B*3801	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.541594	-0.127574	-4.669169	34801.218517
HLA B*4002	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.613256	-0.055989	-4.669245	41044.606132
HLA A*3201	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.543373	-0.127574	-4.670947	34944.031693
HLA B*3801	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.535354	-0.135764	-4.671118	34304.746806
HLA A*2301	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.454494	-0.216975	-4.671469	28477.007029
HLA B*4501	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.559822	-0.112631	-4.672453	36292.9069
HLA A*3301	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.609184	-0.066090	-4.675274	40661.5973
HLA B*0803	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.479610	-0.196676	-4.676287	30172.4333
HLA A*6801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.559817	-0.116983	-4.676800	36292.5142
HLA A*3201	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.560433	-0.116983	-4.677416	36343.9914
HLA A*3301	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.621472	-0.055989	-4.677461	41828.495261
HLA B*0802	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.480879	-0.196676	-4.677556	30260.7061
HLA B*4002	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.550050	-0.127574	-4.677625	35485.444277
HLA A*1101	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.481271	-0.196676	-4.677948	30288.0576
HLA A*0202	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.561969	-0.116983	-4.678952	36472.8066
HLA A*3201	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.622995	-0.055989	-4.678983	41975.386897
HLA A*3301	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.567018	-0.112631	-4.679649	36899.3085
HLA A*0202	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.493108	-0.186575	-4.679683	31124.911730
HLA B*4002	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.612408	-0.067515	-4.679923	40964.5254
HLA A*1101	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.465020	-0.216975	-4.681995	29175.616063
HLA B*1509	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.485324	-0.196676	-4.682001	30572.0305
HLA B*4403	1:92-100	9	ELIRHRHFS	0.968949	-1.036464	-4.615051	-0.067515	-4.682566	41214.6009
HLA B*1502	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.621045	-0.062772	-4.683816	41787.3312
HLA A*2603	1:136-144	9	ADAARATYS	0.939404	-0.973069	-4.650286	-0.033665	-4.683952	44697.8182
HLA B*0803	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.498129	-0.186575	-4.684704	31486.832793
HLA B*1502	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.549024	-0.135764	-4.684788	35401.651461
HLA B*0702	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.467886	-0.216975	-4.684861	29368.813876
HLA A*2603	1:40-48 9	GRACYQSWS	0.834688	-0.890677	-4.629738	-0.055989	-4.685726	42632.198541
HLA A*0211	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.490228	-0.196676	-4.686904	30919.1580
HLA A*0250	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.560454	-0.127574	-4.688028	36345.761008
HLA A*2402	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.574337	-0.116983	-4.691320	37526.3974
HLA B*1801	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.475362	-0.216975	-4.692337	29878.753009
HLA B*5101	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.507525	-0.186575	-4.694100	32175.445469
HLA B*3801	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.578190	-0.116983	-4.695173	37860.8211
HLA A*2603	1:97-105	9	RHFSYSQLS	0.762603	-0.828693	-4.629489	-0.066090	-4.695578	42607.7581
HLA A*2603	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.578878	-0.116983	-4.695862	37920.8818
HLA A*2603	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.635186	-0.062772	-4.697958	43170.4112
HLA A*6801	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.586519	-0.112631	-4.699150	38593.9254
HLA A*2602	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.571858	-0.127574	-4.699433	37312.828049
HLA B*3901	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.482817	-0.216975	-4.699792	30396.066371
HLA B*1503	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.514199	-0.186575	-4.700775	32673.785627
HLA B*5401	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.518837	-0.186575	-4.705412	33024.582711
HLA A*3301	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.643008	-0.062772	-4.705779	43954.9328
HLA B*5301	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.593182	-0.112631	-4.705813	39190.6162
HLA A*2603	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.580093	-0.127574	-4.707668	38027.091674
HLA A*2402	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.492168	-0.216975	-4.709143	31057.631623
HLA A*2603	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.598722	-0.112631	-4.711353	39693.7544
HLA B*5301	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.584078	-0.127574	-4.711652	38377.602319
HLA A*0250	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.595694	-0.116983	-4.712677	39417.9189
HLA B*4403	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.605825	-0.112631	-4.718455	40348.2470
HLA B*1502	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.601748	-0.116983	-4.718732	39971.3038
HLA A*2301	1:230-238	9	FEVTTLADG	0.535215	-0.731891	-4.522167	-0.196676	-4.718843	33278.7158
HLA A*2602	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.583281	-0.135764	-4.719046	38307.284122
HLA B*5301	1:113-121	9	DSRVVVPPG	0.543505	-0.660488	-4.603428	-0.116983	-4.720411	40126.2150
HLA B*7301	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.534429	-0.186575	-4.721004	34231.704237
HLA B*7301	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.504968	-0.216975	-4.721943	31986.618363
HLA A*2402	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.586698	-0.135764	-4.722462	38609.796626
HLA A*3201	1:94-102	9	IRHRHFSYS	0.730701	-0.843332	-4.614022	-0.112631	-4.726653	41117.0572
HLA A*0250	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.592461	-0.135764	-4.728225	39125.581092
HLA B*5301	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.512125	-0.216975	-4.7291[illegible]	32518.077371
HLA B*7301	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.601532	-0.127574	-4.7291[illegible]	
HLA A*6801	1:236-244	9	ADGTEVATS	1.034343	-1.097115	-4.667886	-0.062772	

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HLA A*2301	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.545013	-0.186575	-4.731588	35076.233389
HLA A*2602	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.537379	-0.196676	-4.734056	34465.0945
HLA A*0202	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.598487	-0.135764	-4.734251	39672.286330
HLA B*0803	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.519176	-0.216975	-4.736150	33050.319678
HLA B*3801	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.549583	-0.186575	-4.736158	35447.262342
HLA A*3201	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.602510	-0.135764	-4.738274	40041.427145
HLA B*4002	1:113-121 9	DSRVVVPPG	0.543505	-0.660488	-4.628034	-0.116983	-4.745018	42465.3153
HLA B*4501	1:113-121 9	DSRVVVPPG	0.543505	-0.660488	-4.629747	-0.116983	-4.746730	42633.1210
HLA A*2402	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.561889	-0.186575	-4.748464	36466.098597
HLA A*3002	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.532279	-0.216975	-4.749254	34062.674337
HLA B*1509	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.569365	-0.186575	-4.755941	37099.269919
HLA A*0250	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.560851	-0.196676	-4.757527	36379.0060
HLA B*3801	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.560980	-0.196676	-4.757657	36389.8320
HLA A*3301	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.622896	-0.135764	-4.758660	41965.850528
HLA A*3301	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.543655	-0.216975	-4.760630	34966.724259
HLA B*4403	1:69-77 9	HFSVLEHAS	0.830528	-0.958102	-4.634237	-0.127574	-4.761811	43076.161204
HLA B*5301	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.565834	-0.196676	-4.762511	36798.8364
HLA B*1509	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.549087	-0.216975	-4.766062	35406.822852
HLA B*1502	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.571494	-0.196676	-4.768170	37281.5531
HLA A*0250	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.581937	-0.186575	-4.768513	38188.927114
HLA B*4403	1:113-121 9	DSRVVVPPG	0.543505	-0.660488	-4.653804	-0.116983	-4.770787	45061.2779
HLA A*3002	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.578256	-0.196676	-4.774932	37866.5566
HLA A*2402	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.580767	-0.196676	-4.777444	38086.1798
HLA B*4002	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.646508	-0.135764	-4.782273	44310.673764
HLA B*3801	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.566259	-0.216975	-4.783234	36834.887178
HLA B*4501	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.650888	-0.135764	-4.786652	44759.764594
HLA B*4002	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.600137	-0.186575	-4.786712	39823.237901
HLA A*2603	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.651198	-0.135764	-4.786962	44791.739197
HLA B*4403	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.654661	-0.135764	-4.790425	45150.344326
HLA B*5301	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.605106	-0.186575	-4.791681	40281.508774
HLA B*1502	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.579882	-0.216975	-4.796856	38008.581169
HLA A*2602	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.610340	-0.186575	-4.796916	40769.969035
HLA B*4501	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.613507	-0.186575	-4.800083	41068.372014
HLA A*6801	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.614215	-0.186575	-4.800790	41135.301269
HLA A*3001	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.315757	-0.487391	-4.803149	20689.8457
HLA B*5301	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.318170	-0.487391	-4.805562	20805.1175
HLA A*6801	1:23-31 9	VPWTTDADG	0.560397	-0.696161	-4.670266	-0.135764	-4.806031	46802.208397
HLA A*3301	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.621672	-0.186575	-4.808247	41847.734123
HLA A*2603	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.613482	-0.196676	-4.810158	41065.9281
HLA A*3201	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.594112	-0.216975	-4.811087	39274.664941
HLA B*1502	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.624879	-0.186575	-4.811454	42157.902470
HLA B*4403	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.626145	-0.186575	-4.812721	42281.011374
HLA A*3201	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.617819	-0.196676	-4.814495	41478.0940
HLA A*2603	1:14-22 9	KTDFLAPPD	0.574641	-0.761216	-4.632679	-0.186575	-4.819254	42921.934256
HLA B*4501	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.604166	-0.216975	-4.821141	40194.435621
HLA B*4002	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.606501	-0.216975	-4.823476	40411.160566
HLA A*2602	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.609112	-0.216975	-4.826086	40654.778660
HLA A*3301	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.631610	-0.196676	-4.828287	42816.4118
HLA A*6801	1:230-238 9	FEVTTLADG	0.535215	-0.731891	-4.640686	-0.196676	-4.837363	43720.6217
HLA B*5801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.356025	-0.487391	-4.843417	22699.9591
HLA A*0301	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.369462	-0.487391	-4.856853	23413.2542
HLA A*0101	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.375761	-0.487391	-4.863152	23755.3126
HLA A*2603	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.646353	-0.216975	-4.863328	44294.855343
HLA B*4403	1:38-46 9	FAGRACYQS	0.921032	-1.138007	-4.651821	-0.216975	-4.868795	44855.999610
HLA A*6901	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.395931	-0.487391	-4.883323	24884.6237
HLA A*0201	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.396551	-0.487391	-4.883943	24920.1896
HLA A*2601	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.408557	-0.487391	-4.895949	25618.7072
HLA A*0212	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.421576	-0.487391	-4.908967	26398.2846
HLA B*0801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.422180	-0.487391	-4.909571	26435.0128
HLA B*4001	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.423218	-0.487391	-4.910609	26498.2991
HLA B*5701	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.427393	-0.487391	-4.914785	26754.2659
HLA B*4601	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.427846	-0.487391	-4.915238	26782.2144
HLA B*1501	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.430548	-0.487391	-4.917940	26949.3559
HLA B*4402	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.435527	-0.487391	-4.922918	27260.0689
HLA A*8001	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.438868	-0.487391	-4.926259	27470.5856
HLA B*4801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.439545	-0.487391	-4.926936	27513.4194
HLA A*6802	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.440235	-0.487391	-4.927627	27557.2145
HLA A*2403	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.440731	-0.487391	-4.928123	27588.6887
HLA A*0203	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.456529	-0.487391	-4.943920	28610.7337
HLA B*5101	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.462187	-0.487391	-4.949578	28985.8844
HLA A*3101	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.464557	-0.487391	-4.951949	29144.5387
HLA B*0702	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.468189	-0.487391	-4.955581	29389.3168
HLA A*2902	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.474110	-0.487391	-4.961502	29792.7225
HLA A*0219	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.478017	-0.487391	-4.965409	30061.9664
HLA A*2501	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.496872	-0.487391	-4.984263	31395.8325
HLA B*0802	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.500274	-0.487391	-4.987666	31642.7381
HLA A*0216	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.500821	-0.487391	-4.988213	31682.6491
HLA B*1801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.511340	-0.487391	-4.998732	32459.3734
HLA B*3901	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.515062	-0.487391	-5.002453	32738.7215
HLA A*1101	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.517442	-0.487391	-5.004833	32918.6293
HLA B*1517	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.527465	-0.487391	-5.014856	33687.1792
HLA B*2705	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.530909	-0.487391	-5.018300	33955.4110
HLA B*0803	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.535838	-0.487391	-5.023230	34342.9986
HLA A*0206	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.542494	-0.487391	-5.029886	34873.4009
HLA A*2301	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.544548	-0.487391	-5.031939	35038.6813
HLA B*1509	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.546709	-0.487391	-5.034101	35213.5069
HLA B*1503	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.550515	-0.487391	-5.037907	35523.4751
HLA A*0211	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.558884	-0.487391	-5.046276	36214.6515
HLA B*3801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.582609	-0.487391	-5.070001	38248.0598
HLA B*7301	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.588100	-0.487391	-5.075492	38734.6964
HLA A*2402	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.600369	-0.487391	-5.087761	39844.5721
HLA A*0250	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.603994	-0.487391	-5.091386	40178.5650
HLA A*0202	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.604330	-0.487391	-5.091722	40209.6598
HLA A*3002	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.615991	-0.487391	-5.103382	41303.8840
HLA B*1502	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.621359	-0.487391	-5.108751	41817.6348
HLA A*2602	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.624592	-0.487391	-5.111984	42130.0871
HLA A*3201	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.629489	-0.487391	-5.116880	42607.7581
HLA A*3301	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.643116	-0.487391	-5.130507	43965.8726
HLA B*4002	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.648115	-0.487391	-5.135507	44474.9431
HLA B*4501	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.655044	-0.487391	-5.142436	45190.1759
HLA A*2603	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.669068	-0.487391	-5.156460	46673.2570
HLA B*4403	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.669167	-0.487391	-5.156558	46683.8631
HLA A*6801	1:119-127 9	PPGMEDDAD	0.692523	-1.179914	-4.685585	-0.487391	-5.172976	48482.4980

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