```
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 n

Predictions
Allele  Position        PepLength       Sequence        Proteasome      TAP     MHC
HLA B*1503      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1517      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -0.8
HLA A*2902      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*8001      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -0.9
HLA B*1517      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*3002      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -1.2
HLA A*2602      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -1.2
HLA B*1517      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0101      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*8001      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1502      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2902      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -1.4
HLA A*3002      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1501      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1517      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0101      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1517      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2902      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1501      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -1.7
HLA A*2902      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*3501      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1503      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*8001      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0203      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0250      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3001      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3002      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0250      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -0.4
HLA A*2403      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0211      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -0.4
HLA A*0203      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0101      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*3501      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0206      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0212      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1517      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1501      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1517      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1503      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -1.4
HLA A*3002      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.2
HLA B*1517      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1517      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0250      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0211      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1502      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1502      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.3
HLA A*0202      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0202      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3001      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2603      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.3
HLA A*0203      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -0.7
HLA B*1517      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.1
HLA A*0203      1:238-246       9       KINIAVAPL       1.111426        0.535215
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HLA B*3501      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.3
HLA B*4601      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1501      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -1.5
HLA A*2902      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*3301      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*6802      1:33-41 9       TAARLANHL       1.682942        0.504172        -1.7
HLA B*1502      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*1101      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0250      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*1503      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2602      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0211      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.2
HLA A*0206      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1501      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*3501      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0211      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0301      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2602      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1503      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3201      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.6
HLA A*0301      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -2.7
HLA A*2301      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0202      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0212      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -1.1
HLA A*0202      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2403      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0212      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0301      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0201      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3001      1:34-42 9       AARLANHLV       0.964146        0.245998        -1.0
HLA B*5301      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0203      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*0702      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0216      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0216      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*6802      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -1.1
HLA A*6802      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0211      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*3201      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.6
HLA A*6901      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.6
HLA A*3001      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -1.1
HLA B*1501      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*1101      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0206      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.6
HLA A*0212      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.6
HLA B*1503      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1501      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*1503      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*6801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -1.4
HLA A*0301      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0216      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1517      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*6802      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*8001      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0206      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*3501      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.1
HLA A*0250      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*1101      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*4001      1:180-188       9       AQIMADTGL       1.532715        0.528739
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HLA A*2602      1:7-15  9       DVAARLGTL       1.463313        0.301089        -1.8
HLA A*0202      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0219      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*6801      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0202      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -1.4
HLA A*0211      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2602      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1517      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*1101      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*1101      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*1101      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.0
HLA A*2601      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.0
HLA A*0206      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*3001      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*6801      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*6801      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -1.3
HLA A*0206      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -1.4
HLA A*0250      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4501      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*0702      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -1.9
HLA A*6901      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0216      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -1.5
HLA A*3001      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0206      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0250      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -1.9
HLA A*0203      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.3
HLA A*0202      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2602      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0250      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0201      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*6802      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0211      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*6802      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*6801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*3001      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.2
HLA B*3501      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*5401      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3201      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.4
HLA A*0202      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.4
HLA B*5801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*3501      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -2.0
HLA B*1502      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.4
HLA A*0216      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -2.0
HLA B*1501      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*4002      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1517      1:4-12  9       VGFDVAARL       1.701239        0.380386        -2.4
HLA B*1503      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.3
HLA A*3101      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*1101      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -1.5
HLA A*6802      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*5801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*6802      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*3002      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0206      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0203      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -2.0
HLA A*6901      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*3901      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -2.1
HLA A*3201      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*1517      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0202      1:280-288       9       ATPEQIDAL       1.534469        0.530441
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HLA A*0211      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3101      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*6802      1:7-15  9       DVAARLGTL       1.463313        0.301089        -2.2
HLA A*3001      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*1517      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0206      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0206      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*6802      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1517      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2501      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.4
HLA A*0219      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -1.7
HLA A*0250      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.6
HLA A*0206      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0250      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0202      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0250      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0203      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0203      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*3101      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*3001      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0211      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*2603      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1503      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1502      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*0801      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2501      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*6802      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0202      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0216      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*6901      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6802      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2601      1:7-15  9       DVAARLGTL       1.463313        0.301089        -2.4
HLA A*3001      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0216      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0203      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*6801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*6801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*6802      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*3201      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*1517      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1501      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3901      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0250      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*6901      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*0702      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0202      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1517      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0201      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*1101      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0206      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.8
HLA B*1517      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -2.8
HLA B*1801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*8001      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0203      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*6801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3301      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0211      1:4-12  9       VGFDVAARL       1.701239        0.380386        -2.8
HLA B*3501      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0203      1:182-190       9       IMADTGLAY       1.494684        1.318082
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HLA A*0203      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*0801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0203      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0206      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*3201      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0206      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0202      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*6801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.7
HLA B*3501      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2602      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0250      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1501      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0250      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1503      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0250      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5701      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -3.7
HLA A*0301      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0202      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.1
HLA A*0203      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.1
HLA A*6801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3101      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*5401      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*3201      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1503      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0250      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -1.7
HLA A*0206      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -2.5
HLA A*0212      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0250      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0202      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0206      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1517      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1501      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.2
HLA A*0216      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3201      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*6802      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -1.6
HLA A*0201      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -2.2
HLA A*6901      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*3501      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0202      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -2.6
HLA A*0202      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.0
HLA A*3201      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*1501      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0202      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0250      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*1501      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0206      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0206      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*3501      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2301      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0202      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0206      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*2705      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -2.2
HLA A*2501      1:7-15  9       DVAARLGTL       1.463313        0.301089        -2.7
HLA B*5401      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3201      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*0702      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3101      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -2.4
HLA B*4001      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0202      1:201-209       9       WLAMGATGF       1.086667        1.040666
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HLA A*6901      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.1
HLA A*0202      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.2
HLA A*0206      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*3501      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0203      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0211      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0203      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2601      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*5801      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.2
HLA B*1503      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -2.7
HLA A*0202      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4601      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0212      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1503      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1501      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*6802      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0203      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*3901      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0211      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.3
HLA A*6802      1:30-38 9       DTATAARLA       1.317804        -0.349852       -2.0
HLA A*0203      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1502      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6901      1:7-15  9       DVAARLGTL       1.463313        0.301089        -2.8
HLA A*0216      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -1.9
HLA B*1503      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0206      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.0
HLA A*6901      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*3101      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0216      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*6801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0211      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -1.9
HLA A*0206      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1501      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*3901      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*2602      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*5701      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0202      1:8-16  9       VAARLGTLL       1.373046        0.413198        -2.9
HLA A*0212      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4002      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*6901      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0211      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0202      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*2705      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.0
HLA B*0702      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.0
HLA B*1801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -2.7
HLA A*0211      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*1501      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*5801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -2.9
HLA B*0702      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*3101      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.1
HLA B*4002      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1501      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -2.4
HLA B*1503      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3201      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.4
HLA B*1517      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0219      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*2602      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2902      1:201-209       9       WLAMGATGF       1.086667        1.040666
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HLA A*0219      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0206      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*6801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -2.6
HLA A*3201      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.2
HLA B*1501      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2601      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*6802      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1502      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.1
HLA A*0301      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0203      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0219      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -2.0
HLA B*5801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.3
HLA B*1502      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*2403      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.1
HLA A*2501      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1517      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0301      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -2.4
HLA B*3501      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*0702      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*6801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -2.7
HLA A*6801      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3901      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0202      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0211      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4601      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.1
HLA A*0216      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0206      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3201      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3001      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*1101      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3001      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*0702      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3301      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -2.7
HLA A*6901      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*3001      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -2.1
HLA A*2603      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4001      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*0702      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1503      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0203      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA B*3501      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4403      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0219      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0201      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -2.9
HLA A*2501      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2603      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*3801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA B*1502      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6901      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -2.9
HLA A*0203      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*6901      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0101      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA B*0702      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0202      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6901      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA A*3001      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1503      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1517      1:108-116       9       GLLVVTPYY       1.162301        1.198349
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HLA B*1801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*4501      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -2.1
HLA A*0211      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0206      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.4
HLA A*3001      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0211      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0211      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*5301      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA A*0211      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4001      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.2
HLA A*3101      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*3201      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*5701      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*3101      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0250      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0211      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3101      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0211      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.4
HLA B*3901      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.5
HLA B*3901      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA B*1509      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6802      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -3.1
HLA B*2705      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*4801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA B*1517      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*2501      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*6901      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0212      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.6
HLA A*0201      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0201      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0301      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0206      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0202      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2603      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*3101      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0250      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4402      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*6801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -3.2
HLA B*0803      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*3101      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -2.9
HLA A*0211      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2603      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.2
HLA A*0206      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*2601      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0206      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0202      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4002      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*5801      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*0803      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*0212      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA B*1509      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*3101      1:28-36 9       SLDTATAAR       0.953732        0.586069        -2.9
HLA A*0201      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4002      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -3.3
HLA A*0250      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.1
HLA A*2601      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5301      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1503      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5301      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -3.1
HLA B*4402      1:152-160       9       IEPDTIRAL       1.667218        0.297959
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HLA B*0802      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*3301      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*1501      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2601      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*3301      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*0801      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*0219      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1517      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.2
HLA B*4801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0201      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*0250      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5401      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*2705      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -2.3
HLA A*0250      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*1509      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*2402      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*0250      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*3901      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0211      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*0216      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*6901      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0206      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*6802      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.3
HLA A*2601      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2902      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1502      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*5801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0212      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0206      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0219      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.4
HLA B*1517      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*1517      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.1
HLA B*5701      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.6
HLA A*6801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4402      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*6802      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.5
HLA B*1503      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1502      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*0801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.5
HLA B*4001      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1503      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*0702      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*3501      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*0801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0201      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0802      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*1501      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0203      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0206      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*4801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0250      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3301      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -3.0
HLA B*3901      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*0801      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*3101      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0250      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5101      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.4
HLA A*2403      1:182-190       9       IMADTGLAY       1.494684        1.318082
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HLA B*1503          1:11-19 9           RLGTLLTAM           1.041303            0.243197            -2.8
HLA A*0250          1:220-228           9         QLRELLSAF           1.194681            1.121923
HLA A*0250          1:139-147           9         MLLYDIPGR           1.114213            0.618034
HLA A*0216          1:280-288           9         ATPEQIDAL           1.534469            0.530441
HLA A*6901          1:68-76 9           ELLRAVLEA           1.116657            -0.299496           -2.3
HLA A*0250          1:34-42 9           AARLANHLV           0.964146            0.245998            -2.7
HLA A*3001          1:213-221           9         IAHLAAGQL           1.575399            0.482201
HLA A*0250          1:11-19 9           RLGTLLTAM           1.041303            0.243197            -2.8
HLA B*0803          1:182-190           9         IMADTGLAY           1.494684            1.318082
HLA A*2501          1:183-191           9         MADTGLAYY           1.304460            1.240624
HLA A*0216          1:208-216           9         GFISVIAHL           1.665341            0.445641
HLA A*6802          1:87-95 9           GTYDTAHSI           1.371192            0.292110            -3.2
HLA A*2501          1:155-163           9         DTIRALASH           0.889608            -0.411090
HLA A*0250          1:4-12  9           VGFDVAARL           1.701239            0.380386            -3.6
HLA A*0212          1:262-270           9         GLRLQGIDV           1.072956            0.154057
HLA A*2602          1:33-41 9           TAARLANHL           1.682942            0.504172            -3.7
HLA B*3901          1:180-188           9         AQIMADTGL           1.532715            0.528739
HLA B*1517          1:202-210           9         LAMGATGFI           1.174521            0.259665
HLA A*6802          1:104-112           9         EGAHGLLVV           1.230292            0.004958
HLA A*0206          1:250-258           9         MSRLGGVTL           1.727249            0.542308
HLA B*1801          1:220-228           9         QLRELLSAF           1.194681            1.121923
HLA A*1101          1:3-11  9           TVGFDVAAR           0.785469            0.628205            -2.9
HLA A*0211          1:183-191           9         MADTGLAYY           1.304460            1.240624
HLA A*0301          1:139-147           9         MLLYDIPGR           1.114213            0.618034
HLA A*0206          1:33-41 9           TAARLANHL           1.682942            0.504172            -3.7
HLA A*2301          1:81-89 9           RVIAGAGTY           1.391808            1.523551            -4.4
HLA B*3901          1:89-97 9           YDTAHSIRL           1.591071            0.262701            -3.4
HLA A*3101          1:91-99 9           TAHSIRLAK           0.996404            0.168531            -2.7
HLA A*0202          1:81-89 9           RVIAGAGTY           1.391808            1.523551            -4.4
HLA A*0212          1:280-288           9         ATPEQIDAL           1.534469            0.530441
HLA A*2402          1:182-190           9         IMADTGLAY           1.494684            1.318082
HLA A*0202          1:204-212           9         MGATGFISV           1.066312            0.114153
HLA A*0203          1:216-224           9         LAAGQLREL           1.347147            0.438424
HLA A*0202          1:66-74 9           KIELLRAVL           1.605726            0.383191            -3.5
HLA B*1503          1:159-167           9         ALASHPNIV           1.037611            0.271475
HLA A*0250          1:81-89 9           RVIAGAGTY           1.391808            1.523551            -4.4
HLA A*3002          1:107-115           9         HGLLVVTPY           0.949800            1.189146
HLA B*1517          1:102-110           9         AAEGAHGLL           1.273066            0.436296
HLA A*3001          1:202-210           9         LAMGATGFI           1.174521            0.259665
HLA B*3501          1:216-224           9         LAAGQLREL           1.347147            0.438424
HLA A*6802          1:182-190           9         IMADTGLAY           1.494684            1.318082
HLA A*3001          1:183-191           9         MADTGLAYY           1.304460            1.240624
HLA A*6801          1:72-80 9           AVLEAVGDR           0.741732            0.832221            -3.1
HLA B*1502          1:120-128           9         PQRGLQAHF           1.353492            0.881664
HLA A*0206          1:228-236           9         FGSGDIATA           1.183338            -0.323057
HLA A*2403          1:280-288           9         ATPEQIDAL           1.534469            0.530441
HLA B*5101          1:182-190           9         IMADTGLAY           1.494684            1.318082
HLA A*0201          1:11-19 9           RLGTLLTAM           1.041303            0.243197            -2.8
HLA B*2705          1:180-188           9         AQIMADTGL           1.532715            0.528739
HLA A*2602          1:208-216           9         GFISVIAHL           1.665341            0.445641
HLA A*0212          1:257-265           9         TLSKAGLRL           1.467227            0.434259
HLA A*2602          1:189-197           9         AYYSGDDAL           1.460439            0.696245
HLA A*0202          1:108-116           9         GLLVVTPYY           1.162301            1.198349
HLA B*3501          1:189-197           9         AYYSGDDAL           1.460439            0.696245
HLA A*3001          1:291-299           9         DMRAASVLR           1.068485            0.647236
HLA B*4403          1:81-89 9           RVIAGAGTY           1.391808            1.523551            -4.5
HLA A*3101          1:238-246           9         KINIAVAPL           1.111426            0.535215
HLA B*1502          1:21-29 9           TPFSGDGSL           1.381186            0.343982            -3.3
HLA A*2402          1:208-216           9         GFISVIAHL           1.665341            0.445641
HLA A*3002          1:189-197           9         AYYSGDDAL           1.460439            0.696245
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HLA A*2602      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*1503      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.4
HLA A*3201      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*0702      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.6
HLA A*0219      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3001      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0206      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*3001      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.2
HLA A*0202      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0250      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5401      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.5
HLA B*4601      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0219      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*6901      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0201      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.7
HLA B*3501      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0216      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0212      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0211      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*0203      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1517      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1503      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.8
HLA A*2301      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0201      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0203      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3201      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1503      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3301      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.5
HLA A*0206      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -2.9
HLA A*3001      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*2902      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.7
HLA A*3301      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2601      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*3001      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5701      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*1517      1:32-40 9       ATAARLANH       0.780469        -0.166695       -2.2
HLA B*7301      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.5
HLA A*0206      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1517      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0203      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0203      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2602      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -3.3
HLA B*5801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*3001      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.6
HLA B*1517      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.8
HLA A*0211      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*1101      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0202      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2403      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*6901      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*3501      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0201      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0211      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2902      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*3101      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0211      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4402      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*5401      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA B*5801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1501      1:208-216       9       GFISVIAHL       1.665341        0.445641
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HLA B*4403      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0202      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0202      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.3
HLA B*5101      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*1101      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0219      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0201      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0216      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.3
HLA A*2403      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4501      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.6
HLA A*0216      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0216      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*1801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*1503      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3201      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2603      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*1503      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*6801      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.8
HLA B*4002      1:81-89 9       RVIAGAGTY       1.391808        1.523551        -4.6
HLA B*0801      1:33-41 9       TAARLANHL       1.682942        0.504172        -3.8
HLA A*6801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0211      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*0801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.4
HLA A*2402      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*5701      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*6801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*0702      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.5
HLA A*0203      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0206      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*5801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*1801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0206      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*8001      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0206      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -2.9
HLA A*0203      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.5
HLA A*3001      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*6901      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2602      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.8
HLA A*0206      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0219      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*4501      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0202      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2301      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4601      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0216      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1502      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*3801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0216      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0212      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0216      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.8
HLA A*6802      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1517      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*1101      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -3.3
HLA B*3901      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.7
HLA B*1503      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0250      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2403      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.8
HLA B*2705      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0250      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -2.6
HLA A*0212      1:183-191       9       MADTGLAYY       1.304460        1.240624
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HLA A*0250      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -2.9
HLA B*5401      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0802      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*3301      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0201      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*3002      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*0801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.7
HLA B*1509      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0211      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4402      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*6802      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0216      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0203      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4001      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0250      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0211      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1503      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0250      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0203      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*0803      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*7301      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*2602      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1502      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*2705      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0802      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0301      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*0801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0202      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*1503      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3101      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*4601      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*2603      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*4002      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*6801      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*6802      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4403      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2403      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0206      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0201      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2301      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1501      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1503      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.4
HLA A*0206      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0201      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*3001      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4501      1:182-190       9       IMADTGLAY       1.494684        1.318082
HLA A*0250      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4801      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5301      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*6901      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*4501      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*2602      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0203      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*6802      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*3501      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.0
HLA B*3901      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*0702      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0250      1:183-191       9       MADTGLAYY       1.304460        1.240624
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HLA A*6802      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4403      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*3201      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4001      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0202      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0206      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4001      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*0702      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5701      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0203      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*2705      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*2403      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*0801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*6901      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -3.5
HLA A*0211      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.5
HLA B*5101      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0211      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3201      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0203      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0212      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0203      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.0
HLA B*0802      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*4002      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*4601      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.9
HLA A*0202      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*3501      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0203      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.6
HLA B*3801      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0206      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.6
HLA A*3101      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.8
HLA B*1509      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0211      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0202      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0212      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4403      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1501      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.0
HLA A*0250      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0216      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -3.9
HLA B*5301      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*3501      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*3901      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2602      1:32-40 9       ATAARLANH       0.780469        -0.166695       -2.4
HLA A*0219      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1509      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*4403      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*4001      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0211      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*5801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.9
HLA A*0216      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*0803      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*2705      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2902      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4601      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5301      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0219      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*3901      1:4-12  9       VGFDVAARL       1.701239        0.380386        -3.9
HLA A*0211      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.5
HLA A*6802      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*4801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*0203      1:149-157       9       AVPIEPDTI       1.400742        0.371065
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HLA B*0702      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0101      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5101      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*5801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3101      1:73-81 9       VLEAVGDRR       1.117023        0.684017         -3.6
HLA A*0212      1:15-23 9       LLTAMVTPF       0.994564        1.098786         -3.9
HLA B*5401      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1503      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*2602      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1502      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2403      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0203      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1503      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0206      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*3301      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*3101      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2402      1:15-23 9       LLTAMVTPF       0.994564        1.098786         -3.9
HLA B*1503      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0206      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*3001      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6901      1:41-49 9       LVDQGCDGL       1.264073        0.392133         -3.5
HLA B*1801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1517      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0203      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2402      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0250      1:66-74 9       KIELLRAVL       1.605726        0.383191         -3.8
HLA A*0206      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1503      1:69-77 9       LLRAVLEAV       1.184331        0.094353         -3.1
HLA A*6901      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*4002      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*2705      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0301      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5701      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*0802      1:33-41 9       TAARLANHL       1.682942        0.504172         -4.1
HLA A*2301      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*6901      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2602      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3901      1:61-69 9       TTDGEKIEL       1.342355        0.325527         -3.5
HLA A*2902      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0211      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4002      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4601      1:4-12  9       VGFDVAARL       1.701239        0.380386         -4.0
HLA B*4402      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5401      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*0802      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5301      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*1501      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4403      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5701      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0203      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0202      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0211      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*0702      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0211      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*6802      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0216      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*1517      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*1503      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1503      1:4-12  9       VGFDVAARL       1.701239        0.380386         -4.0
HLA B*4001      1:250-258       9       MSRLGGVTL       1.727249        0.542308
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HLA A*0211      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*3001      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.1
HLA B*5701      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*2402      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.0
HLA A*2603      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0206      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*6802      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.7
HLA B*0702      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0301      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.4
HLA A*0216      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0211      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*3301      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*6901      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*0801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*6901      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2902      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0202      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2403      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*1101      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.4
HLA B*5801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4402      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4601      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3301      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0250      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0301      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0206      1:66-74 9       KIELLRAVL       1.605726        0.383191        -3.9
HLA B*4501      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*8001      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1509      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.1
HLA B*1801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2402      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*3001      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6901      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*3501      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.0
HLA A*3002      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0250      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6901      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0211      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0212      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2301      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*2301      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.0
HLA A*6802      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3201      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*2601      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0301      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*6802      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0201      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*3101      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.0
HLA A*0211      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0250      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*3001      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*3101      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3901      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*1503      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2603      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3901      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4002      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -2.7
HLA B*3501      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -3.8
HLA B*1503      1:213-221       9       IAHLAAGQL       1.575399        0.482201
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HLA B*5401      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*0206      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0211      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*3201      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*6901      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*4801      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2301      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*2402      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0206      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0250      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0201      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.0
HLA B*4801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1517      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3101      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -3.5
HLA B*5801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1501      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.0
HLA B*4001      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*4002      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2402      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*6801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0216      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0702      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.0
HLA B*1801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0212      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0216      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*0702      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2603      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*3501      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*3101      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0702      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3002      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.6
HLA A*0201      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*5301      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*5701      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5801      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5701      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*5101      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.1
HLA B*4001      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*5401      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*2705      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0216      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*2501      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*3801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*0801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0201      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*5301      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.1
HLA A*0216      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0202      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*3901      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1503      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*3001      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0202      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3301      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3301      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*2402      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA A*2501      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*2403      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA A*6802      1:116-124       9       YSKPPQRGL       1.485583        0.401798
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HLA A*3101      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2403      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1502      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0206      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*1101      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0203      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.0
HLA B*0802      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*4002      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA B*1517      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*2902      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.6
HLA A*3101      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0219      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0203      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0203      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5101      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0101      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4402      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*5301      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*0803      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0206      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0206      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*6802      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5701      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.1
HLA A*0212      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*6802      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*2705      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*3002      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0212      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2501      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0212      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*0702      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5701      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*3002      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.1
HLA B*0702      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA A*0201      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2902      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2402      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*1101      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*6802      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.7
HLA A*3002      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1501      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1501      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*2705      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.1
HLA B*2705      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1503      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0206      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.0
HLA B*3801      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*0702      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6802      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5801      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4402      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*6802      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1503      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*7301      1:134-142       9       ATELPMLLY       1.374221        1.200195
HLA A*3001      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0216      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA A*2602      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*3801      1:108-116       9       GLLVVTPYY       1.162301        1.198349
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HLA A*2603      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*0803      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*2902      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*4403      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*3901      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*6901      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.1
HLA A*2603      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0250      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA A*0301      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*1509      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*3501      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*0803      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0219      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.7
HLA A*3001      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3301      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0202      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*1503      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*6802      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.1
HLA A*0201      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2301      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0250      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*4001      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0203      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.1
HLA A*6802      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -3.7
HLA B*1517      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.0
HLA A*2601      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.1
HLA B*4501      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA A*0101      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*7301      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*1503      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*1509      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0211      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*5301      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0250      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*0803      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.1
HLA A*2602      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1501      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0216      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*6802      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*2501      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3501      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.8
HLA A*0219      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*0801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -3.9
HLA B*0803      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0212      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0201      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3901      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5101      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0202      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.8
HLA A*0203      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5401      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0203      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2602      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2602      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*6901      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2601      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*0802      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*3301      1:229-237       9       GSGDIATAR       1.288849        0.467193
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HLA B*3901      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*0801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0216      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*3201      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA B*4402      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*5301      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0212      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*2403      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4002      1:183-191       9       MADTGLAYY       1.304460        1.240624
HLA B*5301      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -3.7
HLA A*0202      1:29-37 9       LDTATAARL       1.609902        0.292450        -3.9
HLA B*1501      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.7
HLA B*5801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1517      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0202      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3501      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0250      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.8
HLA B*4501      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*2603      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*2402      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0206      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0216      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*5301      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.1
HLA A*0216      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.3
HLA A*3101      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.2
HLA B*1501      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*2301      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3101      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1509      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2602      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0203      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0201      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0201      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.7
HLA A*3201      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0702      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0206      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*5301      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*3001      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*1101      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*0206      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0250      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.7
HLA A*6802      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2403      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*5301      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*6901      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*3001      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.1
HLA A*6901      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*5101      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4001      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*1502      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0201      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*8001      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA A*0250      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0212      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1503      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4402      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*3201      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.3
HLA A*6901      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.3
HLA B*5701      1:129-137       9       TAVADATEL       1.437454        0.418113
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HLA B*1509      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*3501      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0301      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA A*0219      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3901      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*6802      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*8001      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*2601      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*8001      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*3901      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.0
HLA A*0219      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA A*2601      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*0201      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*2603      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0301      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4402      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0216      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2601      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0702      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2403      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3001      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0101      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*5801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*5101      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*4002      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*4601      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*2402      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0250      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*5701      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*6802      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0203      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*3002      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*3801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*4601      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0202      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*0801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*4801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*3501      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA B*4601      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1503      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.1
HLA A*0212      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*4601      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1509      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0101      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0211      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*3001      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA A*0201      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0212      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0211      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*3002      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0101      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*2402      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4001      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0206      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6901      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*0801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -3.4
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HLA A*0216      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*3901      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0202      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -3.9
HLA B*4801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2602      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*6901      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4601      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*0206      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -3.1
HLA B*0702      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4002      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA A*3001      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*8001      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1503      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0201      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*2705      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*4001      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.0
HLA A*2301      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*6901      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*2601      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*8001      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*3501      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*3901      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*6802      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*3201      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0202      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0219      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0203      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0203      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*3301      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*6901      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3002      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.1
HLA A*0202      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.2
HLA B*5101      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*2602      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2602      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*0702      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0101      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*2403      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0301      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*1101      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0203      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2501      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0212      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*3001      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0219      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.8
HLA A*0219      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4402      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1503      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -3.4
HLA A*0201      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1517      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0101      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.8
HLA A*3001      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -3.4
HLA A*6802      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0250      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0802      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4001      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0219      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA B*5701      1:8-16  9       VAARLGTLL       1.373046        0.413198        -3.9
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HLA A*6802      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -3.4
HLA A*0212      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA B*5401      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0219      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*6802      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*3001      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*6801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*4402      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4402      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*1501      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.1
HLA A*2902      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*0202      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*4801      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*3201      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1509      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA A*6802      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0216      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.8
HLA B*3501      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0202      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.0
HLA B*1517      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*3901      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.8
HLA B*4403      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*1501      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*3801      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*3201      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*0802      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6802      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*3901      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*5801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0203      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1509      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*1517      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1509      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0301      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2501      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA B*3801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*6901      1:30-38 9       DTATAARLA       1.317804        -0.349852       -3.1
HLA B*1503      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -3.9
HLA A*6901      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*3001      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1509      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4001      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*3901      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*0803      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA B*1517      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*3101      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA A*0202      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0216      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*7301      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0206      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*3901      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*4801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*2902      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA A*0201      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5401      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA B*5301      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0206      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2301      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
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HLA A*6901      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0212      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.1
HLA B*1509      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*5801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*6901      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*2603      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*2705      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*6801      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*5701      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA B*0801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*3001      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0101      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.2
HLA B*3501      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0202      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*3901      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*5401      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*0801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*0801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6901      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*6802      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0219      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0301      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0219      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4001      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.2
HLA A*0219      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2301      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.3
HLA A*0211      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*6901      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*0702      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2603      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0206      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2603      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.4
HLA B*0702      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.9
HLA B*4801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*0801      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3201      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5301      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2403      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*3501      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*3901      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*5801      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1503      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0219      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*1509      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2501      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.4
HLA B*1801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4501      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.3
HLA B*3801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0802      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0211      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3001      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*3501      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*0702      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*2501      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0203      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*4601      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3201      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA B*4601      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*1101      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.4
HLA B*5301      1:191-199       9       YSGDDALNL       1.544375        0.332060
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HLA A*0203      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1503      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.1
HLA A*0201      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA B*4801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*0803      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*3002      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*6802      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*7301      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -3.5
HLA B*0802      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*1503      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0101      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4601      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0201      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0206      1:7-15  9       DVAARLGTL       1.463313        0.301089        -3.9
HLA B*4001      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5301      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA A*8001      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1517      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.1
HLA A*6801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*1503      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5401      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*2705      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*6801      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0301      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*0702      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*7301      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*5701      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1503      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.1
HLA A*0202      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4002      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*2601      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4002      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*6901      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*4001      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3002      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1503      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2603      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4402      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA B*4002      1:62-70 9       TDGEKIELL       1.477276        0.206949        -3.9
HLA A*0219      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*3001      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -3.4
HLA B*0802      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5101      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4403      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1509      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0250      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1503      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0803      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*3501      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*6901      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*5301      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1503      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.1
HLA A*3301      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.0
HLA A*0219      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0803      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA B*0801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA B*5101      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*1101      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA A*2403      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*2705      1:290-298       9       ADMRAASVL       1.629911        0.440584
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HLA B*3501      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0219      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*3002      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA A*3001      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2501      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*6901      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -3.9
HLA B*4001      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0101      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0250      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0206      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.1
HLA B*4601      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*8001      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*3001      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*0801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*2705      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0212      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*0802      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0216      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1501      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2403      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1501      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3101      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0201      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*4402      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*0801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*6801      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*5701      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1509      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*1101      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0802      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1517      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2603      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA A*0301      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*6801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2603      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*4501      1:108-116       9       GLLVVTPYY       1.162301        1.198349
HLA A*0211      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*0702      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1503      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0219      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0802      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*4001      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.3
HLA A*0212      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0702      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*1503      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0101      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*3101      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0206      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.9
HLA B*1509      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4002      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.1
HLA B*5101      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -3.9
HLA A*0101      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*5801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0201      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*4801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA A*3001      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2602      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0301      1:257-265       9       TLSKAGLRL       1.467227        0.434259
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HLA A*2301      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1501      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0211      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.0
HLA B*0802      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*1517      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*3301      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.0
HLA B*5701      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0203      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*1101      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA B*4501      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*0801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*1801      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.4
HLA A*0216      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3301      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.8
HLA A*2602      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.2
HLA B*5701      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.9
HLA A*0216      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*2601      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0803      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0201      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1501      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*5101      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*2402      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*1501      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.0
HLA A*0219      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*5801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*4402      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4601      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*6802      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4403      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4402      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3101      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0202      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5401      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.4
HLA A*0211      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*7301      1:220-228       9       QLRELLSAF       1.194681        1.121923
HLA B*1801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2402      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0219      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0301      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -3.8
HLA B*0801      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*7301      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0301      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4501      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA A*0203      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.9
HLA B*4501      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2603      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1517      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.0
HLA A*3301      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*3301      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*0216      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*6901      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0702      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.5
HLA A*6901      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.1
HLA A*0250      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*3501      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -3.9
HLA A*2601      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*1101      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.0
HLA A*0101      1:290-298       9       ADMRAASVL       1.629911        0.440584
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HLA B*5101      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5301      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4402      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.1
HLA A*0101      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*0202      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0212      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0211      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0203      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0301      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*8001      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*1801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*2403      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*1101      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.9
HLA B*0801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*5801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA A*6801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.9
HLA B*3801      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*8001      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*4002      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*0801      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0803      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*3801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*2402      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.0
HLA B*0702      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*6801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0203      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.5
HLA A*6802      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA A*0301      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0211      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA B*1502      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*0301      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*1503      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -3.5
HLA A*3301      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -3.8
HLA A*0211      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.1
HLA A*3001      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2602      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.4
HLA B*0801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2501      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5301      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*3001      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0201      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1517      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.9
HLA B*2705      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA B*0803      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4002      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*3201      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -3.9
HLA B*0702      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*2402      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3001      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -3.8
HLA A*8001      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*1101      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*2501      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1517      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*2705      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0101      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*2705      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.2
HLA A*2902      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3101      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4402      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*6802      1:217-225       9       AAGQLRELL       1.446320        0.452192
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HLA A*8001      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*3501      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.9
HLA A*2601      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3001      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0250      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*3901      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0206      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -3.6
HLA B*4801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*2601      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0202      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.5
HLA A*0216      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4001      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.2
HLA A*0211      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*3801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*1101      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*0216      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*0803      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4402      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*0202      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3101      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*2403      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.3
HLA A*3002      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3201      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*1501      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*0216      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*0702      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4402      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*1509      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.0
HLA A*3101      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0101      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*1501      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0203      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.2
HLA B*5301      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.1
HLA A*0202      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1801      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*1801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*0702      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*4601      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1509      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.4
HLA A*0250      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*6802      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5701      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*5801      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0702      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4403      1:250-258       9       MSRLGGVTL       1.727249        0.542308
HLA B*5701      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*0802      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*3801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA B*5301      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0206      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.5
HLA B*7301      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*1503      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0212      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -3.9
HLA A*0219      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5401      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0216      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*3501      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*4601      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0201      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*1801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.0
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HLA A*2403      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0802      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA A*1101      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2301      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -3.9
HLA A*0216      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*5301      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*0211      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*0803      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA A*2602      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*2403      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*6801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0211      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*5101      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1502      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.5
HLA A*3002      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*6901      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3801      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*1502      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*8001      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0250      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5101      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0211      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*4402      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*0802      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*5101      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.4
HLA A*2403      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*3002      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2501      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*5801      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*6801      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA A*2902      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0211      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*5101      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*5101      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*5701      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*1801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*8001      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0203      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*6901      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.1
HLA B*3801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0250      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.1
HLA B*3501      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*2705      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*5401      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3201      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0803      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*0250      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*4001      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*1501      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0206      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4601      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0206      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.2
HLA A*3301      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*0301      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.1
HLA A*0216      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.1
HLA A*3201      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3201      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2403      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0212      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*5101      1:280-288       9       ATPEQIDAL       1.534469        0.530441
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HLA A*6901      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.2
HLA A*8001      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*3801      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.4
HLA A*0202      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0301      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2602      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0201      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*3301      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.5
HLA A*0202      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.0
HLA A*6901      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*3001      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*6802      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5701      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*6801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3301      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.4
HLA B*0802      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*0702      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*1101      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*6901      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*7301      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA B*0801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*3501      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.2
HLA B*5101      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4002      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*3501      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.1
HLA A*0203      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5401      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*3001      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4801      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*4001      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*3801      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*3201      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*2402      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*0702      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.5
HLA A*3001      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.2
HLA A*0219      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2603      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.0
HLA B*1502      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3101      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5301      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1503      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2301      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*1502      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1503      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5701      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*0212      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*0801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.0
HLA A*3001      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2902      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*6901      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2403      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2601      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*3002      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1509      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*5301      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA A*0301      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0250      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*3801      1:213-221       9       IAHLAAGQL       1.575399        0.482201
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HLA A*0101      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*1801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2402      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA B*5101      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0202      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*1101      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*3301      1:63-71 9       DGEKIELLR       1.103206        0.332352        -3.8
HLA A*0219      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*4601      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0219      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0212      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5101      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.1
HLA A*2902      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*3001      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2403      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*3101      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4501      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA A*2301      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2601      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*4001      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.4
HLA B*5101      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1517      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*0801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.2
HLA A*6801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.1
HLA A*0206      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*4002      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3501      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.5
HLA B*1801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*1517      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.5
HLA A*3001      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0206      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2501      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.4
HLA B*4501      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*3501      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2902      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*1509      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2403      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0203      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3101      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*0803      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*3001      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2501      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1503      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3001      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*6802      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*0801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.1
HLA A*0211      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4001      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0101      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*5801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*0801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2902      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*1101      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*4403      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*3501      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*3901      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*4403      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*3501      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1503      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0216      1:129-137       9       TAVADATEL       1.437454        0.418113
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HLA A*0201      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5401      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0201      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*2402      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*6901      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3501      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*5301      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*6901      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.2
HLA B*0801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0219      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*5401      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA B*2705      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3002      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4601      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*1503      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0101      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0203      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*2601      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0201      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*6901      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*4801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3001      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA A*1101      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0202      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*5401      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.4
HLA A*2603      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1503      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4002      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*4403      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.5
HLA B*5101      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*8001      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*0201      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*2705      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2301      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*4601      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.0
HLA A*2601      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2601      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0201      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4402      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*5701      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4601      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2601      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA A*2403      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0201      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*6802      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2501      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*6801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*2705      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0212      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -3.6
HLA A*0216      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1509      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.1
HLA A*2301      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1501      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0250      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*1517      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0301      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2601      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*0801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*1501      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
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HLA B*1502      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*2902      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.3
HLA B*1509      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*5101      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*3501      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5701      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*5101      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2501      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*6802      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0216      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*4001      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0250      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0203      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*2705      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*0702      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*5101      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2501      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.0
HLA B*0702      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3002      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*0801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*2603      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*7301      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.5
HLA B*4801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*3901      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0202      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2402      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*3201      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*5801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*1517      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0219      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2902      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0216      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0212      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.2
HLA A*1101      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA A*2402      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*5401      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3001      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0219      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.6
HLA A*0202      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.1
HLA B*0802      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA A*3101      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2501      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA A*3001      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*0203      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*4002      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.6
HLA B*7301      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*5801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3201      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.3
HLA A*0101      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1503      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*3101      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*2601      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0206      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2603      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.0
HLA B*4001      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3001      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*6901      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0203      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*1501      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA B*2705      1:255-263       9       GVTLSKAGL       1.514430        0.369798
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HLA A*6802      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.4
HLA B*5301      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0211      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.9
HLA B*1509      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0101      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0803      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA A*2603      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.3
HLA A*3301      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -3.5
HLA A*3101      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0201      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3101      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA B*5401      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0212      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2601      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.1
HLA A*2402      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0219      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*6802      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.3
HLA A*6901      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1503      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2603      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*0801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*2705      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*6802      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*5101      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1509      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*3101      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*0702      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*6901      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0216      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*4001      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5701      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0211      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*4501      1:33-41 9       TAARLANHL       1.682942        0.504172        -4.6
HLA A*0212      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*0803      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*0802      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*6801      1:189-197       9       AYYSGDDAL       1.460439        0.696245
HLA A*3001      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*2705      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*6802      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0206      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4402      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA B*4002      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*3201      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4601      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*6801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -2.7
HLA A*6801      1:120-128       9       PQRGLQAHF       1.353492        0.881664
HLA B*2705      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1502      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*4001      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*0802      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2402      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA A*6802      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*0801      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0202      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5401      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4402      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1503      1:126-134       9       AHFTAVADA       0.878182        -0.138289
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HLA A*0206      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4002      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*4402      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3501      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*8001      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*3501      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3201      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0250      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*4001      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4601      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*0212      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*2902      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.2
HLA A*2602      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*3901      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*0250      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.9
HLA B*7301      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA B*5701      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*2705      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*3101      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2403      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*8001      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0201      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1517      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5101      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*0201      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*2603      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA A*2602      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*0203      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4001      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0202      1:28-36 9       SLDTATAAR       0.953732        0.586069        -3.9
HLA B*4801      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2301      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*3002      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2501      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0212      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1517      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*3801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0201      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.1
HLA B*5401      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA B*5401      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3201      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0216      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0301      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*4402      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*3901      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0201      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2301      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3201      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0212      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0301      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*2705      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1509      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0702      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0203      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0201      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4403      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*0802      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*1509      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1509      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*3501      1:235-243       9       TARKINIAV       1.205835        0.236791
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HLA A*0219      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1509      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2601      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2602      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2902      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3201      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1509      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2301      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2501      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2301      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*0803      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5301      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*2402      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -3.9
HLA A*0202      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*0101      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2301      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA B*4501      1:107-115       9       HGLLVVTPY       0.949800        1.189146
HLA A*3301      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA A*3201      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*0801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.7
HLA B*3901      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*3901      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA B*5301      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*0702      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1503      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0301      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0219      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*3301      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0206      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.2
HLA A*0301      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*4403      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA B*3801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*3001      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA B*4001      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0212      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*7301      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*3901      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3001      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1509      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4402      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2902      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2603      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0202      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.2
HLA A*6901      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA A*2602      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*4601      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*3001      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0219      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3002      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*7301      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*2501      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*5701      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*3501      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*4801      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*5401      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*4002      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2402      1:191-199       9       YSGDDALNL       1.544375        0.332060
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HLA A*0301      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*3801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*6801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.6
HLA B*4601      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3301      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1501      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5701      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2603      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA A*2902      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*5101      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*2603      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*0801      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*2705      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*0211      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA A*0301      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*8001      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0803      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2602      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -3.8
HLA B*1502      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*1502      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA A*3001      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.2
HLA B*4402      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2601      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*0803      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*0216      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*0301      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0211      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*1801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2402      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*4601      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1509      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA B*4403      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.5
HLA A*2402      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*3101      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2601      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*6901      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1517      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5701      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*1801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*1501      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0212      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0702      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*4403      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA A*0216      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*0802      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4402      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0250      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*0702      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*3002      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0101      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*0201      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*5301      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*6801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*1101      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0202      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0219      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2902      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*6802      1:233-241       9       IATARKINI       1.331664        0.187951
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HLA A*3201      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1501      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*8001      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*4601      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2902      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1509      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*0702      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0216      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA B*3501      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*0801      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0203      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.3
HLA A*0216      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5701      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*2403      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5101      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.1
HLA B*4501      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*3501      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3001      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*2705      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*1801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*1501      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA B*1503      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0250      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0203      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2403      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0301      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.1
HLA A*6801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*0702      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.1
HLA A*2601      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0803      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0212      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA B*0801      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.1
HLA B*5401      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0101      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA B*5801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*4601      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4402      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0206      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*3001      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0212      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0250      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*2403      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*0702      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.1
HLA B*7301      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA A*1101      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.1
HLA A*3001      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0101      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0201      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0250      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2602      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0211      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.2
HLA A*0219      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.3
HLA A*0219      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*3901      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*1101      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1502      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3002      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*5401      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA A*0301      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2402      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
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HLA B*0802      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*8001      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3001      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2602      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0101      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*5101      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.4
HLA A*2603      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1501      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2501      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3002      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA B*1517      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6901      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0212      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2902      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0201      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2601      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*4501      1:208-216       9       GFISVIAHL       1.665341        0.445641
HLA B*2705      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*1801      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*8001      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*0301      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*3001      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*0802      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*2601      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*1503      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0301      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -3.9
HLA A*0202      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.7
HLA B*4001      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*2301      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*4801      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*2402      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1502      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -3.7
HLA A*0219      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA A*0202      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1503      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA A*3101      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*8001      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2403      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*3301      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0216      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*0801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4601      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0301      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*6901      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5701      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2902      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.2
HLA A*2902      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*2602      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA A*0206      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3201      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA B*5301      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*6901      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3301      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4501      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*3501      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4402      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2601      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3101      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3101      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*3801      1:191-199       9       YSGDDALNL       1.544375        0.332060
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HLA A*2402      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6801      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*4002      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.5
HLA B*1509      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2902      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*4001      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*8001      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*2602      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.1
HLA A*1101      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*0801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*3901      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0212      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.2
HLA A*1101      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*1101      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4402      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*1503      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4501      1:201-209       9       WLAMGATGF       1.086667        1.040666
HLA B*1517      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA A*2601      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4403      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*3901      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*1501      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*6802      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -3.5
HLA B*1502      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4402      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3301      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*0212      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*8001      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA A*3101      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*0212      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*0802      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0101      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*0203      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*5101      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*3002      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*3201      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*0802      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*0803      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4002      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*4402      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*1509      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.1
HLA B*3801      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*7301      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA B*4801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*7301      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*2601      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0101      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*6802      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.1
HLA A*0219      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*3801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*7301      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.6
HLA A*3101      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*6802      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2602      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*0702      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*2403      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*0201      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5701      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*0803      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2601      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.1
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HLA B*0801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0203      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5301      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*3002      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2603      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA A*2602      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.1
HLA A*0211      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3501      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -3.3
HLA A*2403      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.1
HLA B*4001      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.1
HLA B*1502      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*1101      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*8001      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0212      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA B*1801      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0301      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3002      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*0803      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*5101      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA A*2603      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0301      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*4001      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*6901      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1501      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0219      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*3901      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*4001      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4501      1:15-23 9       LLTAMVTPF       0.994564        1.098786        -4.6
HLA B*5101      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5801      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1501      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0101      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA B*0803      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1502      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*3201      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*1501      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0219      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*3901      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3301      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*3801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*0301      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*5101      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*2705      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*5101      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0201      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*6801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*1517      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2301      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.3
HLA B*4403      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2602      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0219      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*3901      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA A*1101      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*2501      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*2705      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1801      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1517      1:245-253       9       PLCNAMSRL       1.448212        0.287348
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HLA A*6802      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*6901      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*0801      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0203      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2602      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*3801      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1502      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1801      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*3501      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0202      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*3101      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.1
HLA B*2705      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*2705      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*5801      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2301      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*5701      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA A*1101      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0216      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0301      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2501      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*2601      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2603      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA A*2403      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*0801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*0250      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*1101      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*0702      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA B*4403      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*0203      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4801      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0202      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*1101      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA A*3101      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1501      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA B*1801      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*2705      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2603      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*2902      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*6802      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA B*4501      1:280-288       9       ATPEQIDAL       1.534469        0.530441
HLA A*3002      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*2501      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*3002      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*3801      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0101      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*3001      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*0203      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3301      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*4801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*0216      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2501      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2602      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2501      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0301      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2902      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1502      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*5301      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*2301      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*0702      1:150-158       9       VPIEPDTIR       1.171388        0.635900
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HLA A*2301      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*0201      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3301      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1502      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0203      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4801      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1503      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0201      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0211      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0216      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*4801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA B*1501      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2402      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2902      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2301      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*6802      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.2
HLA B*5401      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*5801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4501      1:4-12  9       VGFDVAARL       1.701239        0.380386        -4.6
HLA B*4501      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -3.8
HLA A*6801      1:290-298       9       ADMRAASVL       1.629911        0.440584
HLA B*1501      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA A*2403      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA A*2902      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3201      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*0802      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*0206      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.2
HLA B*1502      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*0212      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*4801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*1101      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*4403      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA A*6801      1:180-188       9       AQIMADTGL       1.532715        0.528739
HLA B*2705      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*2501      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA B*1517      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA B*5401      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*1501      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0101      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0211      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2902      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0101      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5401      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.2
HLA A*3101      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*5801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*3001      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1801      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*0203      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*3801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*0803      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*0201      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*1502      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*3901      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0301      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0802      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0250      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*3001      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4002      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*5701      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA B*1801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
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HLA B*1503      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4001      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*2501      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4601      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*4801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2403      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*6901      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.7
HLA B*5301      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.5
HLA B*4801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*0211      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*6801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA A*3201      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*5301      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*2601      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*3501      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*1501      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA A*2601      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA A*2601      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0219      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*3101      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0212      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3001      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -3.9
HLA A*2403      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA A*3001      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.2
HLA A*6901      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2403      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*0212      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2902      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*6901      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*3101      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3001      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3101      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*1501      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2301      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*2501      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA B*3901      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*6901      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4601      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*3901      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0202      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0101      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*3901      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0211      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*4601      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*2501      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*5801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3002      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*4002      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*2705      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*0219      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1502      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.4
HLA A*2601      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*2402      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA A*0206      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*6901      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*6802      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0250      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*1101      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*1517      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1509      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
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HLA B*4601      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3501      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*0801      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0301      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA B*4601      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1501      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*4001      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2403      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1501      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4501      1:213-221       9       IAHLAAGQL       1.575399        0.482201
HLA B*5801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA B*3501      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3001      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA B*3501      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA B*4801      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2501      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA A*8001      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*0101      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA A*0301      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*3002      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0101      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2501      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0201      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0212      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*6901      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*0216      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA A*2603      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*1517      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4001      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1509      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*4801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2602      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1501      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.3
HLA B*1503      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*1501      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1517      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3002      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*1509      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1517      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2402      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA B*0801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3002      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*2902      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0301      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5101      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*1801      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3201      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*1501      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*0802      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*1503      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5401      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*2705      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2301      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1501      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0216      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.1
HLA B*5801      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*3501      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*0803      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
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HLA A*0219      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0206      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.6
HLA A*2902      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*2902      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*7301      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA A*0101      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*8001      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5101      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*1101      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.1
HLA A*0101      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA B*1502      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*0802      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4002      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3101      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA B*3901      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*2601      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2402      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA A*1101      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA B*5701      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*0212      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*2705      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*5801      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4001      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*0206      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*0702      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0212      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5801      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4501      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*1101      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4402      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*8001      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2601      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5401      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*4801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*4001      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA B*0801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*6901      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -3.3
HLA B*5701      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4001      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3101      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*0211      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.2
HLA B*5401      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA B*5701      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5301      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0212      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3001      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.2
HLA B*0803      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3101      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4601      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA A*2603      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.8
HLA A*0212      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*0803      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.3
HLA A*0201      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*6802      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2902      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*0801      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*4402      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.2
HLA A*2601      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*5701      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5701      1:102-110       9       AAEGAHGLL       1.273066        0.436296
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HLA A*0301      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*6802      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3002      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0301      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4601      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2602      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA A*6901      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2601      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*8001      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*0203      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*3002      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA A*2403      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*4801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*5701      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2601      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0216      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*3002      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2402      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*5801      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*2902      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5101      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2902      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*2705      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0216      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2602      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4402      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2602      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*3201      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0201      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0250      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2403      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*8001      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*0803      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*4001      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*4001      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4402      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA A*6801      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.6
HLA B*5101      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*5801      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*6801      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*6802      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*6901      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*0101      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*2705      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2402      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2601      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0219      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.2
HLA A*0203      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*8001      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA A*6801      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*0801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*2705      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*0301      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA A*2301      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA A*0206      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*2705      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3002      1:133-141       9       DATELPMLL       1.554399        0.353260
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HLA B*4001      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2601      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*6802      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0301      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0250      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0101      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*1501      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4601      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA A*3101      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4001      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4002      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2403      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2902      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5701      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.3
HLA B*0801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3002      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*1801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2301      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5401      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*4801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*7301      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.6
HLA A*3201      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1509      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA A*3101      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2403      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*2403      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4402      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*6901      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*1501      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*8001      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*0802      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2301      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA B*4402      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2902      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4001      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0212      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*5801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*2705      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*0702      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1517      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.5
HLA A*0101      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*0803      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.2
HLA B*0802      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*1101      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*4801      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0101      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0203      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*5801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*1517      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4403      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*6802      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*1501      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0201      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*6901      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2403      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA A*0219      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4403      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.4
HLA B*5801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA B*4601      1:238-246       9       KINIAVAPL       1.111426        0.535215
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HLA A*0203      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*3801      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA B*0702      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3101      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*6901      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3002      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*0801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0201      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*5401      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA A*2403      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.1
HLA A*3001      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0206      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.1
HLA A*2902      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5401      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2501      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1503      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0212      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.1
HLA B*3801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*2501      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4001      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*3001      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA B*5701      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*4402      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*6801      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*2402      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*1101      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0201      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*3901      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*8001      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*6801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*3501      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1509      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*3801      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*4001      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.2
HLA B*4601      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3002      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*2601      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*0802      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5801      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*5701      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0203      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*2501      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0203      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA B*0801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*0201      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.4
HLA B*4501      1:66-74 9       KIELLRAVL       1.605726        0.383191        -4.6
HLA A*3002      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2403      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0301      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*5301      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0206      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*0212      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0219      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*6802      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.8
HLA B*0802      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1503      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*1517      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0219      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*2705      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2501      1:101-109       9       CAAEGAHGL       1.249461        0.495475
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HLA B*1517          1:11-19 9           RLGTLLTAM           1.041303            0.243197            -3.9
HLA A*1101          1:114-122           9         PYYSKPPQR           1.113255            0.635690
HLA A*3201          1:8-16  9           VAARLGTLL           1.373046            0.413198            -4.4
HLA B*1501          1:235-243           9         TARKINIAV           1.205835            0.236791
HLA A*3301          1:152-160           9         IEPDTIRAL           1.667218            0.297959
HLA B*0702          1:245-253           9         PLCNAMSRL           1.448212            0.287348
HLA A*0206          1:262-270           9         GLRLQGIDV           1.072956            0.154057
HLA A*3002          1:202-210           9         LAMGATGFI           1.174521            0.259665
HLA B*4402          1:149-157           9         AVPIEPDTI           1.400742            0.371065
HLA B*1509          1:75-83 9           EAVGDRRVI           1.485818            0.219873            -4.3
HLA B*0802          1:291-299           9         DMRAASVLR           1.068485            0.647236
HLA B*4801          1:114-122           9         PYYSKPPQR           1.113255            0.635690
HLA A*3101          1:21-29 9           TPFSGDGSL           1.381186            0.343982            -4.3
HLA A*3301          1:116-124           9         YSKPPQRGL           1.485583            0.401798
HLA A*0101          1:291-299           9         DMRAASVLR           1.068485            0.647236
HLA A*2402          1:132-140           9         ADATELPML           1.429339            0.373138
HLA B*0801          1:175-183           9         DLHSGAQIM           1.347999            0.083270
HLA B*3501          1:73-81 9           VLEAVGDRR           1.117023            0.684017            -4.4
HLA A*2603          1:194-202           9         DDALNLPWL           1.675726            0.139754
HLA B*1503          1:7-15  9           DVAARLGTL           1.463313            0.301089            -4.4
HLA B*4601          1:245-253           9         PLCNAMSRL           1.448212            0.287348
HLA B*5801          1:291-299           9         DMRAASVLR           1.068485            0.647236
HLA B*0801          1:267-275           9         GIDVGDPRL           1.401875            0.296531
HLA A*6901          1:69-77 9           LLRAVLEAV           1.184331            0.094353            -3.9
HLA A*2501          1:8-16  9           VAARLGTLL           1.373046            0.413198            -4.4
HLA A*0211          1:241-249           9         IAVAPLCNA           1.122147            -0.103628
HLA A*2403          1:150-158           9         VPIEPDTIR           1.171388            0.635900
HLA B*4001          1:161-169           9         ASHPNIVGV           1.362164            0.249139
HLA B*4403          1:194-202           9         DDALNLPWL           1.675726            0.139754
HLA A*0216          1:214-222           9         AHLAAGQLR           1.045022            0.721608
HLA A*0219          1:161-169           9         ASHPNIVGV           1.362164            0.249139
HLA B*1517          1:73-81 9           VLEAVGDRR           1.117023            0.684017            -4.4
HLA A*0216          1:150-158           9         VPIEPDTIR           1.171388            0.635900
HLA B*0803          1:101-109           9         CAAEGAHGL           1.249461            0.495475
HLA B*4601          1:235-243           9         TARKINIAV           1.205835            0.236791
HLA A*0201          1:114-122           9         PYYSKPPQR           1.113255            0.635690
HLA A*0203          1:249-257           9         AMSRLGGVT           0.737166            -0.132110
HLA B*5401          1:217-225           9         AAGQLRELL           1.446320            0.452192
HLA B*1502          1:133-141           9         DATELPMLL           1.554399            0.353260
HLA B*3901          1:41-49 9           LVDQGCDGL           1.264073            0.392133            -4.3
HLA A*2902          1:149-157           9         AVPIEPDTI           1.400742            0.371065
HLA B*2705          1:7-15  9           DVAARLGTL           1.463313            0.301089            -4.4
HLA A*0301          1:102-110           9         AAEGAHGLL           1.273066            0.436296
HLA B*0801          1:291-299           9         DMRAASVLR           1.068485            0.647236
HLA B*0702          1:73-81 9           VLEAVGDRR           1.117023            0.684017            -4.4
HLA B*4402          1:87-95 9           GTYDTAHSI           1.371192            0.292110            -4.3
HLA A*3101          1:149-157           9         AVPIEPDTI           1.400742            0.371065
HLA A*2603          1:29-37 9           LDTATAARL           1.609902            0.292450            -4.5
HLA B*0802          1:102-110           9         AAEGAHGLL           1.273066            0.436296
HLA A*6801          1:217-225           9         AAGQLRELL           1.446320            0.452192
HLA A*3201          1:89-97 9           YDTAHSIRL           1.591071            0.262701            -4.5
HLA B*1801          1:132-140           9         ADATELPML           1.429339            0.373138
HLA B*5301          1:158-166           9         RALASHPNI           1.140241            0.372113
HLA B*3801          1:216-224           9         LAAGQLREL           1.347147            0.438424
HLA B*4402          1:73-81 9           VLEAVGDRR           1.117023            0.684017            -4.4
HLA B*4402          1:21-29 9           TPFSGDGSL           1.381186            0.343982            -4.3
HLA A*0216          1:102-110           9         AAEGAHGLL           1.273066            0.436296
HLA B*5301          1:61-69 9           TTDGEKIEL           1.342355            0.325527            -4.3
HLA B*4801          1:245-253           9         PLCNAMSRL           1.448212            0.287348
HLA B*0802          1:168-176           9         GVKDAKADL           1.258099            0.417879
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HLA B*5101      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.4
HLA A*8001      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3301      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*4601      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0211      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*2705      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4403      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0101      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*4402      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.4
HLA A*0203      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.1
HLA B*2705      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0216      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2602      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA A*2902      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*2601      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2402      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3801      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1503      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*5801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4801      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4001      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2603      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA B*0702      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0212      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0203      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4601      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*5401      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2402      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0203      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*1101      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4001      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*0801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA B*4001      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*3901      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*3001      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.1
HLA B*0803      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0219      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4601      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*0201      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*5101      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*1509      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0101      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*1801      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.7
HLA B*0803      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*1502      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.4
HLA B*1501      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0301      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*0201      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0101      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*5401      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0216      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA A*0206      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*3002      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*3501      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0803      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*0702      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0101      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA B*0802      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0201      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*0101      1:114-122       9       PYYSKPPQR       1.113255        0.635690
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HLA A*8001      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4601      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*6802      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*3101      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0301      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*2705      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*3201      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*1509      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*6802      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4601      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*0803      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4403      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4501      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*3501      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA B*5701      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0219      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*3301      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0211      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*6901      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*0802      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*5701      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA A*6901      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2603      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA B*3501      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*0801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2402      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2902      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*1101      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0201      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*0203      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*1101      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3001      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.1
HLA A*0219      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2601      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*5801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*0803      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*3002      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*8001      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.3
HLA A*8001      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*5401      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0201      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2902      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*4601      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3201      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA B*1503      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3002      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*8001      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2601      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*0801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4601      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*0802      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*2601      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0216      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*0702      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*0801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*3501      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.9
HLA A*0216      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*5701      1:114-122       9       PYYSKPPQR       1.113255        0.635690
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HLA B*4002          1:116-124           9       YSKPPQRGL       1.485583        0.401798
HLA B*4601          1:285-293           9       IDALAADMR       1.213710        0.506246
HLA B*4402          1:114-122           9       PYYSKPPQR       1.113255        0.635690
HLA B*5701          1:139-147           9       MLLYDIPGR       1.114213        0.618034
HLA A*0219          1:229-237           9       GSGDIATAR       1.288849        0.467193
HLA B*0802          1:149-157           9       AVPIEPDTI       1.400742        0.371065
HLA A*0211          1:228-236           9       FGSGDIATA       1.183338        -0.323057
HLA B*3801          1:150-158           9       VPIEPDTIR       1.171388        0.635900
HLA A*2403          1:75-83 9           EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*5101          1:41-49 9           LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*0801          1:114-122           9       PYYSKPPQR       1.113255        0.635690
HLA B*4801          1:75-83 9           EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*6801          1:116-124           9       YSKPPQRGL       1.485583        0.401798
HLA B*1502          1:159-167           9       ALASHPNIV       1.037611        0.271475
HLA A*2301          1:194-202           9       DDALNLPWL       1.675726        0.139754
HLA B*0702          1:114-122           9       PYYSKPPQR       1.113255        0.635690
HLA B*0702          1:229-237           9       GSGDIATAR       1.288849        0.467193
HLA A*0219          1:21-29 9           TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*3301          1:217-225           9       AAGQLRELL       1.446320        0.452192
HLA A*0212          1:248-256           9       NAMSRLGGV       0.862691        0.199419
HLA B*1501          1:114-122           9       PYYSKPPQR       1.113255        0.635690
HLA A*3201          1:75-83 9           EAVGDRRVI       1.485818        0.219873        -4.3
HLA A*3001          1:174-182           9       ADLHSGAQI       1.261395        0.212062
HLA B*4403          1:66-74 9           KIELLRAVL       1.605726        0.383191        -4.6
HLA B*0803          1:216-224           9       LAAGQLREL       1.347147        0.438424
HLA B*1502          1:216-224           9       LAAGQLREL       1.347147        0.438424
HLA A*0206          1:150-158           9       VPIEPDTIR       1.171388        0.635900
HLA A*2403          1:229-237           9       GSGDIATAR       1.288849        0.467193
HLA A*8001          1:229-237           9       GSGDIATAR       1.288849        0.467193
HLA B*4001          1:168-176           9       GVKDAKADL       1.258099        0.417879
HLA A*0212          1:21-29 9           TPFSGDGSL       1.381186        0.343982        -4.4
HLA B*1501          1:277-285           9       QVAATPEQI       1.207957        0.241161
HLA A*6802          1:214-222           9       AHLAAGQLR       1.045022        0.721608
HLA A*0219          1:102-110           9       AAEGAHGLL       1.273066        0.436296
HLA B*5401          1:129-137           9       TAVADATEL       1.437454        0.418113
HLA B*4801          1:285-293           9       IDALAADMR       1.213710        0.506246
HLA A*0301          1:168-176           9       GVKDAKADL       1.258099        0.417879
HLA B*0702          1:76-84 9           AVGDRRVIA       1.439473        -0.251903       -3.8
HLA A*3002          1:41-49 9           LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*5701          1:245-253           9       PLCNAMSRL       1.448212        0.287348
HLA B*5301          1:116-124           9       YSKPPQRGL       1.485583        0.401798
HLA A*1101          1:101-109           9       CAAEGAHGL       1.249461        0.495475
HLA A*2501          1:139-147           9       MLLYDIPGR       1.114213        0.618034
HLA B*0802          1:61-69 9           TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0206          1:75-83 9           EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*5301          1:132-140           9       ADATELPML       1.429339        0.373138
HLA B*1509          1:62-70 9           TDGEKIELL       1.477276        0.206949        -4.3
HLA B*1801          1:139-147           9       MLLYDIPGR       1.114213        0.618034
HLA A*0216          1:291-299           9       DMRAASVLR       1.068485        0.647236
HLA A*0211          1:21-29 9           TPFSGDGSL       1.381186        0.343982        -4.4
HLA B*0802          1:238-246           9       KINIAVAPL       1.111426        0.535215
HLA B*2705          1:114-122           9       PYYSKPPQR       1.113255        0.635690
HLA B*1517          1:214-222           9       AHLAAGQLR       1.045022        0.721608
HLA B*0803          1:123-131           9       GLQAHFTAV       1.301654        0.109394
HLA A*3101          1:75-83 9           EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*0802          1:229-237           9       GSGDIATAR       1.288849        0.467193
HLA A*2902          1:168-176           9       GVKDAKADL       1.258099        0.417879
HLA B*1503          1:110-118           9       LVVTPYYSK       0.828598        0.319191
HLA A*3201          1:216-224           9       LAAGQLREL       1.347147        0.438424
HLA B*5401          1:191-199           9       YSGDDALNL       1.544375        0.332060
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HLA B*3901      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*4801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0301      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*2301      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.2
HLA B*3801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*4601      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*3001      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0101      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*3901      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0212      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*5701      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0219      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*5701      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1502      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA A*2602      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*3001      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0301      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0216      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*6901      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4402      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.3
HLA B*0802      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0101      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA A*0301      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0203      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2602      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*1101      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*2403      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0702      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*0803      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*2603      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.5
HLA B*4002      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA B*4001      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*2705      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*3501      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2601      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0212      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3002      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*1801      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2601      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA B*1503      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.6
HLA B*3901      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.0
HLA B*0803      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1801      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*3801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4402      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1503      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*6801      1:152-160       9       IEPDTIRAL       1.667218        0.297959
HLA B*7301      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.5
HLA A*2301      1:132-140       9       ADATELPML       1.429339        0.373138
HLA B*3801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*3801      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.4
HLA A*3301      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*5401      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.5
HLA B*1503      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1501      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*2402      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*1503      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*2403      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0212      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*1101      1:161-169       9       ASHPNIVGV       1.362164        0.249139
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HLA B*1509      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*1517      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2501      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA B*7301      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA B*7301      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0211      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.0
HLA B*0702      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2402      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2301      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*5101      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*0203      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0203      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4002      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*8001      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA B*4601      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*4001      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*0803      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*1517      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4403      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*0802      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*7301      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA B*0801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*2705      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA B*1801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.4
HLA A*2601      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*2403      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*1501      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -3.9
HLA A*0250      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2602      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*2705      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*1502      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1509      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*6802      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2402      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*3101      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA B*4001      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2501      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0203      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4402      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*2601      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0201      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0212      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*8001      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*8001      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*1501      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3501      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*4601      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*6802      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*6802      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*3901      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.2
HLA A*3101      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA B*3901      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*2705      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -3.9
HLA B*7301      1:217-225       9       AAGQLRELL       1.446320        0.452192
HLA B*1509      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0206      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2301      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA B*1502      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1501      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0212      1:175-183       9       DLHSGAQIM       1.347999        0.083270
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HLA A*2301      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.4
HLA B*5701      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1509      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*7301      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2501      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*3901      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2902      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*1509      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA A*0301      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*4402      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*5301      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0212      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0202      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*3901      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.6
HLA A*6801      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*0250      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*3901      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*3501      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*5701      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2501      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3201      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6801      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.6
HLA B*4801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*5101      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*8001      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA B*3901      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*0101      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3001      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2301      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2902      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0206      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4402      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5701      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4501      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.6
HLA A*0301      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*6901      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*7301      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*0702      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0219      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*5701      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*1101      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*4002      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0202      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.5
HLA B*4801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.3
HLA A*1101      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*0803      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*0801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*3002      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.5
HLA B*1801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA B*0802      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*3501      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*0702      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0101      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*8001      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*0802      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4002      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*2705      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*0202      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*0202      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1502      1:205-213       9       GATGFISVI       1.492197        0.176075
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HLA B*3801      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA B*1801      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*0803      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*5401      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*0802      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*3001      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2301      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5101      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*3901      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*3301      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*0206      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2603      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*1801      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*1502      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*0802      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*1801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*1801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA A*6802      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.0
HLA A*2601      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*2902      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*6802      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2402      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*3001      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1509      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2501      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1509      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0702      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -3.9
HLA A*3002      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*3501      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*1101      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.4
HLA B*4601      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*6801      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*0216      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*3501      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*4402      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*3801      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*6802      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*6901      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.2
HLA A*0206      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -3.5
HLA A*1101      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0101      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*0702      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4601      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.3
HLA A*0212      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*0211      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.9
HLA B*1502      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*8001      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*2403      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*3201      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*3001      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3002      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*1509      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2902      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*8001      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1517      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*3301      1:29-37 9       LDTATAARL       1.609902        0.292450        -4.6
HLA A*8001      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2403      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*3501      1:158-166       9       RALASHPNI       1.140241        0.372113
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HLA A*0211      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2603      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*3201      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0203      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.7
HLA A*0206      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0219      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*2705      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*8001      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*1101      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*2301      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*2501      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2601      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*7301      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*1101      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*1101      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*7301      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*5701      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*4402      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*0801      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*0803      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4402      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*8001      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*0206      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0206      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5401      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*1101      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2301      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*2705      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2602      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.0
HLA A*0101      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1503      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.9
HLA A*2501      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2602      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA A*2403      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1502      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3101      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.0
HLA A*0211      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*3801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2403      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0211      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*0219      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0211      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*4403      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*3002      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0250      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*3201      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.2
HLA B*5101      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*0803      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA A*3101      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*0802      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*1801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2301      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA B*4402      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*5101      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*8001      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*3201      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*0802      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.3
HLA A*0206      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*2902      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*2301      1:101-109       9       CAAEGAHGL       1.249461        0.495475
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HLA B*0702      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2603      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4402      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0216      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0203      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*4403      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*0702      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3301      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*3101      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1517      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3801      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4002      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0211      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2501      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*1503      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*3801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0301      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.2
HLA A*0301      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*3901      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*5101      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3501      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.2
HLA B*4501      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*0802      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4402      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*3801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*2603      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3301      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA B*4403      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3101      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5701      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.3
HLA B*7301      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA B*3901      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.2
HLA B*3901      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*3901      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*1502      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*2602      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*3201      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA B*5101      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*7301      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.5
HLA A*0206      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -3.9
HLA B*3901      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2501      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*5101      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*6801      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.5
HLA B*5401      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1509      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4501      1:133-141       9       DATELPMLL       1.554399        0.353260
HLA A*0212      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2501      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0201      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1502      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0216      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4501      1:257-265       9       TLSKAGLRL       1.467227        0.434259
HLA A*0211      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0203      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0201      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.2
HLA B*0803      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2402      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*3901      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1501      1:204-212       9       MGATGFISV       1.066312        0.114153
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HLA B*4501      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.6
HLA A*2501      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2902      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4403      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*3201      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*1101      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*1801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*3901      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*4002      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.8
HLA A*0216      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3201      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5101      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*3801      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.4
HLA A*0206      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*6802      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0202      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4501      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2603      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA B*0803      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*3801      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*0801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3101      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6801      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*2602      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*7301      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*6901      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.2
HLA A*0211      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2402      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA A*2603      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*5401      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3002      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0201      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1503      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*0203      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -3.9
HLA B*1517      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0203      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1509      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*1503      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*4001      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3201      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*2501      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*5301      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*3301      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3002      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*3002      1:34-42 9       AARLANHLV       0.964146        0.245998        -3.9
HLA A*3301      1:89-97 9       YDTAHSIRL       1.591071        0.262701        -4.6
HLA B*2705      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*3801      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*0203      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*5301      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*4501      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA B*5401      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA B*3801      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*3901      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1801      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4501      1:116-124       9       YSKPPQRGL       1.485583        0.401798
HLA A*2902      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*0803      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2902      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*5301      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.5
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HLA A*3201      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2402      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*1101      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*2301      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*3101      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.1
HLA B*1503      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*3301      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1509      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.2
HLA A*2601      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*2602      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA A*0212      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2902      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*4501      1:129-137       9       TAVADATEL       1.437454        0.418113
HLA A*3002      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*2705      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*0802      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0250      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*0803      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*3002      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*2301      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*4001      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2402      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*4403      1:255-263       9       GVTLSKAGL       1.514430        0.369798
HLA A*0202      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*5401      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA B*1501      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5401      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0201      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6901      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2603      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*5101      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*8001      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*4402      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*6801      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.4
HLA A*0202      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4403      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*1501      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1509      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2402      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0212      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0211      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*0101      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*0801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*1101      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*2603      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*1801      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4501      1:191-199       9       YSGDDALNL       1.544375        0.332060
HLA A*3002      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2402      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*2603      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0250      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*0803      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA A*2301      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*3301      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*7301      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2301      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1517      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*5101      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1502      1:149-157       9       AVPIEPDTI       1.400742        0.371065
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HLA B*5101      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0203      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4601      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*1101      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2602      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.0
HLA B*1501      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*5801      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*7301      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3101      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*2301      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4002      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*2705      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0803      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*1503      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -3.9
HLA B*5801      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*0201      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2902      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*1801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0206      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -3.9
HLA B*5401      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.5
HLA A*6901      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1503      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*5401      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*4002      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5401      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0211      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2301      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*7301      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0202      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*3001      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0250      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.4
HLA A*0250      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*4002      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA B*1503      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*5401      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0211      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0301      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2301      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1502      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0203      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*8001      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*2705      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4402      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.8
HLA A*2602      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*4501      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA A*0202      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*1501      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*0202      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5401      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*3301      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*2602      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.5
HLA A*3301      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.5
HLA A*2403      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0250      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.5
HLA B*0803      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*2403      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*2705      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*1101      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*5401      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
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HLA A*3001      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5101      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*6802      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4403      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA B*4402      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2402      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*0801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*3201      1:194-202       9       DDALNLPWL       1.675726        0.139754
HLA B*1509      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*4501      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*4002      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3201      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*1101      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*0201      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2602      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4002      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1517      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -3.6
HLA B*7301      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2902      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*6901      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*6801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -3.7
HLA B*1801      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*3301      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA A*2301      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*1503      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0702      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*5101      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*3201      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0202      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3001      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.2
HLA A*6901      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1502      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*2902      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*2705      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4601      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*6801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*5101      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*2705      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*6901      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*6802      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2402      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*5401      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*3201      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*3001      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1509      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0206      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4501      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*0212      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0219      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*0201      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*3901      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0206      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1502      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*3801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*4002      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.4
HLA B*5101      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2602      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA B*5301      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.4
HLA B*5401      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2402      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.5
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HLA B*5301      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
HLA B*0702      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*2301      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2603      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*6801      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.4
HLA B*0803      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.0
HLA A*2902      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*3501      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*0702      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4501      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0201      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3201      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*3501      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*4501      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*7301      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*4002      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.5
HLA A*3201      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*2301      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*0702      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*4002      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0216      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0202      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA B*7301      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.5
HLA A*0211      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2501      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*2402      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*1517      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*2402      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*1503      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -3.7
HLA B*5101      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0211      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.0
HLA A*0202      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*6802      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3002      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA B*1502      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1501      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0301      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*2603      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA A*2902      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*7301      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.4
HLA B*5101      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0250      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*0301      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0211      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*0802      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*2501      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5301      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA B*4403      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -3.9
HLA B*0702      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*7301      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*6802      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.2
HLA A*2603      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0250      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3001      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2402      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*0101      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4402      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2603      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
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HLA A*0206      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*3201      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*8001      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*3001      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.1
HLA A*6901      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5401      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -3.8
HLA A*0216      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*3002      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.1
HLA A*0211      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*3801      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*5801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*3501      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2301      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1517      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.0
HLA B*4501      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3301      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*3801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4801      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4001      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*2501      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2902      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*4001      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.3
HLA B*1503      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5301      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1502      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA B*5401      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0206      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -3.8
HLA B*2705      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0250      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2601      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*5401      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*1503      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6802      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*7301      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
HLA B*4001      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*7301      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA B*0801      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0206      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*3801      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1503      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*4501      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0211      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*6802      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*7301      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0212      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2603      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2402      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*0206      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0203      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.0
HLA B*5801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*0219      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*4403      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1502      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2601      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*5801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*4402      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*4002      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA B*5301      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*3001      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.0
HLA B*5101      1:277-285       9       QVAATPEQI       1.207957        0.241161
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HLA A*3201      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA B*5701      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*5301      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*0203      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2603      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2402      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.4
HLA A*0219      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*1801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4403      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4001      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*4601      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0101      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1501      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4403      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA B*1502      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2602      1:214-222       9       AHLAAGQLR       1.045022        0.721608
HLA A*3101      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.1
HLA B*5401      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*0803      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4403      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0206      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1502      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*7301      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*1509      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*2705      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0206      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*5301      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*3301      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*0202      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*0211      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*7301      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*3801      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*0702      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0202      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*0801      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*2602      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4501      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*7301      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.6
HLA B*1503      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2403      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4403      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*0803      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*0802      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*4001      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*7301      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*5301      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*5301      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2402      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0219      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0206      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5701      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4501      1:150-158       9       VPIEPDTIR       1.171388        0.635900
HLA A*0206      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.7
HLA B*4801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4001      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4801      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*3501      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0211      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2902      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1502      1:262-270       9       GLRLQGIDV       1.072956        0.154057
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HLA A*0216      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4402      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0201      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4403      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.5
HLA A*3301      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA A*8001      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*5301      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5401      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.5
HLA B*4601      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3301      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.5
HLA A*2301      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.5
HLA A*6801      1:132-140       9       ADATELPML       1.429339        0.373138
HLA A*3002      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4002      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
HLA B*0801      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2603      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA A*2601      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*5801      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2602      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*5301      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*3501      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2902      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4501      1:8-16  9       VAARLGTLL       1.373046        0.413198        -4.6
HLA A*8001      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*0203      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.1
HLA A*2902      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*6802      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*0802      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3301      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*1801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*4501      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
HLA A*6901      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*2705      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA B*1509      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*0702      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*1517      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4501      1:216-224       9       LAAGQLREL       1.347147        0.438424
HLA A*6901      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5401      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*4601      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*0219      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0212      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1501      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0203      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0211      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.0
HLA B*3501      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3001      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.2
HLA B*0801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*0803      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.3
HLA A*6901      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2301      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0212      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*0202      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4501      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*2705      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2601      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*0801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*5801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
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HLA A*3002      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA A*0202      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*1101      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4403      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3501      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2603      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0803      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*6901      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4002      1:229-237       9       GSGDIATAR       1.288849        0.467193
HLA B*4501      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.5
HLA B*4002      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*1801      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*0202      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5701      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*6801      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2603      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4002      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*5401      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4002      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*3301      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0203      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.0
HLA A*0301      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*0702      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5401      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*0803      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2602      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*0101      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*6802      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2603      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*3501      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*5701      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6901      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0212      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2603      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2501      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.8
HLA A*2603      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*2705      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3301      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.5
HLA A*2601      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*0702      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4403      1:73-81 9       VLEAVGDRR       1.117023        0.684017        -4.6
HLA B*0802      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA A*3201      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0216      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.0
HLA B*4601      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4002      1:101-109       9       CAAEGAHGL       1.249461        0.495475
HLA B*1501      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*5401      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*6802      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.1
HLA A*0202      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0201      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA B*0802      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2403      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*3002      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*0101      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.3
HLA A*6801      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2501      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA A*0219      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0219      1:235-243       9       TARKINIAV       1.205835        0.236791
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HLA B*1502      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0201      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*3301      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*0216      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*8001      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2403      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0216      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA B*1501      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2902      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*7301      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*5401      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.5
HLA B*4801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*2403      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4403      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA B*4501      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5301      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*6801      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA A*0211      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.8
HLA A*2602      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.5
HLA B*1801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0101      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*5701      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA B*0801      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*5101      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2403      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA A*3201      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.1
HLA A*0212      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4002      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*1101      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4601      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4601      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*3901      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*7301      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*3901      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*4403      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0250      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*1801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*1517      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1502      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4002      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.6
HLA A*2403      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*4402      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA B*4403      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.6
HLA A*0250      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.9
HLA A*6901      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5401      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.5
HLA B*0803      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*3002      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1517      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA A*2301      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*2601      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4002      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*3301      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*1501      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*5701      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*4403      1:149-157       9       AVPIEPDTI       1.400742        0.371065
HLA B*5301      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2902      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0201      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
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HLA B*7301      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0202      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA A*2602      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*6901      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.2
HLA B*5401      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*5701      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.1
HLA A*0206      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*5801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4002      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*3201      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.5
HLA A*6802      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*8001      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1501      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*3901      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2602      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*4501      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.6
HLA A*0101      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*5701      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*2705      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*3301      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*4501      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA A*2602      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0216      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*3801      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA B*3501      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2403      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4001      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*5301      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA A*0216      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA A*0101      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0301      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3001      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.8
HLA B*4801      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*3101      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4601      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*6802      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*1509      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1509      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3201      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*2602      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1509      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0206      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*5401      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*4403      1:7-15  9       DVAARLGTL       1.463313        0.301089        -4.6
HLA A*0219      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*5301      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*1501      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*0201      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0301      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*3101      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*0801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1502      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0201      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2902      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*7301      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2603      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*3101      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*5401      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.5
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HLA B*1501      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.0
HLA A*3201      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA B*0803      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1517      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -3.7
HLA A*3002      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.5
HLA A*0203      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*1801      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1502      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.5
HLA B*5401      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*4002      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0202      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4002      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4501      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.0
HLA A*6901      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0212      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*2602      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*2501      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*6801      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*2705      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2601      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0301      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6801      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.5
HLA B*4001      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0216      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.9
HLA B*5401      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0301      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.1
HLA A*0219      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*6801      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2601      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2601      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3501      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4002      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*3501      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*3002      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0202      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -3.8
HLA B*4403      1:139-147       9       MLLYDIPGR       1.114213        0.618034
HLA B*5801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0101      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1502      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.5
HLA A*0219      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3101      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0201      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*6801      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*4501      1:87-95 9       GTYDTAHSI       1.371192        0.292110        -4.5
HLA A*8001      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4403      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.6
HLA B*1502      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0211      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.8
HLA B*4403      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*3101      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*2705      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2603      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.1
HLA B*5101      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA A*8001      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*0301      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4501      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA B*4501      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*2402      1:161-169       9       ASHPNIVGV       1.362164        0.249139
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HLA A*3201      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0301      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4001      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*1501      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*5701      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1509      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA A*3002      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*3002      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*1801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.1
HLA A*3301      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*5801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.1
HLA B*5801      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*6802      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0250      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.4
HLA B*2705      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0101      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*2705      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2501      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*6802      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*4601      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*8001      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*2601      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*6901      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2601      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*4402      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*3501      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1502      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0250      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA B*7301      1:102-110       9       AAEGAHGLL       1.273066        0.436296
HLA A*2402      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*2601      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4403      1:114-122       9       PYYSKPPQR       1.113255        0.635690
HLA A*2602      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0219      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*0802      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2902      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*3801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4001      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*4002      1:75-83 9       EAVGDRRVI       1.485818        0.219873        -4.6
HLA A*0203      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4403      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4002      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.5
HLA A*0203      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*0212      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*3901      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*0702      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0101      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0301      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA A*3301      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*1101      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2603      1:285-293       9       IDALAADMR       1.213710        0.506246
HLA A*6901      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -3.9
HLA A*2501      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*4501      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.6
HLA A*0203      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*1509      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*3901      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3301      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*0702      1:174-182       9       ADLHSGAQI       1.261395        0.212062
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HLA B*5801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA B*5701      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*5801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*6802      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0206      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -3.7
HLA B*4601      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA A*2501      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0250      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*0803      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*5401      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*4501      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA B*0802      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2501      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0216      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.8
HLA A*2301      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4501      1:21-29 9       TPFSGDGSL       1.381186        0.343982        -4.6
HLA A*1101      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0301      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3301      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.6
HLA A*0201      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4501      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4403      1:245-253       9       PLCNAMSRL       1.448212        0.287348
HLA A*0101      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0203      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*1501      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4501      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*3901      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*0301      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0219      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*5101      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*5101      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*7301      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.6
HLA B*1503      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*3901      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0250      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0101      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4601      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*6901      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA B*4002      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*4002      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2902      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2601      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*8001      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3101      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*1509      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*1801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2501      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*4801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*2705      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0101      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA B*5801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0203      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.8
HLA B*4002      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -3.3
HLA A*0216      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*3301      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.5
HLA B*3801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*0203      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2402      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*3901      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*4601      1:175-183       9       DLHSGAQIM       1.347999        0.083270
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HLA B*3501      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*0702      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1502      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA A*6901      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.1
HLA B*1517      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*8001      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA A*2501      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*4501      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1517      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0219      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4601      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*6901      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*3501      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*7301      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2601      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA B*7301      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA B*2705      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2602      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*1101      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1509      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*0801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2501      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*4403      1:291-299       9       DMRAASVLR       1.068485        0.647236
HLA B*1501      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*0801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0702      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3201      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*0801      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2301      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0202      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -3.8
HLA B*0802      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*2603      1:205-213       9       GATGFISVI       1.492197        0.176075
HLA A*3001      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*6801      1:62-70 9       TDGEKIELL       1.477276        0.206949        -4.6
HLA A*0203      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*4501      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA A*0203      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0201      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.1
HLA B*4402      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0101      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4001      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0212      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA B*1509      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*3901      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA B*7301      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.6
HLA B*4601      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.2
HLA A*0101      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2603      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.4
HLA A*6801      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*6901      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA A*3201      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0101      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4001      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA B*4001      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*2403      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0206      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3101      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2902      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0212      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1501      1:104-112       9       EGAHGLLVV       1.230292        0.004958
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HLA A*6801      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA B*0802      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4402      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*4801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA A*3002      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -3.9
HLA B*5101      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5401      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.2
HLA B*0801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.1
HLA B*1517      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3101      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0216      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0211      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.8
HLA B*3801      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA B*4002      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*7301      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.6
HLA B*3901      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1501      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*2705      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4001      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*3801      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA B*0702      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5301      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA B*1502      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA A*2902      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA A*0216      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.1
HLA B*4801      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*3801      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0202      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA B*4402      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*8001      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*1503      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2601      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*4501      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*7301      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*1503      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.8
HLA A*8001      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4501      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*3201      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.2
HLA A*0301      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2301      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA A*0301      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4403      1:267-275       9       GIDVGDPRL       1.401875        0.296531
HLA A*2501      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0202      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*4402      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0219      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.4
HLA A*3201      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*4403      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.6
HLA A*0219      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*2705      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*8001      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*7301      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*0212      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*5801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*5701      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0101      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*4601      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0101      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0216      1:231-239       9       GDIATARKI       1.387075        0.073052
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HLA A*0250      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4001      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*1801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*2705      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0211      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*0801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA A*6801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2501      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0201      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.3
HLA B*4001      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0219      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1502      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*0219      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0212      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4403      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA B*3901      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0219      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.1
HLA B*1503      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.1
HLA A*0211      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.0
HLA A*2403      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3002      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1509      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*6901      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.9
HLA A*0250      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1509      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA B*4801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0211      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*6802      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*3801      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4601      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4002      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.6
HLA B*5801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*8001      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2403      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4501      1:61-69 9       TTDGEKIEL       1.342355        0.325527        -4.6
HLA B*5301      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*1101      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*1101      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*0803      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3002      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*0801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*2501      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*0802      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2402      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0203      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.0
HLA B*0702      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2403      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*6802      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.7
HLA A*0201      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2402      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA A*6802      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*0801      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA B*1501      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5701      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1509      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0219      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.2
HLA A*2902      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0201      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5401      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2403      1:256-264       9       VTLSKAGLR       0.762607        0.656403
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HLA A*2403      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*1501      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4501      1:168-176       9       GVKDAKADL       1.258099        0.417879
HLA A*2301      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*0802      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0803      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0212      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0301      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1502      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*4601      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*5301      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.2
HLA B*4402      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*5101      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.5
HLA B*4801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1501      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.1
HLA B*4402      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*5101      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA A*2603      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*2301      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0203      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0206      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2902      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*2501      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*2705      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0101      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0201      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0206      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0101      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*4002      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*3501      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*0212      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*8001      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2902      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*0702      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2601      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.1
HLA B*1801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*0803      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5301      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*5701      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4001      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA B*3501      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*0801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*3001      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.2
HLA A*0201      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.3
HLA A*3201      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*0801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0211      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2403      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*3501      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2301      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1501      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -3.8
HLA B*0702      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*3501      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0202      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*1101      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*2705      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*4601      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*0801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*8001      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
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HLA A*3002      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*6901      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.2
HLA B*0801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.1
HLA A*0203      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*0803      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*4601      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*4001      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1503      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*3801      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5701      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0211      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5301      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0101      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*8001      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*2402      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1502      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2402      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*0702      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3101      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.1
HLA B*1502      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*3101      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*4403      1:238-246       9       KINIAVAPL       1.111426        0.535215
HLA B*0802      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2501      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*0702      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*5401      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA B*5701      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2601      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0201      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.1
HLA B*1503      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*4801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*4801      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0202      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4601      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*3201      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3001      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*0803      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1517      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*6801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*1101      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0206      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0201      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*2603      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*5701      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*0801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5301      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*3501      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0250      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*3201      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2601      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5701      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*1501      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*2603      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0216      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0216      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*3301      1:161-169       9       ASHPNIVGV       1.362164        0.249139
HLA A*8001      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5101      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
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HLA B*1801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*1502      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.2
HLA B*5401      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2403      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA B*4501      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.6
HLA A*0211      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*6802      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*0201      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*6801      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*3301      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4402      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0212      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4403      1:41-49 9       LVDQGCDGL       1.264073        0.392133        -4.6
HLA A*0219      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2301      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.5
HLA A*0202      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2501      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.1
HLA A*0211      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*0802      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1501      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.1
HLA B*1517      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -3.5
HLA B*0803      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2602      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.5
HLA B*7301      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*4403      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*3901      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*2501      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*0802      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*3901      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*3301      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*3801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*5701      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*6802      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*1101      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*6801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -3.7
HLA B*1503      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2402      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*4001      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*4501      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2603      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.2
HLA B*0802      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0211      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -3.9
HLA B*4601      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2403      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA B*0803      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*2902      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA B*1801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*8001      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*6802      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.2
HLA B*7301      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*6801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -3.7
HLA B*4402      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*8001      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*5401      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0206      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA A*3002      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*3101      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*0802      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2501      1:231-239       9       GDIATARKI       1.387075        0.073052
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HLA A*0206      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*0216      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0101      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4402      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*5301      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1509      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*2403      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1503      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2602      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA A*6901      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*2603      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*1517      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*3801      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*2402      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.5
HLA A*0203      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -3.9
HLA A*2603      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5401      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0211      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA A*6802      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.1
HLA A*0202      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5401      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*0219      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*2403      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0212      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*1503      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0101      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0212      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA B*4402      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0212      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*2705      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0219      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3002      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0211      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.2
HLA B*3501      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*5801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*0219      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*0802      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4601      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*5301      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*3901      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1503      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*4801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*4801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*3501      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.1
HLA A*3002      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6802      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4402      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*2501      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*6901      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1517      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*2902      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0219      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0202      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0219      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*5301      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.5
HLA B*3501      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0202      1:65-73 9       EKIELLRAV       0.851830        0.084898        -3.9
HLA B*3901      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0203      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*0803      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
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HLA A*0202	1:103-111	9	AEGAHGLLV	1.003584	0.135355
HLA B*5101	1:175-183	9	DLHSGAQIM	1.347999	0.083270
HLA B*4402	1:252-260	9	RLGGVTLSK	1.136726	0.270032
HLA B*5401	1:28-36 9	SLDTATAAR	0.953732	0.586069	-4.5
HLA A*2403	1:63-71 9	DGEKIELLR	1.103206	0.332352	-4.4
HLA A*0201	1:225-233	9	LSAFGSGDI	1.011406	0.278764
HLA A*2403	1:59-67 9	PTTTDGEKI	1.283399	0.020942	-4.3
HLA B*1517	1:123-131	9	GLQAHFTAV	1.301654	0.109394
HLA B*1517	1:193-201	9	GDDALNLPW	0.935099	0.118725
HLA A*0203	1:270-278	9	VGDPRLPQV	1.259480	-0.090215
HLA B*4001	1:225-233	9	LSAFGSGDI	1.011406	0.278764
HLA A*0211	1:104-112	9	EGAHGLLVV	1.230292	0.004958
HLA A*2603	1:88-96 9	TYDTAHSIR	0.867128	0.660107	-4.5
HLA B*1501	1:249-257	9	AMSRLGGVT	0.737166	-0.132110
HLA B*1801	1:93-101	9	HSIRLAKAC	1.327808	0.080369
HLA B*5101	1:241-249	9	IAVAPLCNA	1.122147	-0.103628
HLA A*2603	1:256-264	9	VTLSKAGLR	0.762607	0.656403
HLA B*0803	1:260-268	9	KAGLRLQGI	1.143236	0.252977
HLA B*3801	1:174-182	9	ADLHSGAQI	1.261395	0.212062
HLA A*0216	1:59-67 9	PTTTDGEKI	1.283399	0.020942	-4.3
HLA A*2602	1:244-252	9	APLCNAMSR	0.945216	0.602816
HLA B*0702	1:94-102	9	SIRLAKACA	1.337108	-0.141865
HLA A*2902	1:10-18 9	ARLGTLLTA	1.327543	-0.004208	-4.3
HLA B*1501	1:10-18 9	ARLGTLLTA	1.327543	-0.004208	-4.3
HLA B*4601	1:225-233	9	LSAFGSGDI	1.011406	0.278764
HLA B*4002	1:10-18 9	ARLGTLLTA	1.327543	-0.004208	-4.3
HLA A*8001	1:242-250	9	AVAPLCNAM	1.074859	0.266154
HLA A*3201	1:14-22 9	TLLTAMVTP	0.951502	0.038214	-4.0
HLA B*1801	1:174-182	9	ADLHSGAQI	1.261395	0.212062
HLA B*1801	1:277-285	9	QVAATPEQI	1.207957	0.241161
HLA B*3501	1:159-167	9	ALASHPNIV	1.037611	0.271475
HLA B*2705	1:3-11  9	TVGFDVAAR	0.785469	0.628205	-4.4
HLA A*2603	1:165-173	9	NIVGVKDAK	1.187218	0.245244
HLA B*2705	1:242-250	9	AVAPLCNAM	1.074859	0.266154
HLA A*6802	1:94-102	9	SIRLAKACA	1.337108	-0.141865
HLA A*0219	1:195-203	9	DALNLPWLA	1.164585	-0.398227
HLA B*7301	1:72-80 9	AVLEAVGDR	0.741732	0.832221	-4.6
HLA B*5801	1:10-18 9	ARLGTLLTA	1.327543	-0.004208	-4.3
HLA A*2602	1:110-118	9	LVVTPYYSK	0.828598	0.319191
HLA B*0802	1:93-101	9	HSIRLAKAC	1.327808	0.080369
HLA A*0216	1:76-84 9	AVGDRRVIA	1.439473	-0.251903	-4.2
HLA B*0801	1:104-112	9	EGAHGLLVV	1.230292	0.004958
HLA B*4001	1:159-167	9	ALASHPNIV	1.037611	0.271475
HLA B*1509	1:252-260	9	RLGGVTLSK	1.136726	0.270032
HLA B*1502	1:88-96 9	TYDTAHSIR	0.867128	0.660107	-4.5
HLA A*2603	1:244-252	9	APLCNAMSR	0.945216	0.602816
HLA A*0301	1:69-77 9	LLRAVLEAV	1.184331	0.094353	-4.3
HLA A*0202	1:244-252	9	APLCNAMSR	0.945216	0.602816
HLA A*0203	1:59-67 9	PTTTDGEKI	1.283399	0.020942	-4.3
HLA B*0802	1:256-264	9	VTLSKAGLR	0.762607	0.656403
HLA B*3901	1:43-51 9	DQGCDGLVV	1.245484	-0.019858	-4.2
HLA B*0702	1:10-18 9	ARLGTLLTA	1.327543	-0.004208	-4.3
HLA A*2301	1:260-268	9	KAGLRLQGI	1.143236	0.252977
HLA A*0219	1:63-71 9	DGEKIELLR	1.103206	0.332352	-4.4
HLA A*0250	1:174-182	9	ADLHSGAQI	1.261395	0.212062
HLA B*0802	1:242-250	9	AVAPLCNAM	1.074859	0.266154
HLA A*0203	1:98-106	9	AKACAAEGA	1.151290	-0.119087
HLA B*0801	1:91-99 9	TAHSIRLAK	0.996404	0.168531	-4.1
HLA A*2501	1:11-19 9	RLGTLLTAM	1.041303	0.243197	-4.3
HLA A*0216	1:2-10  9	TTVGFDVAA	1.389378	-0.196146	-4.2
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HLA B*1509      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*0702      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*3501      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0702      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*3501      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*8001      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*1101      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.2
HLA B*5801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*0201      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.2
HLA B*5401      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA B*0803      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1503      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5101      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0212      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0206      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0202      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.2
HLA B*0801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1517      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*4403      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2501      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*0211      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0250      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1509      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3002      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*4402      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0101      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*4002      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -3.3
HLA A*2902      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2403      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*7301      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*0202      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA B*4403      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.6
HLA B*5101      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0216      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0206      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*3501      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*0301      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*0206      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0101      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*2601      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*0101      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*0702      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*3501      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*7301      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*3001      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2601      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2402      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2902      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5401      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.1
HLA B*4402      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*3201      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA B*1503      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5101      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*5101      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*2902      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*3501      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*6801      1:242-250       9       AVAPLCNAM       1.074859        0.266154
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HLA B*1801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0212      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*0202      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0702      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -3.9
HLA A*2403      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*2501      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*0801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1501      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*1101      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*3901      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*1503      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2603      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0216      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3901      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA A*0301      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*6802      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2501      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0211      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0211      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0211      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0203      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA A*1101      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*4501      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.6
HLA B*1509      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2301      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2603      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0250      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA B*1801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*4002      1:72-80 9       AVLEAVGDR       0.741732        0.832221        -4.6
HLA B*3801      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*3201      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA A*0212      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.0
HLA A*1101      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*5101      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2402      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*4001      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA A*3301      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0216      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.4
HLA B*4501      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA B*1502      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4001      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.2
HLA A*2402      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0216      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.0
HLA B*4501      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*2301      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*1517      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1502      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0216      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4001      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*2601      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA A*2601      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*0803      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*0202      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.5
HLA B*0702      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0206      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.4
HLA A*3002      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*1101      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2602      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*0203      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.0
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HLA A*2402      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*7301      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA A*6801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5401      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*6801      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0301      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*3101      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*0212      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*0212      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.2
HLA A*0101      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA A*2601      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*7301      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*5301      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.6
HLA B*4002      1:244-252       9       APLCNAMSR       0.945216        0.602816
HLA A*2402      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4601      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA A*0216      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*1101      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*3002      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA B*4002      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2902      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*5401      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*1509      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*5301      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*1502      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0202      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*0201      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*1801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0219      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*3001      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4402      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3001      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5701      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA B*1517      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*3001      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*3001      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.2
HLA B*4001      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*0216      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2601      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*5101      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*1509      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*1501      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*4801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4501      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3002      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*3801      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*1801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2601      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.3
HLA B*5101      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*7301      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*1101      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA B*5101      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2602      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*3101      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.2
HLA B*1501      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5701      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA A*0201      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*5101      1:159-167       9       ALASHPNIV       1.037611        0.271475
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HLA B*1503      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*5301      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.6
HLA A*2301      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3002      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5701      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*0216      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*6802      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*3201      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*8001      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3001      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0202      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.0
HLA A*6901      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.1
HLA A*0250      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA A*0216      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5701      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*3301      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*0206      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*6802      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1509      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*5101      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*5401      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5701      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0212      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.0
HLA A*8001      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*4601      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2602      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0212      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*2705      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA A*0101      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.2
HLA B*1503      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.1
HLA A*0219      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0201      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1509      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0219      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5701      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA A*8001      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4801      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*5301      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0202      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3201      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2501      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4403      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA A*6901      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.5
HLA B*1517      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*0301      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3001      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.1
HLA A*2902      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*0212      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*3001      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2603      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2301      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*0206      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*3101      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*5401      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*2902      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*0801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.9
HLA A*2602      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0216      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -3.9
HLA B*5701      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*1517      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
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HLA A*0216      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.0
HLA B*3901      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.2
HLA B*1517      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0211      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*3501      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*7301      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.6
HLA B*1502      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*0803      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*4801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*0212      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2301      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1509      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*0803      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*3901      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*2301      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA B*5401      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.2
HLA A*0219      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*3001      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5101      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA B*3801      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*0702      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*1101      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.3
HLA B*7301      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.6
HLA B*3501      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*0101      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2601      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.0
HLA B*1509      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA B*4601      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.3
HLA A*3301      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2402      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3101      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5801      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*2501      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0802      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*0702      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0216      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.1
HLA A*0101      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4002      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -3.8
HLA B*5301      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*3301      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*3301      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*6802      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*0101      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*5401      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*3501      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*0250      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5701      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*1101      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2603      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*7301      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -3.9
HLA A*2402      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*4002      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*4001      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*3001      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2603      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3801      1:256-264       9       VTLSKAGLR       0.762607        0.656403
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HLA A*2403      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.2
HLA B*2705      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*3501      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -3.8
HLA A*3002      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*0801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*2301      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0250      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*1517      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5101      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*3002      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*8001      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*5401      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*3801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*3301      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*8001      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA B*4002      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.6
HLA A*6801      1:158-166       9       RALASHPNI       1.140241        0.372113
HLA B*3801      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*2603      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*3101      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*1501      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.0
HLA B*3801      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA B*4501      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.6
HLA B*4403      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*0803      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*2301      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2902      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.2
HLA A*0212      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*7301      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*0802      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1801      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*0219      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*0250      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1517      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*4002      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.6
HLA B*1801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0206      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2602      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4402      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*1801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4002      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*2402      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*4402      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4601      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*0802      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*2601      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*1517      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5101      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*0216      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3001      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*6802      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*3501      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0301      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.0
HLA A*0211      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*3001      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*3901      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*3101      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*0801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4402      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
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HLA B*0702      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*0203      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*6901      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*7301      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -3.6
HLA A*0202      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*1517      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0202      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0301      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*2705      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*1801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4501      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.6
HLA A*0201      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4403      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3501      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*2402      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA B*4801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0250      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA A*2602      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA A*0206      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2501      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*2602      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3501      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1501      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*4403      1:28-36 9       SLDTATAAR       0.953732        0.586069        -4.6
HLA A*1101      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*5801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*2902      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2402      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*0212      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.0
HLA A*2301      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.3
HLA A*6802      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0101      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*5801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA B*0803      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA A*3002      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*4501      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2501      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*6901      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4402      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*4501      1:233-241       9       IATARKINI       1.331664        0.187951
HLA B*3801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*0101      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*0211      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*3001      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*3001      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.1
HLA B*5801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*5401      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*6901      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0211      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*3101      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3001      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3002      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4403      1:88-96 9       TYDTAHSIR       0.867128        0.660107        -4.6
HLA B*5801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*6802      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.2
HLA B*2705      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*1509      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*3501      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*4001      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0802      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
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HLA A*0101      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4002      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA B*4001      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4403      1:233-241       9       IATARKINI       1.331664        0.187951
HLA A*2601      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.0
HLA A*2301      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*5401      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*3101      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*0250      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*6802      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2501      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA B*2705      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0301      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4001      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA B*4402      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA A*3002      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1509      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0203      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0219      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*1509      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5101      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*0802      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA A*2301      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*1503      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -3.9
HLA B*1517      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1501      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3101      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0206      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA B*5401      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*1509      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA B*3801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA A*0206      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA A*2603      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*7301      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA B*1502      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3901      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*5401      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*6901      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0202      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*6802      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*2902      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*1501      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*4002      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*6801      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA A*6901      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*4001      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0301      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*3101      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.1
HLA B*1503      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4601      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1503      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA A*0216      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4001      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3101      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*5401      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA B*1501      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA A*2501      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*2902      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0301      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0301      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
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HLA B*1502      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2602      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*1101      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4402      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA B*1501      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0250      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.1
HLA B*0801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5301      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2602      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*0212      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0201      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*7301      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*0803      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6901      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5401      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2402      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA A*2402      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*0802      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*2403      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*1101      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*3801      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3501      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*4001      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*2705      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*0802      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*6901      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*2902      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*0202      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*0201      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA A*0211      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2601      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3201      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*4801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*2501      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*2601      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA B*0801      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*7301      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*5301      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*1502      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA A*0250      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*0216      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*3501      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -3.9
HLA A*0202      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*0301      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*0802      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*2705      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*0203      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.0
HLA A*2601      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*0301      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*2902      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA B*3901      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA A*0301      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*3901      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*0201      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0250      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2601      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*3101      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.1
HLA B*1501      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.1
HLA A*3001      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.2
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HLA B*4601      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4002      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0202      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*3001      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4402      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -3.9
HLA B*4403      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*5401      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0211      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*7301      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*0702      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*3001      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.7
HLA B*5301      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*0203      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -3.8
HLA A*3002      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0206      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*8001      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*5701      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*5401      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*0803      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*2301      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*0216      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA A*2403      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4601      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA B*4501      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4601      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*0803      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3002      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*3501      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0211      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0201      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*8001      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*3001      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*1517      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4601      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*0250      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.5
HLA A*3301      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*0101      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*3301      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*5801      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*1509      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA B*2705      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA B*5401      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA A*3101      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0211      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0203      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA B*0803      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA B*4402      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*8001      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*5301      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*5801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*4501      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*1517      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*0803      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.4
HLA B*1501      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2402      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*0803      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*2902      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1501      1:99-107        9       KACAAEGAH       0.993752        -0.091603
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HLA A*0250      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*3901      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA B*7301      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*2403      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*3001      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA B*0803      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2602      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*5301      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*1502      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*3801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*2705      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1509      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4501      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1801      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1509      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*0206      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*4501      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*1801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA B*5101      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3002      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5101      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*1801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*1501      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3002      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA A*2403      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0219      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA B*5301      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.5
HLA A*0101      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*4801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1509      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA A*2602      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA A*0101      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*5701      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*5301      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3002      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0250      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.3
HLA A*1101      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*2501      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*5401      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*2601      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -3.9
HLA A*0250      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5401      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*5301      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0206      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.4
HLA A*2601      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*0801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*1101      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA B*3901      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.3
HLA A*2603      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA B*1501      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*4801      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4501      1:202-210       9       LAMGATGFI       1.174521        0.259665
HLA A*3301      1:93-101        9       HSIRLAKAC       1.327808        0.080369
HLA B*1509      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*4801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA B*5701      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*8001      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*2301      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
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HLA A*0211      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.2
HLA A*3001      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.4
HLA A*3001      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*6901      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3801      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA B*4501      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*5301      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*3101      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0101      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4001      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA B*2705      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -3.7
HLA B*0801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4403      1:235-243       9       TARKINIAV       1.205835        0.236791
HLA B*5801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1502      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA A*3301      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA A*3001      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.1
HLA A*2501      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*3201      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA A*0212      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2403      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*0250      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1501      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0101      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*1503      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.1
HLA A*0219      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*7301      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA B*1509      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2501      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*1503      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*5801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2601      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0203      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*4002      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA B*4601      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*1101      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*1503      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2602      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*2705      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3001      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.1
HLA A*0250      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*1501      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*3001      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*3901      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*0702      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*1502      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*7301      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.6
HLA A*2301      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA B*5701      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA B*5801      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*3001      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.1
HLA A*3201      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*0801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*6801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*0802      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4601      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*3002      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2601      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA A*2603      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0250      1:234-242       9       ATARKINIA       1.117852        -0.166757
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HLA A*0202      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2602      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA A*0250      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.4
HLA B*7301      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4402      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4001      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*2603      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*3002      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA A*2602      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*2705      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*2705      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA A*6901      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0301      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*3001      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0212      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1502      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0203      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0201      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*7301      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*0216      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2403      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*6802      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3101      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*3101      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.1
HLA B*4403      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA B*2705      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*2403      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*8001      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*6801      1:174-182       9       ADLHSGAQI       1.261395        0.212062
HLA B*1502      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*6901      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2601      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*6801      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0202      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*8001      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA A*0216      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*3101      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2902      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*4403      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -3.9
HLA B*4402      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*8001      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.3
HLA B*0802      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4601      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*6901      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*0702      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*1101      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*1101      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*3501      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4501      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1503      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*5101      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.4
HLA B*4001      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*1502      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4403      1:277-285       9       QVAATPEQI       1.207957        0.241161
HLA A*6801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0211      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2403      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*0802      1:204-212       9       MGATGFISV       1.066312        0.114153
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HLA B*1517      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*4501      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*1517      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4601      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*4001      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*2705      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4002      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*2501      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA A*0101      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA A*2603      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA A*2602      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*6901      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2902      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA A*6801      1:231-239       9       GDIATARKI       1.387075        0.073052
HLA B*1501      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA A*2403      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4601      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*3501      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA B*4501      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*2602      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4002      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA A*2403      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.3
HLA B*4801      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*7301      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*2705      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*1502      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*1101      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*3901      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA B*1502      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2902      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*7301      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*6901      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2403      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA B*1801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA B*0801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0212      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2902      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3101      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0202      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*4403      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*3301      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA B*1501      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2402      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA A*6901      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.2
HLA B*5101      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*6802      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*3001      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1501      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5701      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5701      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*0802      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*0216      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*2705      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*4402      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA B*1517      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
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HLA B*4801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*5101      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA B*4001      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*3001      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -3.9
HLA B*4002      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA B*4001      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5101      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0101      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2402      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.4
HLA B*4002      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*3801      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4501      1:175-183       9       DLHSGAQIM       1.347999        0.083270
HLA A*0211      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*3501      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*7301      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4501      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*4002      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA B*5801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0203      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.1
HLA B*5701      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*3501      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*8001      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*1501      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5401      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*0802      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2603      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA A*3001      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0201      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0301      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*2403      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*1502      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5401      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4501      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.6
HLA B*1801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2301      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.5
HLA B*5101      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*6802      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4002      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*1501      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0219      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3101      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4501      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA A*2601      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1801      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*0101      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*3501      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0201      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.1
HLA B*5801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0101      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*4501      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*2301      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0212      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*4501      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA B*5701      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA A*0301      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0202      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA A*2501      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0702      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*1101      1:207-215       9       TGFISVIAH       0.983515        -0.240948
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HLA B*7301      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*2705      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*1517      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*4402      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*4402      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*4002      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3001      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.0
HLA A*1101      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0219      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2601      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*0702      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3301      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*0801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4002      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA B*4403      1:63-71 9       DGEKIELLR       1.103206        0.332352        -4.6
HLA B*4402      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*0211      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*6901      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0202      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*4601      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*1517      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*3501      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0702      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4403      1:165-173       9       NIVGVKDAK       1.187218        0.245244
HLA A*6901      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*3002      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*0801      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*2402      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4501      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*3101      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0201      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.3
HLA B*4002      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.6
HLA A*0202      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0250      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*5801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA A*2402      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA B*4801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*6802      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4601      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.1
HLA B*0803      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA B*4402      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*5801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4501      1:256-264       9       VTLSKAGLR       0.762607        0.656403
HLA A*8001      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*2601      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0219      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0250      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3301      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA B*4501      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.1
HLA B*1503      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3001      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0203      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0203      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*5701      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*4403      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA A*0101      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2603      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA B*1503      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*3002      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
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HLA B*5101      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1501      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA A*3002      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*6801      1:123-131       9       GLQAHFTAV       1.301654        0.109394
HLA B*4402      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*5801      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0101      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4801      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*8001      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*0801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA B*1501      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0219      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*1101      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1509      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2501      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*1503      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*3001      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0101      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.2
HLA A*0201      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*7301      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*3501      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0212      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0211      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*3901      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0101      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*0802      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0219      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0212      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.1
HLA A*0250      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0206      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5701      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*6901      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0203      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1502      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA B*1502      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA B*3901      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*2705      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0219      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*1509      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*3901      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*3501      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*2603      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*0101      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*1502      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA B*1517      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1503      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*6802      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0211      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3901      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2602      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA B*1509      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6802      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5301      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.5
HLA A*0212      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*4801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*2705      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4001      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
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HLA B*4403      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA B*4601      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2902      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0101      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0206      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*3002      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1509      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*0216      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*7301      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*0201      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA A*3201      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.2
HLA B*4601      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0203      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*0201      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.2
HLA B*5701      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5401      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA A*2403      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0212      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*3501      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4403      1:252-260       9       RLGGVTLSK       1.136726        0.270032
HLA B*4402      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2603      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.8
HLA B*1501      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2601      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*3002      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*2902      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*0803      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*0203      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4402      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.1
HLA B*4403      1:3-11  9       TVGFDVAAR       0.785469        0.628205        -4.6
HLA A*2601      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*3901      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*6901      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4402      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*1801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5101      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*6901      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2402      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*3801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.5
HLA B*4501      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*3001      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2501      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*2601      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2601      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0206      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3101      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2403      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.2
HLA B*1517      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*0301      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*1517      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*0201      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2403      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1502      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA B*1501      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.0
HLA A*3002      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*8001      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4001      1:110-118       9       LVVTPYYSK       0.828598        0.319191
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HLA B*1501      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.2
HLA B*0803      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0212      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*5801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*5801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*0801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.1
HLA A*2501      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*0101      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*0802      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA B*7301      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -3.2
HLA B*4801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1501      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*0203      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0702      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0219      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*1101      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*8001      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*2402      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0803      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2601      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*3001      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.1
HLA A*0301      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*3201      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0211      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.1
HLA A*2603      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1517      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.7
HLA B*4601      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*1101      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0201      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*6901      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*7301      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3001      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0212      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4403      1:242-250       9       AVAPLCNAM       1.074859        0.266154
HLA A*3002      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2301      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.4
HLA A*2902      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*2301      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2403      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2602      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.2
HLA B*4601      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*2705      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1501      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*3801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0201      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0219      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0702      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0211      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.0
HLA A*0201      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*3201      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0301      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2902      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2501      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2301      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0203      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0216      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.0
HLA B*1517      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*5301      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*3301      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4402      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
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HLA B*3501      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0211      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0219      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4001      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*5301      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*5701      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0101      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*1101      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0201      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*1503      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*1501      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*6901      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*8001      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*0301      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1501      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3201      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.1
HLA A*0212      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5401      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.5
HLA B*0802      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*1503      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*2402      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*3101      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*6801      1:260-268       9       KAGLRLQGI       1.143236        0.252977
HLA A*6901      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*8001      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5301      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*2603      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*3901      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*0802      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3002      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0206      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.1
HLA B*1501      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*3101      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3301      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA A*2603      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*4801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4001      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0219      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*0101      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0101      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*2501      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*2301      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.4
HLA B*3501      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA A*6801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0301      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*4002      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*5701      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2403      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2501      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*2603      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3001      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3901      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*5701      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.3
HLA B*0803      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3002      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*6801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*0801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4601      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*3801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA A*0212      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
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HLA B*7301      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.5
HLA A*0216      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*3002      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA B*0702      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5301      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.5
HLA A*0212      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0219      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*1509      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0219      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*6901      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1501      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3002      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*0201      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5401      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5801      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*4801      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*5101      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA A*2403      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5301      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*5701      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2501      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*0802      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*3901      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*6901      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5701      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0203      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*4402      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*3901      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0202      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3901      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0250      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.1
HLA A*2402      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA A*2601      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*2301      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*6802      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*5801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*6802      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4402      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3801      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*0301      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*6901      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0216      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.1
HLA A*0301      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3001      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*5101      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*1509      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*3901      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*4402      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0212      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*3101      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0803      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*0219      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.2
HLA A*2602      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0101      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2902      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*6802      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0301      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4501      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0201      1:130-138       9       AVADATELP       0.883886        0.178246
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HLA B*1503      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*7301      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -3.4
HLA A*0301      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*1801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA B*1503      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*5101      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0802      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*7301      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.5
HLA A*2902      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*0801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.2
HLA A*0203      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.1
HLA B*0802      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4002      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*5301      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*0801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2403      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*1509      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*0802      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA A*0301      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.2
HLA B*1502      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0216      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*4002      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*5101      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*0801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5801      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0211      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3002      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2403      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*5101      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3002      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.2
HLA B*0702      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*1801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4501      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA B*5701      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*1501      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*1801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5301      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4601      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0219      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*2705      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*0101      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1509      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA A*0212      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*4501      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*4002      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA A*2403      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*3501      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*2705      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0216      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0219      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3101      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*1517      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0216      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*7301      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*6802      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.1
HLA B*3901      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*5301      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*5101      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*5301      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.5
HLA B*1503      1:106-114       9       AHGLLVVTP       0.952677        0.025889
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HLA B*5701      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0250      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2603      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*3101      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4002      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3001      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2403      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0219      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*7301      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.4
HLA A*3201      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*0301      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3101      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0101      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0216      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*3002      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0201      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*0301      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*5401      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0212      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*3501      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*3301      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*6901      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0250      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*5701      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*6802      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.1
HLA B*7301      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*2705      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA B*4402      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1501      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.1
HLA B*4801      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*4601      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*8001      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0211      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0216      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0101      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.2
HLA B*4402      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*3001      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*4501      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA B*4403      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA A*6901      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*3001      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0203      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*3002      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*3201      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA B*1509      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0211      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4001      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*3501      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.2
HLA B*1503      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*2705      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0211      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*3801      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*1509      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.4
HLA A*6802      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA A*3301      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.5
HLA B*4501      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA A*0206      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0212      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0250      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
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HLA A*6801      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA B*0802      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*5101      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*5301      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*0801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*3501      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0203      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0216      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3201      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA A*3301      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*7301      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*3801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*3001      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2902      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4001      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.3
HLA A*2902      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA A*1101      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*0702      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0201      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.2
HLA A*0101      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1501      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2301      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*2301      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*3101      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*6901      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*4402      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.2
HLA A*8001      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0803      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*2603      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*0802      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0301      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*0802      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*3001      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*3301      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.6
HLA A*2602      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA B*0803      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*3801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*0801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0203      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*2902      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.2
HLA B*4601      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*0212      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0250      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*0803      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2601      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*8001      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4402      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*5401      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*0801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA B*4501      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*1517      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA A*0212      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*4001      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3201      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA B*5701      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*4001      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0301      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*1509      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1503      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
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HLA A*6802      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*0202      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0206      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0803      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4402      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA A*3101      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*0201      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1509      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*5401      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA A*3201      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2301      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*0702      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0301      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA B*5401      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*3501      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*2403      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*5401      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2403      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0216      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0212      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*1502      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0202      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4403      1:159-167       9       ALASHPNIV       1.037611        0.271475
HLA A*6802      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0301      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3301      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA B*4001      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*2501      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0216      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.4
HLA A*3201      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*0301      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2902      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*3101      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5101      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4001      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*3001      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.2
HLA A*2403      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4501      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*0219      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*0803      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA A*0250      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA B*5801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.2
HLA B*3501      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*3301      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*2705      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*5701      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*0801      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*3001      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.1
HLA A*0211      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*2705      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*0219      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*0801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4501      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.6
HLA B*3901      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*5801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*8001      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA B*2705      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4601      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*5801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2301      1:196-204       9       ALNLPWLAM       1.101533        0.102489
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HLA B*5701      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*3101      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1517      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*0801      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0201      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*3801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA A*3002      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.9
HLA A*3101      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA B*0801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3002      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*3501      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*7301      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.6
HLA B*5801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*7301      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4001      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0250      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3101      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4501      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA A*2601      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*3001      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*3801      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA A*0201      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5701      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*0702      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*3501      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*5101      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0203      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0216      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*0801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*3301      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.6
HLA A*6801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.9
HLA B*5401      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA A*2601      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*1501      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3801      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*1501      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0216      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2403      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*3201      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA A*2902      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA B*1517      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*2705      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*1517      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3002      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5701      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*1101      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0219      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2501      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0201      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0202      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*2705      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0206      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA B*1801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*2301      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA B*4601      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*8001      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*8001      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*4801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA B*4801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
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HLA A*0212      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*8001      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4501      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.6
HLA B*1501      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*2403      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*6801      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.6
HLA B*1503      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0203      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*6801      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.6
HLA A*0202      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0101      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*4002      1:225-233       9       LSAFGSGDI       1.011406        0.278764
HLA A*6802      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1517      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0301      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*3801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA B*4601      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*6801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0201      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA A*0301      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*5301      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA B*4402      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA A*2602      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*5801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5701      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1509      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*3002      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*8001      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*1501      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*2601      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2402      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*3001      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*8001      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.3
HLA B*5101      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.3
HLA A*2902      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*6801      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*0702      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2402      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*3901      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*5401      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*1501      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5401      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*0702      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0219      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0202      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.1
HLA B*4601      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0301      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0101      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*0803      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*6901      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*0702      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3801      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1503      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2602      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA B*1517      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*8001      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4601      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
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HLA B*5701	1:248-256	9	NAMSRLGGV	0.862691	0.199419	
HLA B*5801	1:99-107	9	KACAAEGAH	0.993752	-0.091603	
HLA A*0101	1:95-103	9	IRLAKACAA	1.125185	-0.100733	
HLA A*3301	1:196-204	9	ALNLPWLAM	1.101533	0.102489	
HLA B*4002	1:43-51	9	DQGCDGLVV	1.245484	-0.019858	-4.5
HLA B*5801	1:95-103	9	IRLAKACAA	1.125185	-0.100733	
HLA B*3801	1:74-82	9	LEAVGDRRV	1.007656	0.105836	-4.4
HLA B*4403	1:225-233	9	LSAFGSGDI	1.011406	0.278764	
HLA A*0301	1:95-103	9	IRLAKACAA	1.125185	-0.100733	
HLA A*0211	1:176-184	9	LHSGAQIMA	1.310862	-0.288602	
HLA B*4501	1:225-233	9	LSAFGSGDI	1.011406	0.278764	
HLA B*7301	1:76-84	9	AVGDRRVIA	1.439473	-0.251903	-4.5
HLA B*4002	1:104-112	9	EGAHGLLVV	1.230292	0.004958	
HLA A*0211	1:236-244	9	ARKINIAVA	1.156331	-0.075958	
HLA A*2902	1:27-35	9	GSLDTATAA	1.309789	-0.344356	-4.3
HLA A*0206	1:91-99	9	TAHSIRLAK	0.996404	0.168531	-4.5
HLA B*3901	1:14-22	9	TLLTAMVTP	0.951502	0.038214	-4.3
HLA B*4001	1:98-106	9	AKACAAEGA	1.151290	-0.119087	
HLA A*3001	1:13-21	9	GTLLTAMVT	0.942628	-0.365430	-3.9
HLA B*0702	1:226-234	9	SAFGSGDIA	1.101652	-0.116187	
HLA A*3301	1:76-84	9	AVGDRRVIA	1.439473	-0.251903	-4.5
HLA B*0702	1:1-9	9	VTTVGFDVA	1.273057	-0.233595	-4.3
HLA B*4402	1:176-184	9	LHSGAQIMA	1.310862	-0.288602	
HLA A*2301	1:76-84	9	AVGDRRVIA	1.439473	-0.251903	-4.5
HLA B*1509	1:248-256	9	NAMSRLGGV	0.862691	0.199419	
HLA A*0216	1:38-46	9	ANHLVDQGC	1.053749	0.036049	-4.4
HLA A*2501	1:239-247	9	INIAVAPLC	1.072040	0.023283	
HLA B*4002	1:59-67	9	PTTTDGEKI	1.283399	0.020942	-4.6
HLA B*5401	1:270-278	9	VGDPRLPQV	1.259480	-0.090215	
HLA B*1501	1:176-184	9	LHSGAQIMA	1.310862	-0.288602	
HLA A*1101	1:234-242	9	ATARKINIA	1.117852	-0.166757	
HLA A*2603	1:262-270	9	GLRLQGIDV	1.072956	0.154057	
HLA B*2705	1:38-46	9	ANHLVDQGC	1.053749	0.036049	-4.4
HLA A*1101	1:1-9	9	VTTVGFDVA	1.273057	-0.233595	-4.3
HLA B*4001	1:210-218	9	ISVIAHLAA	1.212072	-0.215938	
HLA B*1517	1:236-244	9	ARKINIAVA	1.156331	-0.075958	
HLA B*4801	1:236-244	9	ARKINIAVA	1.156331	-0.075958	
HLA B*4001	1:176-184	9	LHSGAQIMA	1.310862	-0.288602	
HLA A*2501	1:1-9	9	VTTVGFDVA	1.273057	-0.233595	-4.3
HLA B*5801	1:226-234	9	SAFGSGDIA	1.101652	-0.116187	
HLA A*3101	1:193-201	9	GDDALNLPW	0.935099	0.118725	
HLA A*2602	1:1-9	9	VTTVGFDVA	1.273057	-0.233595	-4.3
HLA B*0702	1:95-103	9	IRLAKACAA	1.125185	-0.100733	
HLA A*2403	1:226-234	9	SAFGSGDIA	1.101652	-0.116187	
HLA A*8001	1:130-138	9	AVADATELP	0.883886	0.178246	
HLA B*3501	1:287-295	9	ALAADMRAA	1.210552	-0.212923	
HLA A*3002	1:117-125	9	SKPPQRGLQ	0.964588	-0.031766	
HLA B*3501	1:130-138	9	AVADATELP	0.883886	0.178246	
HLA B*3801	1:142-150	9	YDIPGRSAV	1.011917	0.044096	
HLA B*3501	1:38-46	9	ANHLVDQGC	1.053749	0.036049	-4.4
HLA A*0201	1:95-103	9	IRLAKACAA	1.125185	-0.100733	
HLA B*0702	1:193-201	9	GDDALNLPW	0.935099	0.118725	
HLA B*1502	1:266-274	9	QGIDVGDPR	0.540265	0.584720	
HLA A*2402	1:144-152	9	IPGRSAVPI	0.865318	-0.021970	
HLA A*0219	1:284-292	9	QIDALAADM	0.849844	0.044312	
HLA A*1101	1:99-107	9	KACAAEGAH	0.993752	-0.091603	
HLA B*1503	1:146-154	9	GRSAVPIEP	0.740088	-0.009387	
HLA B*3501	1:173-181	9	KADLHSGAQ	0.776480	0.012646	
HLA B*1517	1:162-170	9	SHPNIVGVK	0.837185	0.288907	
HLA A*2601	1:181-189	9	QIMADTGLA	0.925319	-0.075098	

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HLA B*4403      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*4001      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1517      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2902      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3001      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA A*1101      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*0702      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*5101      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2403      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*3501      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*2301      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2402      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0201      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*5701      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*0802      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*1101      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA A*2602      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.0
HLA B*1501      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0211      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.2
HLA A*2402      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*6801      1:10-18 9       ARLGTLLTA       1.327543        -0.004208       -4.6
HLA B*5401      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*4501      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.6
HLA B*1501      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.2
HLA A*2403      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2902      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -3.9
HLA A*0212      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0219      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA B*4403      1:59-67 9       PTTTDGEKI       1.283399        0.020942        -4.6
HLA A*6801      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA A*3001      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0216      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3001      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0202      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0202      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*7301      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1801      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*7301      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2601      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0101      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0211      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*6901      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.2
HLA B*4403      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.6
HLA B*4601      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*3002      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1503      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0212      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*5701      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0216      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4601      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*3101      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*3501      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*0702      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA A*0216      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*7301      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*6802      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*5701      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*1101      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA B*1503      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
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HLA A*6801      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*5301      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.5
HLA A*0203      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.1
HLA B*7301      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*1101      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4402      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1503      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.1
HLA B*4601      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1501      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0212      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*4501      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4403      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.2
HLA B*0801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0203      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4601      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*7301      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4002      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA A*3101      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*4402      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*4801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*3901      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3101      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2403      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*1502      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5701      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*0101      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*1101      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*0101      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA B*5801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*7301      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*4402      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*2601      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0201      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2403      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*5801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*3201      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2601      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*6801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5101      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*6802      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2602      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*0801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2601      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0203      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4002      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*6901      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4001      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2403      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3101      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2601      1:32-40 9       ATAARLANH       0.780469        -0.166695       -3.9
HLA B*1801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*5801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2403      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*0803      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*0702      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*4001      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0211      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*2902      1:136-144       9       ELPMLLYDI       0.811740        0.148983
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HLA A*0301      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0301      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3901      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*4801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*1101      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*3501      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4601      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*1501      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -3.8
HLA A*0250      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0301      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*0801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*6801      1:11-19 9       RLGTLLTAM       1.041303        0.243197        -4.6
HLA B*0801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2601      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*2403      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*8001      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*4403      1:34-42 9       AARLANHLV       0.964146        0.245998        -4.5
HLA B*4501      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*0802      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA A*2601      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2402      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0206      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*1101      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*3801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*1101      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2301      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*3301      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*1517      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2902      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*2705      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4601      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.2
HLA A*2601      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*5801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0219      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0216      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*7301      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*5701      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3201      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5301      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*0801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*1502      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*3101      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2402      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA B*1509      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*2902      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*5801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*0803      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*4601      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3201      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0219      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2601      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*2601      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*2705      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*6802      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2403      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*3301      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*2902      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2402      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA A*0212      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.2
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HLA A*0101      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*0206      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0203      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.1
HLA A*1101      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*2501      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3001      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*3002      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.2
HLA A*2301      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4601      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*7301      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3101      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*5801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2902      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*2705      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*6801      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*2602      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0206      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0250      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0212      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2902      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.2
HLA A*2902      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0250      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA A*2601      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0219      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*1801      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0211      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2402      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*3801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0101      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0301      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4001      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0216      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4403      1:2-10  9       TTVGFDVAA       1.389378        -0.196146       -4.5
HLA A*3001      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0216      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4001      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*4001      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*1501      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*5701      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0212      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4402      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*3002      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0301      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*2705      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*6802      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4402      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0219      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*3002      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*1503      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0219      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0211      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0301      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0301      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*1801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*4002      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*4601      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*8001      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0212      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0101      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
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HLA A*2902      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*0101      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*6802      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*0802      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*3002      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.4
HLA B*0702      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0301      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4001      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*5101      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*8001      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1503      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*4403      1:69-77 9       LLRAVLEAV       1.184331        0.094353        -4.6
HLA B*1502      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0201      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*1517      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -3.8
HLA B*3501      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2603      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA B*5301      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3001      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2601      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*0803      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*1101      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5401      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4402      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0206      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1517      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*6901      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.2
HLA B*1503      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3101      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*2602      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*0219      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*3101      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*6802      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*3901      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0206      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*0301      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0250      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*2403      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2501      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*5801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*4801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2902      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*3201      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*6802      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5701      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0206      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*2902      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*4001      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*0101      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA B*1501      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*5801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5701      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*3901      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2501      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA B*2705      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA A*0301      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*6901      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*5401      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0250      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*0212      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
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HLA A*0101      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2602      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*4801      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3501      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0216      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0202      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0216      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*4801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*2601      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3301      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.6
HLA B*4801      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*4403      1:104-112       9       EGAHGLLVV       1.230292        0.004958
HLA B*4402      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*5801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*0802      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2501      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*5301      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA A*2602      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*4501      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*3002      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5101      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2602      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0250      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA B*5801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0802      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0203      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.2
HLA B*0803      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*1502      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.5
HLA B*4402      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*2705      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*7301      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*4801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*0801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3501      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*0702      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*3801      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*0802      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*0219      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA A*1101      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2902      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0250      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3201      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*2705      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*1509      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*4501      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0202      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0212      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*0801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3101      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0702      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0202      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*1801      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1501      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*3501      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*6901      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1501      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.2
HLA A*2301      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*6801      1:239-247       9       INIAVAPLC       1.072040        0.023283
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HLA B*4601      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*1101      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3201      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0203      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2403      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2902      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4402      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*2705      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*1502      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*0219      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0216      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5701      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3301      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA B*3801      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*5101      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5301      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA A*2501      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*3501      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*2501      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*8001      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*4001      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*0801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*4601      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*1801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*4801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*0702      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0803      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA B*1501      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*1517      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*1101      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA B*1503      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*0702      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0301      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1517      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*6901      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0206      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*0803      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3501      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4001      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*6802      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2601      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2403      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0202      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*0301      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4601      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*7301      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA B*5101      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*1517      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*0250      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*6802      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA A*3002      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0212      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2403      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4001      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*6802      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5401      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*0203      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0206      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2601      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
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HLA B*5701      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.3
HLA A*3101      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*3001      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3002      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2603      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3901      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*5701      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*3001      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2902      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*8001      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*1501      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA A*2403      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4402      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*3001      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2403      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*5101      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2301      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.5
HLA A*8001      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5401      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*5301      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*3901      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA A*6801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*1101      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4601      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5301      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*2705      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5101      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.4
HLA A*6901      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0203      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0101      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5701      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2301      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2601      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*1503      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3001      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA B*0801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA A*3002      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA B*0802      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*4801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA B*4501      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.1
HLA A*0203      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.2
HLA A*0201      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1509      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA B*2705      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*0212      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0216      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4402      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*4402      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*3901      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*5301      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*0702      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2602      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5101      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1503      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4001      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4501      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*3001      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*7301      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
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HLA B*3501      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.2
HLA B*3901      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA B*4801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*4402      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2501      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2601      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*0803      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3901      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*1501      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5101      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*7301      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*2403      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.2
HLA B*2705      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4402      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1509      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*3201      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*2705      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2403      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*0801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*3901      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3101      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.2
HLA B*1517      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4402      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2902      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*0803      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*5401      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*6901      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*2403      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3101      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0216      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*4002      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA A*0219      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4002      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0201      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2501      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*3001      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.1
HLA A*2603      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*4601      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*4001      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*3002      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*4001      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*8001      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*2501      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*1509      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*5101      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*1801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*2902      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*4001      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*4601      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*2902      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.2
HLA B*4601      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0219      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*0803      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3101      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*8001      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*1503      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2403      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
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HLA A*0101      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2501      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*0211      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4501      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*1503      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0201      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.2
HLA A*0201      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5101      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4002      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.5
HLA A*0202      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*3101      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*8001      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*0803      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*5401      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2603      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*1517      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0202      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*3001      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*5701      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*6801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4601      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*0801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2601      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*6901      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*0803      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*5801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0702      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*0802      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*1501      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*1503      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0250      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1502      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0301      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2902      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*1101      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*0702      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*2705      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*4601      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0216      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA B*1503      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*5101      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*0702      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*0702      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA A*2902      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*1101      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*4002      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.6
HLA A*8001      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3101      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*3501      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*1501      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*4002      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*3201      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0216      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5301      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.5
HLA A*2403      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*6901      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.2
HLA B*0702      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5401      1:236-244       9       ARKINIAVA       1.156331        -0.075958
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HLA A*8001      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1509      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*3101      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.3
HLA A*0101      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0802      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0201      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2301      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.4
HLA A*0301      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*3002      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*3001      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.2
HLA B*3501      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0201      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*3002      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*3801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0301      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*7301      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*1101      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*5801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*0802      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0202      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*6901      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.2
HLA B*4403      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA B*4601      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*8001      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*1801      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*2705      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1517      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*0301      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2501      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5701      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0301      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5701      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.3
HLA B*4601      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*2403      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0202      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*6801      1:196-204       9       ALNLPWLAM       1.101533        0.102489
HLA B*1517      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*3201      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0250      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5101      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0206      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*2501      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*1101      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*0802      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2602      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0101      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA A*2902      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*1517      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*7301      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*5401      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5101      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*5801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*6901      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3001      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5701      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5301      1:142-150       9       YDIPGRSAV       1.011917        0.044096
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HLA B*3501      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*1501      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.0
HLA A*0250      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*3801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0301      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*0801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4001      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1517      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*0702      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*4403      1:204-212       9       MGATGFISV       1.066312        0.114153
HLA A*2501      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*0801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4001      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*1509      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*0202      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2403      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4402      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1517      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*3101      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*5701      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*5301      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA A*2402      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*5801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4402      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*3501      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*3901      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*2601      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*2601      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2603      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.9
HLA A*0301      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0250      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0202      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0803      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*0702      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4402      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*8001      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2501      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*3001      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.2
HLA A*3201      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0203      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*6801      1:43-51 9       DQGCDGLVV       1.245484        -0.019858       -4.6
HLA B*4001      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2602      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.2
HLA A*0301      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*3201      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*6802      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3001      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0206      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4601      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*2705      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1517      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*0803      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*0803      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*8001      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*0801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*3901      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2403      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*7301      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*1101      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*5401      1:234-242       9       ATARKINIA       1.117852        -0.166757
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HLA A*2501      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*1509      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA A*2402      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*6802      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1509      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*0201      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*4801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*4402      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*1517      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*0802      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0202      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*0702      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2403      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0802      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1509      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0212      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*3901      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*6901      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2601      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*1501      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*2603      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*2402      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.5
HLA A*2402      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA A*3301      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*2705      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3101      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4001      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0203      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1501      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*8001      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5701      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0219      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0301      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0219      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0202      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*3101      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*3001      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.2
HLA B*0702      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*5801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*2705      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*5101      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4402      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2602      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0219      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*6801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA A*1101      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*6801      1:262-270       9       GLRLQGIDV       1.072956        0.154057
HLA A*0202      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*8001      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*4801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2602      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*5101      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5101      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*7301      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*1801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5301      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0206      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*2402      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*7301      1:162-170       9       SHPNIVGVK       0.837185        0.288907
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HLA A*8001      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0202      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0203      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*3801      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2301      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1502      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*8001      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*0203      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*2501      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0206      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4001      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4002      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*6801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*0201      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*5401      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA A*0206      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*4002      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*4801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*2705      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0219      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1501      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*4002      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA B*1509      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5401      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA B*5801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*6901      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0216      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2301      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*3201      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*4801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*6802      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*5301      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2602      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*2705      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0211      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*3901      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*3501      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*7301      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4601      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*1502      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*0101      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*3201      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0250      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*4402      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -3.9
HLA A*2301      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.4
HLA B*3501      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0212      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0803      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0802      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*0702      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.3
HLA A*3002      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0101      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*1517      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0201      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0101      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*2902      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*0802      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*2705      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0802      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0101      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
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HLA B*0801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*3301      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*3501      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1502      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA A*2501      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*4403      1:76-84 9       AVGDRRVIA       1.439473        -0.251903       -4.6
HLA A*0216      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*1501      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*3201      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*0212      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0216      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*3901      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2501      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4402      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*4801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3201      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*0702      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2301      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*4403      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0250      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*1509      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2301      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*5801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*3501      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0301      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*3001      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*7301      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*0801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*3801      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*2301      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2602      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*4002      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*0202      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*1101      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0219      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*4001      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*4403      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2501      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.0
HLA B*4601      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA A*0301      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0101      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*1801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.2
HLA B*5301      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1502      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4001      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*1101      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*5101      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3002      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2601      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*1509      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0201      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1509      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*3801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1503      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.0
HLA B*0802      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0206      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA B*1801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2603      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*6901      1:99-107        9       KACAAEGAH       0.993752        -0.091603
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HLA A*0301      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5701      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*6802      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.9
HLA B*3501      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*8001      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*5301      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*6901      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4001      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*8001      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*6901      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*2601      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4801      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2902      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2601      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*1801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2601      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2501      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*5701      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0201      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*0801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*3101      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0101      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*2603      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA B*1517      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA A*6802      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5101      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*4001      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.3
HLA B*1503      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0101      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3001      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.2
HLA A*0201      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*0801      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2902      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0202      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*2902      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*3101      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4403      1:94-102        9       SIRLAKACA       1.337108        -0.141865
HLA B*4001      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*2402      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*2601      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*0201      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*3101      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*7301      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1503      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*8001      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*1801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -3.9
HLA A*3001      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0216      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0301      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA B*3501      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4601      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2402      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*6901      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.7
HLA A*0219      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*0702      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*5301      1:266-274       9       QGIDVGDPR       0.540265        0.584720
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HLA A*0101      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5701      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4601      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*4501      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4501      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3001      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2501      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*5401      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*1101      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0202      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0211      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*3201      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*6901      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*0802      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3201      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA B*5401      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2902      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*3901      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*0702      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0211      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*1517      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1517      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*6801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*3801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*8001      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2902      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*3501      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.0
HLA B*0802      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0212      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2403      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA B*1503      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4403      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -3.9
HLA B*1801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2501      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.2
HLA A*6801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*1501      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1801      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3901      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*8001      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*3901      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*3002      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.7
HLA B*5801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*4001      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*0101      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4001      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2501      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*5701      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA B*4501      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*2705      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*2403      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4403      1:91-99 9       TAHSIRLAK       0.996404        0.168531        -4.6
HLA B*0801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0212      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0702      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*0702      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*0202      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4402      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*3101      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*1501      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*0206      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.0
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HLA A*2403      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1509      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4501      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1502      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0301      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*1502      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2902      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0101      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4002      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4001      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0216      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*3501      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*1101      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5301      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.1
HLA B*1501      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*8001      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA A*2601      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*0803      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3001      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2902      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*8001      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2902      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2403      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*8001      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*0801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*7301      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0212      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*5101      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*5101      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0101      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*2601      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4403      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*2501      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0201      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*4601      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2403      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2403      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*1502      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*3201      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0201      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*5801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0702      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0803      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0211      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.9
HLA A*2403      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5401      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*2402      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2601      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0202      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -3.7
HLA A*6901      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA B*1801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*3001      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0206      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*6802      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -3.6
HLA A*3101      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0203      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*1501      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
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HLA B*0702      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0216      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4601      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*3501      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*4601      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*6802      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2602      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.5
HLA B*2705      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4601      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0802      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*0702      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3201      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*3501      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*2602      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*3501      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*0803      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*1101      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3301      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*3801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA B*4801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4002      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*6802      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2902      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0219      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0250      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*2603      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*0802      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0803      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4001      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.2
HLA B*5701      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA A*2402      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*4001      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0301      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA B*5701      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0101      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*3201      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA A*6802      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2602      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3901      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*6802      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*2602      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*5801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2402      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*1502      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA B*0802      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*0801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*1101      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1517      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5701      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4002      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2301      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5101      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*0802      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*4403      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA B*4601      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5701      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*0203      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*3001      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.2
HLA B*0802      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
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HLA B*3901      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2601      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0212      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*4403      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA A*0206      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0206      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0702      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5401      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*0203      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -3.9
HLA A*0219      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*1517      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2403      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0301      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*2902      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0201      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0216      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4002      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*1503      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*0101      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*2501      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*5401      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*1509      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*3801      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1517      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1503      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*3101      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*8001      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0301      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*3002      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1517      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0250      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*3002      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*8001      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*6801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1502      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*1517      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1509      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*5701      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*3201      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.6
HLA A*0203      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*7301      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*2705      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4501      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3301      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*0301      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*0201      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2301      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*3501      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*1503      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*2403      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA A*2501      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3901      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.0
HLA B*4501      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA A*0201      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA A*3301      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*2402      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*4402      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*1503      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*0212      1:131-139       9       VADATELPM       0.607375        0.172412
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HLA B*1509      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*0803      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*0101      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*1502      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*2402      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4601      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*0101      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3002      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*5401      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0212      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5701      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*5401      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0202      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*3501      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0206      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*3901      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*6801      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*2301      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5101      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*2902      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*1501      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*5101      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3002      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*6801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1502      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3301      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*5701      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*4601      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*2705      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0212      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*0219      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*5401      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1509      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5301      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*0801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*0803      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0101      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2601      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*2402      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.5
HLA A*0211      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*6801      1:270-278       9       VGDPRLPQV       1.259480        -0.090215
HLA B*2705      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*2402      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*3501      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3002      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA A*2902      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0802      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0216      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3501      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*4801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*7301      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*3901      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*0802      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA A*0212      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
HLA B*5801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA B*4001      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*7301      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2601      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.3
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HLA A*0202      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.2
HLA B*0803      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*2603      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*0203      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.2
HLA B*4601      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*2301      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4402      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*0211      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*5101      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*2601      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*5301      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*0301      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2602      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*0802      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*4001      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA B*0802      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*3801      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2301      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*0101      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3301      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*3301      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4002      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA A*2402      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.4
HLA A*1101      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2301      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*6802      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4002      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2501      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*3801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1502      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*3201      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA B*4403      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA B*1801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*6901      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2402      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*1801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4402      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*1101      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*8001      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*2602      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*2902      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*6802      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*2301      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*3901      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0216      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0702      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2402      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*3101      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*4001      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*2902      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA B*4402      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*4601      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*2301      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA A*2301      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0219      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2902      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3101      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*6802      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
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HLA A*0301      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5401      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.0
HLA B*1801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1517      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.0
HLA A*3002      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA B*4501      1:266-274       9       QGIDVGDPR       0.540265        0.584720
HLA A*2403      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*6802      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*5701      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*6801      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA A*2601      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*4501      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA B*3801      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA B*5701      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0250      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*5801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA A*2402      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*0803      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*4601      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*8001      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*2501      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*5101      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*5701      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*3801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0202      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3901      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*0803      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*4403      1:110-118       9       LVVTPYYSK       0.828598        0.319191
HLA B*0803      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0216      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2403      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*0803      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*2705      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*0702      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4501      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*2402      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*3002      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*3101      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1517      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0206      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5301      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*6901      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3001      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3301      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.6
HLA A*2301      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*3801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2603      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*6901      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4403      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1509      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2601      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4402      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*3901      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*0801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*2301      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0250      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*3001      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*8001      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
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HLA A*2403      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1509      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*3201      1:142-150       9       YDIPGRSAV       1.011917        0.044096
HLA A*6901      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA A*6802      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0101      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*4002      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.5
HLA A*2602      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*2603      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5301      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.6
HLA B*4801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4501      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*4402      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*0803      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*4402      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*3201      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4601      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2501      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*8001      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4402      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*2705      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*5101      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*2603      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.6
HLA B*1509      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*0802      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA A*6901      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*0802      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4501      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*3801      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*1101      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*2902      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.1
HLA A*3002      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1509      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0101      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.3
HLA A*0211      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0216      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2601      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4601      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA A*2402      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2501      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0212      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*7301      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0202      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0250      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0211      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0301      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5301      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0203      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3002      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0101      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*2403      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*3901      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*2602      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.6
HLA B*1801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*2601      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*2705      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1509      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*0803      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
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HLA A*1101      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*5401      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0250      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*3901      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*1502      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*0203      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0803      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*4001      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0219      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*3501      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4402      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*7301      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*6802      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0101      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4403      1:162-170       9       SHPNIVGVK       0.837185        0.288907
HLA A*3001      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3301      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*0211      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3301      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA A*8001      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0803      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA B*4801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.3
HLA B*4402      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0212      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*2403      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.3
HLA A*3201      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*3101      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2602      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*4601      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*1101      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*4402      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4001      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2603      1:239-247       9       INIAVAPLC       1.072040        0.023283
HLA A*6802      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*5801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0702      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*1101      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.4
HLA A*3002      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*3801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0219      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*3201      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA B*0803      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0216      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*0206      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1501      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -3.6
HLA B*0702      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.3
HLA B*5701      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1509      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0803      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*0802      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*4801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*0801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA B*3501      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2602      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -3.7
HLA A*3301      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0702      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*0250      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5301      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*3002      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0201      1:156-164       9       TIRALASHP       0.818770        0.051162
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HLA B*4001      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5701      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5401      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA B*3801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0211      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0219      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*5401      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*0801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*3301      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*1101      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0101      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3901      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*7301      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.4
HLA B*4002      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*0101      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*4601      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*4501      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*3501      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*1517      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2902      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*5701      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*6802      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1503      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*6801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA A*6901      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1517      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*5801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*1801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0301      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*6901      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*8001      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*2603      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.6
HLA B*5101      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*3801      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*5401      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5101      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0802      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2403      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*5801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*3101      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA B*0801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*8001      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*8001      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0802      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0301      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2403      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*6802      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4002      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0201      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1517      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2301      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*4402      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*0802      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*4801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*7301      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4001      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*5301      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4403      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3301      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.2
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HLA B*3801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*6801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*5101      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1517      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.2
HLA A*2402      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*2603      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA B*1509      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0202      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*0803      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*7301      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA B*3901      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1517      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1509      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA A*0101      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*5401      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA A*2902      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*2705      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1509      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*1801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0203      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*7301      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1502      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2601      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*0101      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3901      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*0801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*5101      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*3901      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*3501      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*3801      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*4501      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*6801      1:103-111       9       AEGAHGLLV       1.003584        0.135355
HLA B*4801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*6901      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3101      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*3501      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*5701      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*2601      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*1517      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5701      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4002      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.5
HLA B*1509      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*0219      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*1101      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA A*3101      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA B*2705      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0201      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*8001      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*5801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*2902      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*2705      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*2602      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0203      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0301      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*5301      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*4402      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA B*5401      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
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HLA A*6901      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*7301      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0203      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*3101      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0212      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*0802      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*2403      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*0250      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA B*5801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4402      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*1501      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*0802      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA A*0206      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0803      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4501      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*8001      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*2501      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*1517      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0206      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*6901      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*0301      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2501      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2902      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*1101      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*2301      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*3301      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*0101      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0702      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*2603      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1509      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4001      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2902      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3002      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*3101      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0219      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*3101      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*3501      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*1501      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA A*2402      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*3001      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4601      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0301      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0206      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0250      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -3.5
HLA A*3301      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA A*0216      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*4801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*3501      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*1801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*6801      1:74-82 9       LEAVGDRRV       1.007656        0.105836        -4.6
HLA A*3201      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*0216      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2301      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*2602      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.6
HLA B*5301      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*5801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*5701      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
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HLA A*8001      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2501      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*3301      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.6
HLA B*0801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0802      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0212      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*6901      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2601      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4403      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA B*0702      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3001      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.2
HLA B*2705      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0301      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*2501      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1502      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA A*0211      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4001      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*3301      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*0202      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4403      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*0803      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*8001      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.1
HLA B*5401      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.2
HLA A*2902      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*1517      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.4
HLA B*4002      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*2501      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0101      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*1101      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4501      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*2403      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*3501      1:31-39 9       TATAARLAN       0.966344        -0.631748       -3.8
HLA A*3101      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*5801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*1501      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA A*0301      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2402      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4001      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA A*1101      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1502      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*1517      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA B*5101      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*6901      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3801      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA B*3801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*7301      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*2301      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2403      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*2705      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*0301      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA A*1101      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*5401      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*3001      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3002      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*3002      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*1509      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA A*0203      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3101      1:281-289       9       TPEQIDALA       1.190185        -0.368479
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HLA B*1503      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -3.8
HLA A*0219      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA A*0201      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2603      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*5301      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*2902      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*8001      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4001      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*5701      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*0802      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4001      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2402      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*4801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*0802      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0216      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*3301      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*3901      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*5801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0250      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0212      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*0201      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2301      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*5701      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*1101      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1502      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4403      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*7301      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA A*0201      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA A*3001      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*5101      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*3801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5101      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0101      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*4403      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*1502      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2301      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*0702      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*3801      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*2705      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4002      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*1801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*1517      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2602      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA B*1503      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*4601      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4402      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*0801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA B*2705      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2501      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*1801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0201      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3201      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*1801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2902      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4001      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*7301      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA B*5801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*1509      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
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HLA A*2601      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*3901      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*0802      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*2705      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*0203      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4002      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4501      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3002      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*1501      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0702      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2902      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*0101      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*2501      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0219      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*8001      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.3
HLA B*5301      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*4001      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*3301      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA A*2601      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0211      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5101      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*0219      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3002      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5701      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*1801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*0219      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2501      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*1101      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4402      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*7301      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2603      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3201      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*1801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*3501      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*4501      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*2402      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*4801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*1517      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0803      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*1502      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4402      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2601      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4002      1:248-256       9       NAMSRLGGV       0.862691        0.199419
HLA A*0202      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*2602      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*2601      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2501      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0101      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4601      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA A*8001      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*5801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA B*1509      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*3801      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*2402      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*3001      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*5801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*2301      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*1502      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*0802      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2402      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
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HLA B*1509      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2603      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -3.7
HLA B*4501      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*2705      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA B*3501      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*2301      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0250      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4601      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA A*0301      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0301      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3201      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*3501      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0101      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1502      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*1101      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*0201      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4402      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*6802      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA B*4402      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4001      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0203      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*1502      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*2403      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*4403      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*5101      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*1502      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1502      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1502      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4002      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0216      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*5101      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*1101      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.2
HLA A*6901      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3301      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5101      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0803      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*6901      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0202      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*0803      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*2705      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*3002      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0212      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2501      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*8001      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*4402      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2501      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4002      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*8001      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5401      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*5101      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5301      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4501      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.6
HLA A*0201      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA B*7301      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*5101      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2603      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*3801      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
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HLA B*1517      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.3
HLA B*4001      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*1801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0301      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0212      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*6801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
HLA B*4403      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1503      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2501      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA B*3801      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1503      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.1
HLA A*3201      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4001      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4002      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0201      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*3801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*1801      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1501      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0212      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*5301      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*1801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*0212      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.3
HLA A*2301      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA A*0250      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA A*0211      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*7301      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4001      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.0
HLA A*3001      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*3801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA A*6801      1:38-46 9       ANHLVDQGC       1.053749        0.036049        -4.6
HLA B*3801      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*2601      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.3
HLA B*1501      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*3501      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3002      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*5701      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA A*6901      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA B*7301      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*6802      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*3901      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0101      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*0203      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1517      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*2602      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*3101      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*1501      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA B*4002      1:130-138       9       AVADATELP       0.883886        0.178246
HLA B*1517      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*2601      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*2403      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*6802      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2301      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2603      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA A*6801      1:236-244       9       ARKINIAVA       1.156331        -0.075958
HLA A*3001      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3901      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*3901      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*1801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3301      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*1801      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.4
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HLA A*3101      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*2602      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0203      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0203      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.1
HLA B*4002      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0301      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*3101      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.2
HLA B*5101      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*3101      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0216      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*1801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*3101      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2902      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1501      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0219      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*3801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4403      1:12-20 9       LGTLLTAMV       0.995694        0.063166        -4.6
HLA B*3901      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*0702      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*3002      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*4402      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*4601      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2603      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*2402      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*4501      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*4403      1:130-138       9       AVADATELP       0.883886        0.178246
HLA A*3201      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA B*0801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*3301      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*2501      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*4403      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2402      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*7301      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*8001      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*0702      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1501      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*0250      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA B*4402      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA A*2403      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2501      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1517      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*2403      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*5701      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*3901      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*6901      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.1
HLA A*2301      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1501      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2602      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*3201      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*3801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*3901      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*0201      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*6801      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*2301      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA B*4403      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*1502      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA A*0216      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0101      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
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HLA B*1501      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5101      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0219      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1517      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA B*4601      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*5801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA B*1502      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA A*2601      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4001      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4601      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*1801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*3001      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*5101      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*1501      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.0
HLA B*4402      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*1509      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*6802      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2301      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0203      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.2
HLA A*1101      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3002      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*3501      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0301      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3101      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2602      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*0802      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*3101      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4402      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0201      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*1503      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA B*3501      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*2902      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*5701      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2402      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*6802      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*1101      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*5801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0203      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA A*8001      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*6801      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA B*4001      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2402      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2501      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*0203      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0702      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*5101      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.5
HLA A*2902      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0250      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*3002      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*3901      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0802      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4601      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0803      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*5301      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA A*2603      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*6802      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0201      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*2501      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA B*5401      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5701      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
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HLA A*3002      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*5301      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*0803      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0212      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*6801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4501      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA A*0250      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*5301      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0212      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*0802      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1502      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*6801      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA B*5401      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*0801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*0803      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*1509      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*2601      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5301      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA B*4001      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0211      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0201      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4601      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3101      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*8001      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4402      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0212      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2403      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4601      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0202      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*0202      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.2
HLA B*5801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*1801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0203      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*0202      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*2603      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0301      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4403      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1501      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2603      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2601      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0301      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA B*5301      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*3901      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*4001      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*3901      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*3301      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2601      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3002      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0211      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*5301      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0250      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3002      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6801      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA A*8001      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*1801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*3901      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2301      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0201      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
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HLA B*0702      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2501      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*3001      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2602      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2403      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*0801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*6901      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*1101      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0203      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*0212      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*1517      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.4
HLA B*5401      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*2705      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*5401      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA B*0801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*4801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*1517      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*2403      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*1801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2501      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2402      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*0802      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*4801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4001      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5701      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1501      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*0801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4402      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0301      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*6802      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*3002      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA B*1801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2602      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*0802      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0206      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*5101      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*1503      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5701      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*3001      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*3101      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*6802      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4402      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4403      1:210-218       9       ISVIAHLAA       1.212072        -0.215938
HLA B*4801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*6802      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*1517      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0101      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3101      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0802      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4403      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA B*5301      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA A*3002      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*3501      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*2705      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2603      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2403      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4402      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*1517      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
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HLA A*2603      1:176-184       9       LHSGAQIMA       1.310862        -0.288602
HLA A*2602      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*3002      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0201      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1502      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0219      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4403      1:1-9   9       VTTVGFDVA       1.273057        -0.233595       -4.6
HLA B*1503      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*6802      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0250      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2301      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*3801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6802      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*4001      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA B*7301      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2603      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.5
HLA A*0201      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*0802      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA B*5301      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0216      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*5701      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*8001      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5101      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0203      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0206      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4601      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*3901      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*0702      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2601      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*7301      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*3101      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2403      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*1503      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*3501      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3002      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*5101      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*4801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0211      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0211      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*3501      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.1
HLA B*1509      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*2501      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2601      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2601      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*1503      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0250      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2301      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*3301      1:98-106        9       AKACAAEGA       1.151290        -0.119087
HLA A*0201      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4601      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*5701      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0216      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*3201      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*4601      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*5401      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA B*5801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0201      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*0201      1:274-282       9       RLPQVAATP       0.674151        0.089466
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HLA B*0802      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA A*2602      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*3301      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA A*2602      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA A*2902      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*7301      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA A*8001      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0101      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0201      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA B*5401      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0212      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0101      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*0803      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.4
HLA A*1101      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*2902      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0301      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*0801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*6901      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA A*2902      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4601      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.3
HLA A*1101      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1502      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA B*5101      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*3501      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*2402      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA A*0203      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA B*4001      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4403      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2603      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA A*0250      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*3301      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*4403      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*3002      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1503      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*6901      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*2603      1:206-214       9       ATGFISVIA       1.265885        -0.261822
HLA B*5801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*5301      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.4
HLA B*5801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2902      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5701      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*2402      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.5
HLA B*4801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4601      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0202      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3101      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*0219      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*5101      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0101      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*5701      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*6801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0101      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA A*3101      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*8001      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*6802      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*2705      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0702      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*6901      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*0803      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2601      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
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HLA A*0219      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*4001      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*2705      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*5801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*3301      1:226-234       9       SAFGSGDIA       1.101652        -0.116187
HLA A*2402      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0301      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*0803      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.4
HLA A*0202      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA A*2403      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*2601      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*2501      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA A*2603      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0201      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA B*0801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*5801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*5301      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*4801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*5301      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.4
HLA A*0216      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2402      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*2603      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA A*0219      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*8001      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2601      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA A*6901      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2601      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*0802      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*5401      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1501      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0211      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3101      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*2601      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3201      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.1
HLA A*0216      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*3801      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*6801      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*8001      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0206      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*1509      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*0802      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*3801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0301      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*6801      1:193-201       9       GDDALNLPW       0.935099        0.118725
HLA A*0301      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*7301      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*1501      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5701      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4601      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*3101      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4402      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*8001      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*1502      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*3301      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*3501      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4402      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4402      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0206      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2402      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
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HLA B*1509      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0101      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2403      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*3101      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA A*2902      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*2705      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*0802      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*0702      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3201      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0250      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*6801      1:95-103        9       IRLAKACAA       1.125185        -0.100733
HLA A*0216      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*3301      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.5
HLA B*5101      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0301      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*6802      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3301      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*5101      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2902      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*3101      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*1509      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*3801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0211      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0201      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3301      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*0702      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*5701      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*7301      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0803      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0216      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA A*0201      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*2402      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0219      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*4402      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5101      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*5701      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*3001      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*3501      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0101      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.3
HLA A*0212      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3001      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2403      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0216      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0803      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*1502      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*5301      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.5
HLA B*0802      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*3501      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*1509      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*3001      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.1
HLA A*0212      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3301      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA B*1501      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0202      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0211      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*2902      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*3901      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*7301      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4001      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0212      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
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HLA A*2602      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4601      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2501      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0219      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*1801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*1509      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA B*0702      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA B*4403      1:241-249       9       IAVAPLCNA       1.122147        -0.103628
HLA B*5401      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*5301      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*0801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*2301      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*6802      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3201      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*0801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0219      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0211      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*0702      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*2705      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2501      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*0801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*1502      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0101      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2403      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5401      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.5
HLA A*6901      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2902      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*5701      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*0212      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.4
HLA B*0803      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2403      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2602      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA B*1502      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*0212      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*1101      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*4402      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0212      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*0803      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0212      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0216      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4402      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*2601      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*2705      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0216      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5301      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*0301      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4002      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*0212      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0211      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*5301      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*6802      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*4801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4601      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*1517      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*1101      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0211      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*0801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*1517      1:274-282       9       RLPQVAATP       0.674151        0.089466
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HLA A*2501      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*1101      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4001      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*1101      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4601      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA A*3101      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*6801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*0216      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0803      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*2705      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.3
HLA B*4002      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*2301      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA A*0219      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0206      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*4801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*6801      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*0802      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*8001      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*5301      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0219      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.1
HLA B*1503      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*6802      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0202      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA A*0219      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5301      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*1502      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2403      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*0803      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*3201      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5701      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*1502      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2301      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*3301      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA B*4403      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA A*0216      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*1502      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*1501      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3501      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.1
HLA A*2602      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0803      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*3801      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*0202      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*3901      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*0702      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*1503      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*0250      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0101      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2301      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4402      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*0702      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2501      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2402      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA B*4002      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2603      1:27-35 9       GSLDTATAA       1.309789        -0.344356       -4.6
HLA A*2902      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5301      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA A*2301      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
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HLA A*0203      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4002      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.6
HLA A*0101      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0206      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*2705      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*0211      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*2602      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*7301      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*1509      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*2705      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1503      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*3002      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2402      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA B*0803      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA A*2301      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*1502      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*2501      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*4501      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.6
HLA A*2601      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1517      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4601      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5701      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3101      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*0201      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*6901      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*0250      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5401      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA A*6801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1503      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4403      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.6
HLA B*5401      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*0802      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*6901      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*4801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*2705      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0216      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*2603      1:124-132       9       LQAHFTAVA       1.154833        -0.202686
HLA A*6802      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*0802      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*3801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*6801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*6801      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0219      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*3002      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0219      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*4501      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.6
HLA B*3801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2402      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*6802      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4001      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3301      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.5
HLA B*1502      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*4501      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*4403      1:234-242       9       ATARKINIA       1.117852        -0.166757
HLA A*2403      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*6801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0802      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0212      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*3901      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
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HLA A*2301      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*1101      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0206      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA A*2403      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5401      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*1101      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4403      1:287-295       9       ALAADMRAA       1.210552        -0.212923
HLA B*0702      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*1501      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*3901      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0702      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*6901      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*1509      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4403      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*7301      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*1801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2603      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0201      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1503      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0206      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*2501      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*2601      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*6801      1:271-279       9       GDPRLPQVA       1.458707        -0.429067
HLA B*3501      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2501      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2402      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4402      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*2301      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*1502      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA A*2902      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1509      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*2602      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*6801      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA B*2705      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*2705      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4002      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*4001      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*5801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5701      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*5101      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*0301      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*1502      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*0802      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*4002      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*5701      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*1501      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0206      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0201      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*3301      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*0219      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*5701      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*4402      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4601      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*5801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*3002      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*5401      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2501      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*7301      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*1517      1:195-203       9       DALNLPWLA       1.164585        -0.398227
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HLA B*5401      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*0702      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0201      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*0802      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0211      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*4001      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3101      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2601      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0206      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*0702      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*1509      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*5401      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*8001      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*4402      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0101      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2301      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2501      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*1101      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*3801      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0211      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*3201      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA B*1501      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*8001      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*1517      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*5401      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*1503      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0216      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA A*2402      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*8001      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*6801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5301      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*0250      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4002      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*1501      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*2902      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*3301      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*6801      1:65-73 9       EKIELLRAV       0.851830        0.084898        -4.6
HLA A*0216      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*1502      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA B*2705      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*0206      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -3.9
HLA B*5801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2603      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*3201      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA B*5801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.2
HLA B*1801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*3501      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2603      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*3101      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*0802      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3002      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0212      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.3
HLA B*1501      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*3901      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*4002      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA A*0212      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*1101      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
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HLA B*3901      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0212      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2602      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*2705      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*1517      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA A*0212      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA A*0202      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4601      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*6801      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0202      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*4601      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0216      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4001      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2603      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*1509      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0301      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*3801      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*3301      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0250      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0203      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2902      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*6802      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6802      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.1
HLA A*0101      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*2403      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*5101      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2301      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0201      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3002      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*3801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA A*2501      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*4801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0301      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2301      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*0801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1509      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*0101      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*5401      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5701      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*7301      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*3801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA A*0250      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*5701      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*0803      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*5101      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*5301      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*4501      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*4403      1:14-22 9       TLLTAMVTP       0.951502        0.038214        -4.6
HLA B*0702      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*3901      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4601      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*1509      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2603      1:237-245       9       RKINIAVAP       0.691673        0.268585
HLA A*0101      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*2705      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3901      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA A*3002      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*1101      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*4601      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
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HLA B*5301      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.5
HLA B*5401      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*4001      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*6802      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*2902      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1509      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.4
HLA B*1502      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2603      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*1502      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*1502      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*4001      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*3201      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2403      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*3901      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*3901      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*1503      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*0803      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*3801      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*2301      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*0801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0203      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*6901      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*3801      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2902      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA B*3901      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4501      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*8001      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0202      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4402      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*0211      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0219      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2501      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4402      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*8001      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2403      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*3901      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2902      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*4402      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*6802      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1509      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4001      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*7301      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0219      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0702      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*1502      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*2501      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*5801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0212      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5101      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4002      1:30-38 9       DTATAARLA       1.317804        -0.349852       -4.6
HLA B*3501      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3201      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*7301      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0250      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*4601      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*3201      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.2
HLA A*2402      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0212      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2402      1:172-180       9       AKADLHSGA       1.103643        -0.200277
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HLA B*0803      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*5301      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2602      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*1509      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*0803      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0211      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*1503      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.4
HLA B*1801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*3101      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5401      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0201      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1517      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*1517      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0101      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*6801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.4
HLA B*2705      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*1101      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*6801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2402      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*8001      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*3301      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*0202      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*0211      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0219      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2501      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0250      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*0206      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*6901      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*2705      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5401      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0212      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0206      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*1509      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*1503      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*2601      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA B*5301      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2602      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*7301      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.6
HLA A*0201      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA B*5301      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0202      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*0702      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*2902      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*1503      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*1101      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0206      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2602      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*2301      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*5701      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*1101      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0203      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1509      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2602      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA A*0219      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*5101      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2301      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
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HLA B*1517      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3201      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*1517      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*4403      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*3201      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*0301      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*7301      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*4403      1:136-144       9       ELPMLLYDI       0.811740        0.148983
HLA B*1501      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*8001      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*3501      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2603      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0802      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0219      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2601      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4403      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA A*3002      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2601      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0206      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0101      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*6901      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2402      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*1502      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3201      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*2402      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*1502      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0250      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2301      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4501      1:258-266       9       LSKAGLRLQ       0.978838        -0.024618
HLA B*2705      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0202      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0202      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*0802      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*3301      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*7301      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1503      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5301      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0211      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*1502      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*0202      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*0803      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA B*0702      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3002      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3201      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*7301      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA B*5801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1509      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*6801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*6901      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3501      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*0802      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*2501      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.1
HLA B*4002      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*6801      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*3901      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0203      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*1101      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
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HLA A*3301      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*3002      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*2601      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0702      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2403      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4002      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0803      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*4501      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*2603      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*0803      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0212      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5301      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2402      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA A*2603      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*0802      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*5301      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.5
HLA B*4001      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0802      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3101      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1502      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*3001      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5101      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*0801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2603      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.6
HLA A*2603      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*0802      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*3801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA A*6801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*3301      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*0211      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*5801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA B*1509      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6801      1:106-114       9       AHGLLVVTP       0.952677        0.025889
HLA A*3002      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*8001      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*4801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*3001      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*1517      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*7301      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*2902      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2301      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*5401      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*0216      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*4001      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0211      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*8001      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0216      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*0803      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*0211      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*0801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4601      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3002      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*5301      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*0801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*5401      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA A*6802      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2402      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*6901      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3901      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0201      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
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HLA A*2601      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*3801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2403      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.3
HLA A*0206      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*3801      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0101      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3101      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4002      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA A*2603      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*1801      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*5401      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*3301      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*4801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0219      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0216      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.2
HLA A*1101      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*6901      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5101      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*2601      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0211      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.2
HLA A*0219      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*1502      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0206      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*1101      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*6802      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*3001      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4501      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA B*0803      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*1503      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*0202      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.1
HLA B*3501      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*0203      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0203      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*7301      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*3201      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*0201      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4501      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0203      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA A*3002      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA B*0802      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*2501      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2402      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*1509      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*3201      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA B*5301      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2501      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*4403      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA B*3801      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*3101      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*6801      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA A*0202      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA B*1509      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0803      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2402      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*8001      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*8001      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*4601      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
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HLA B*5801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1503      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3001      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4402      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4601      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0216      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*3801      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*3201      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0301      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*7301      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2902      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*2902      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*2403      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1501      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0211      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2603      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*4002      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.2
HLA B*5301      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.5
HLA A*6901      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*0801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0702      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*3801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3301      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0301      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3001      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4002      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2501      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA B*3801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2902      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2602      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*0802      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0803      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*0803      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0206      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*3301      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*0801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2603      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA B*5101      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*7301      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.5
HLA B*0803      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5101      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3001      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*1101      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*0203      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*2602      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.5
HLA B*1501      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*4501      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.6
HLA B*0702      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0216      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*5101      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*5401      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*5101      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*3501      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*2603      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*4501      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4002      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.6
HLA B*1509      1:127-135       9       HFTAVADAT       0.823504        -0.222280
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HLA A*6801      1:289-297       9       AADMRAASV       0.746862        0.165392
HLA A*2301      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*7301      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3301      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*2402      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*3002      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA B*0702      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2902      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5301      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0216      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*0802      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2601      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3901      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*0802      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0206      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2403      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0301      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*0702      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*2301      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*3301      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*1801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*3002      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2301      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*0803      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA B*4002      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA A*3301      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*0212      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*5401      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.4
HLA A*2301      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*6802      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -3.8
HLA A*3001      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.2
HLA A*0212      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*4403      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA A*2902      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*1509      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*1101      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*3001      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*5801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0211      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4001      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0202      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.0
HLA B*7301      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*3501      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*3101      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*6901      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA B*4501      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*5301      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA B*1501      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0250      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*2705      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*0301      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*5801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2501      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*5701      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0202      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2402      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2403      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*3002      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*6802      1:155-163       9       DTIRALASH       0.889608        -0.411090
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HLA A*0206      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*2902      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*3301      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*1503      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*2705      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2501      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0301      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*6802      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*0211      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*4002      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA B*5401      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*4501      1:117-125       9       SKPPQRGLQ       0.964588        -0.031766
HLA B*1509      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA B*2705      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*2705      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -3.9
HLA A*3002      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*5701      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*0101      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*8001      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*0801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*0803      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*3801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0201      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1503      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1501      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*1502      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*6802      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA B*7301      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA B*4001      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*1801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0212      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*4402      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*5401      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*0702      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*7301      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2301      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6802      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2602      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2603      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*3901      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2602      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*5101      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*2602      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*3101      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*3001      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*0250      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*3001      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5401      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*5401      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*3901      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4402      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2403      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1501      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*6802      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3301      1:172-180       9       AKADLHSGA       1.103643        -0.200277
HLA B*4601      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4403      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.6
HLA A*0211      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*1101      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
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HLA A*2603      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.5
HLA A*6802      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*3301      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3001      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3201      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*0101      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA B*5701      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4601      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*3001      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA B*4501      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*2501      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*3101      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA B*1509      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4002      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*3001      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.2
HLA B*2705      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*3301      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA A*0216      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2603      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2603      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA B*4001      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*6901      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1517      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*3901      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0202      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*1501      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5301      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*3801      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA B*4402      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2301      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*0212      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4501      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0203      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*0202      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*2402      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*5701      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5301      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4402      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4002      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA B*1509      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*5101      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.4
HLA A*8001      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1502      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*4403      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0206      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3201      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2602      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2602      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*1517      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3301      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*0203      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1509      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0101      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*3801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*0803      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*2603      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*7301      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*2705      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*1503      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA B*1509      1:286-294       9       DALAADMRA       1.145958        -0.333963
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HLA B*4601      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*7301      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4403      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA A*2403      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2402      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*3201      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0201      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*6801      1:92-100        9       AHSIRLAKA       1.095131        -0.163421
HLA A*1101      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*2602      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA B*4601      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3201      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.6
HLA B*3901      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA B*0802      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*3201      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0219      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3101      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*5101      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA A*0250      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4002      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA B*0803      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*1501      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*4403      1:36-44 9       RLANHLVDQ       0.776231        0.142039        -4.6
HLA A*2602      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*3901      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*7301      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2902      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2601      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0202      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*6901      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*0211      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5101      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1502      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2902      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*5401      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*2402      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1502      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*1509      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*1801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*5101      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*5801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*6802      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.2
HLA A*2602      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1503      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2501      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.4
HLA A*6901      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*5701      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2501      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*0802      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3002      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*5101      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3101      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*1101      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0216      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0202      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA A*2902      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4601      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*2403      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3201      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
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HLA B*4801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*1101      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*5301      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4002      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0202      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*3801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*0702      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2602      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.6
HLA B*1503      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3201      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0219      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*3301      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.6
HLA B*1801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6802      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*3801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4002      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*0801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*1101      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*6801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*3501      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2301      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0101      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0301      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*2301      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4002      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0203      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*0202      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*3301      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.6
HLA A*3101      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0202      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*3801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*1503      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4403      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA B*5401      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2501      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5101      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0802      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2603      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*0250      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA A*2602      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2301      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4403      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*5701      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*1502      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4403      1:53-61 9       GTTGESPTT       1.261322        -0.386632       -4.6
HLA B*4403      1:209-217       9       FISVIAHLA       1.132189        -0.231568
HLA B*2705      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0201      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1501      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*6801      1:141-149       9       LYDIPGRSA       1.085554        -0.169978
HLA B*4403      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA B*0801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*3801      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*6801      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.6
HLA A*6802      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5401      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*1801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*0219      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
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HLA A*2402      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2601      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2402      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*5701      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*6802      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*5701      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA B*7301      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4402      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0211      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA A*6801      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA A*0206      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0206      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1502      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4501      1:284-292       9       QIDALAADM       0.849844        0.044312
HLA A*0250      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*2602      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0250      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*4403      1:99-107        9       KACAAEGAH       0.993752        -0.091603
HLA A*0201      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2601      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1502      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*1509      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*3501      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*1517      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0219      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2301      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA A*2601      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1517      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA B*5301      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3301      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*0211      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1501      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*3801      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2301      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*5301      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA A*0212      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*5801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.2
HLA A*0201      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA B*7301      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*0801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*3501      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0206      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*7301      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*3201      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*0802      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4601      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*0803      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*1801      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*2602      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*1101      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2601      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*0802      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*2705      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*0219      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*3301      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*4501      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*4501      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*1101      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2902      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*0801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
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HLA B*3501      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0203      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0301      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5701      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1502      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA A*2501      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2301      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4501      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2402      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.5
HLA B*7301      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*0802      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*3801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA A*1101      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*5301      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*4403      1:9-17  9       AARLGTLLT       1.054002        -0.180052       -4.6
HLA A*6801      1:122-130       9       RGLQAHFTA       1.137884        -0.254443
HLA B*1801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*6802      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2603      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5301      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*7301      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*5701      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*8001      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*0803      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*2403      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*5801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA A*0216      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*1509      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1503      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*0219      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0216      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0203      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.0
HLA B*1517      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.2
HLA A*2301      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*8001      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*0101      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*5101      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*0803      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*3901      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.4
HLA B*5401      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4501      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.2
HLA A*1101      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.0
HLA B*1502      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0101      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*6901      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5101      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0211      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4402      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*3001      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3001      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*8001      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4002      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA B*5401      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2902      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5301      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*2402      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*3301      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*1503      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
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HLA B*4402      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2501      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2402      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*3101      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0250      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*6901      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2501      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0211      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.0
HLA A*0206      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0101      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4001      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*2603      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*2603      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA B*5801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.2
HLA B*4001      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*1101      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*0250      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*1503      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0212      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4001      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2603      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*0201      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA B*4001      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3201      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0301      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2603      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA A*0206      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*6802      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4002      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA B*7301      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*7301      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*8001      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*3301      1:84-92 9       AGAGTYDTA       1.144522        -0.273227       -4.6
HLA A*8001      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*3801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*7301      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA B*2705      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2603      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.6
HLA A*0250      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*3001      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.2
HLA A*0203      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4601      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1517      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0702      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2403      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3001      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.2
HLA B*0803      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*3001      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.1
HLA A*6802      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0206      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*1502      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.5
HLA A*0250      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6801      1:219-227       9       GQLRELLSA       1.111095        -0.201908
HLA A*3201      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0219      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*3301      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA B*4801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*6801      1:80-88 9       RRVIAGAGT       1.030720        -0.137805       -4.6
HLA A*2602      1:281-289       9       TPEQIDALA       1.190185        -0.368479
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HLA B*4402      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*3001      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4002      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA A*2402      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*4001      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*0803      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*2403      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*3801      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*4002      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*3101      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*7301      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0202      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0212      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0101      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0250      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*2601      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2603      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*1503      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*1503      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5701      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0250      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA A*0250      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2601      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0216      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0201      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*0801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0301      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2501      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0212      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*4501      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3001      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2301      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*1801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*5301      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2301      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*3201      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA A*2403      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1502      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*4601      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0101      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0202      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0206      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*6802      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0202      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0219      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*5101      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*0803      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*1517      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA A*2603      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.6
HLA B*0801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*0201      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4001      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*0212      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2403      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*0802      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4403      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*5401      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*0801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1501      1:282-290       9       PEQIDALAA       1.082927        -0.508857
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HLA A*6802      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2601      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*0702      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*3801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA B*5801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2603      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*7301      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2501      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*4501      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*2601      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*8001      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*6801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*6801      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*2402      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2602      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*3201      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*4501      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA B*4402      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4403      1:68-76 9       ELLRAVLEA       1.116657        -0.299496       -4.5
HLA B*4501      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1501      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*3901      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2602      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*4001      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0203      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3301      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*1509      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4501      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.6
HLA A*3002      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0212      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.3
HLA A*3301      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3002      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*3201      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*3101      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0206      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1509      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA A*2602      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*2501      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*8001      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*0702      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3101      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0301      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*3501      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*4801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0250      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*6802      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*2501      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*5401      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2301      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*0219      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0212      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*1517      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4402      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4402      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4002      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0211      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1517      1:160-168       9       LASHPNIVG       0.939536        -0.515513
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HLA A*0212      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.2
HLA A*0101      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0203      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1503      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA A*3201      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.5
HLA B*5301      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*5801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0201      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.2
HLA B*3501      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*2602      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0301      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4501      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA B*7301      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.6
HLA B*1517      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*2301      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*5701      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2902      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*5801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0802      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0203      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*3501      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*0212      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*3801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*1502      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*0250      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*3901      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0101      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*0211      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*4403      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5701      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2602      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*0802      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2501      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*2705      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*5401      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4002      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.6
HLA A*2403      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1503      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA B*4403      1:198-206       9       NLPWLAMGA       1.046312        -0.191729
HLA B*0702      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3501      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*0801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5301      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3101      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4403      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*3201      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*3501      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*1502      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0301      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1517      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*0203      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2403      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*3002      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*1502      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*3801      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*4403      1:85-93 9       GAGTYDTAH       1.125748        -0.290385       -4.6
HLA A*6801      1:144-152       9       IPGRSAVPI       0.865318        -0.021970
HLA A*2603      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
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HLA A*6801      1:42-50 9       VDQGCDGLV       0.838419        0.035498        -4.6
HLA B*2705      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4601      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*1517      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*1101      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*0702      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*2402      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*1101      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0201      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3002      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA A*3002      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*1509      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*7301      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA B*3901      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2902      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4403      1:228-236       9       FGSGDIATA       1.183338        -0.323057
HLA A*3001      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0301      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4501      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA B*3901      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*0201      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0206      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.4
HLA B*5301      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*6801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0216      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*3001      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*3002      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0216      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*5801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*2501      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2602      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*5801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*5301      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA B*1502      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*5401      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*5801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4501      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2301      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0101      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*3801      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*2501      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*4403      1:156-164       9       TIRALASHP       0.818770        0.051162
HLA A*3002      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*0203      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -3.8
HLA A*0301      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*5101      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*1503      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0202      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*5801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*2402      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.5
HLA A*0219      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*6802      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4601      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1501      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*2601      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*4001      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2601      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*5301      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*1517      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2301      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
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HLA B*5401      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4002      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*2601      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4601      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*6901      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*0802      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*6801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*3101      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*8001      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2601      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*3801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5701      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4403      1:181-189       9       QIMADTGLA       0.925319        -0.075098
HLA A*0216      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*6802      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0250      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1501      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*1101      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4501      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA B*4801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2403      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2301      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*2402      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*3201      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*0803      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*5101      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2603      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*0206      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA A*2601      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*1501      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*1101      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4002      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*3301      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0216      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0203      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3001      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*1502      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA A*6801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.0
HLA B*2705      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1517      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*0201      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*3801      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA B*3801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2501      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2601      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA A*2403      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*8001      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*1509      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4601      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*5701      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA A*3201      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4002      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2603      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA A*2403      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA B*5301      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA A*1101      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*1501      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*6801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4002      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
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HLA A*2603      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0219      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*0202      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4002      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4001      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1517      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3101      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0802      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0202      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*3101      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0301      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*2902      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*7301      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*4001      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0101      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA B*0801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA A*6901      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4402      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*3901      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*3201      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*8001      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.3
HLA B*1503      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*8001      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5701      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*3301      1:276-284       9       PQVAATPEQ       0.978949        -0.168517
HLA A*0201      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*2705      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3101      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*1801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5101      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2402      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*2402      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA B*4403      1:286-294       9       DALAADMRA       1.145958        -0.333963
HLA A*2601      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0201      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*0801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0216      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4402      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3301      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
HLA B*4403      1:281-289       9       TPEQIDALA       1.190185        -0.368479
HLA B*4002      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
HLA A*2601      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1502      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2602      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*2603      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*2301      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5401      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*0802      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*2603      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA B*1509      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA B*4001      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA A*0201      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1502      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0101      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*0301      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0202      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*5101      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5701      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3201      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
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HLA A*0211      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*4501      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.6
HLA B*7301      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA B*5801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0216      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5301      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*1501      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*5801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*1501      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4501      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
HLA B*4601      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*0803      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*3301      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*1503      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4601      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6901      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*2902      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0203      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA A*0212      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0101      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0301      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*0702      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2403      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA B*5801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4402      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA B*5701      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2602      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA B*5701      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4501      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*0101      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*5301      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2602      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2402      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*3002      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*2705      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4002      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*2602      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*5801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2902      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4001      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4403      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA A*0206      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0211      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0301      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3002      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0301      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1502      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA A*0219      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*6801      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
HLA A*0206      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.0
HLA B*3901      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*2705      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*3002      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*1501      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2902      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*5301      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.5
HLA A*3201      1:112-120       9       VTPYYSKPP       0.288012        0.075481
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HLA B*1509      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*3901      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0212      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3301      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*2501      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2603      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*0803      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0301      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4002      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA A*6801      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0250      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4601      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*5401      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0219      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*1502      1:195-203       9       DALNLPWLA       1.164585        -0.398227
HLA B*4002      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1509      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*0301      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0219      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2301      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*0801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4402      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0212      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA B*2705      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5701      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0216      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*3001      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0206      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*2705      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3301      1:131-139       9       VADATELPM       0.607375        0.172412
HLA A*0101      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2602      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4601      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*5301      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2603      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0206      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*1503      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*2402      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.5
HLA A*0211      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*5401      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*3801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4403      1:166-174       9       IVGVKDAKA       1.003463        -0.170676
HLA A*2501      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0201      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6802      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*2602      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*7301      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*0702      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4402      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1501      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0203      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*4402      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA B*1509      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3001      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -3.9
HLA A*2301      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA B*4002      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*1801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
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HLA B*1501      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*0203      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*7301      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0301      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA B*1501      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0250      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0250      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*3101      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA A*2501      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4002      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.6
HLA A*8001      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*0301      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3101      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0206      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0212      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*6801      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4403      1:51-59 9       VSGTTGESP       0.782841        0.037884        -4.6
HLA B*5101      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*4002      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4601      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1502      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*6901      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*7301      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*0211      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0206      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*0702      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0206      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0203      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0301      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*3301      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*1517      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*2705      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*3501      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0101      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA A*3101      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA A*3001      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*0212      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0203      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*8001      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0301      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*6901      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*8001      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*7301      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*1509      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1502      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA A*2902      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3101      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1502      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*5401      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0201      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.3
HLA B*1801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5101      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.3
HLA B*5701      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*0801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA A*0301      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6901      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*0702      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0101      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2602      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
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HLA B*4601      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*4002      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA A*1101      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*8001      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*2402      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0250      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2301      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0202      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*3501      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0250      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*0211      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA A*3001      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*6901      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0211      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4501      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*5301      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4501      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*2403      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*5701      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*3002      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*2705      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2902      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0219      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1502      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*2902      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5301      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
HLA B*3501      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*6801      1:121-129       9       QRGLQAHFT       1.142797        -0.345550
HLA B*3501      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5101      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*0802      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4501      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA B*4601      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*6801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3201      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*4402      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*1503      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5701      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5701      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0803      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2301      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*2402      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*5701      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*2403      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*6801      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*4801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*3301      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2601      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*2602      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*3901      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*3002      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4403      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*3801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*5801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4002      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*0803      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*2403      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
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HLA A*2602      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5701      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*3002      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*8001      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4402      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*0803      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA B*1503      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3301      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA A*3101      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*4801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*4501      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA A*3301      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA A*0219      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0206      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.1
HLA B*4001      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3201      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2402      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*0802      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0803      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*1517      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0101      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3301      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*0101      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*5301      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.5
HLA A*0216      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*6901      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0219      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*3301      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*0212      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6901      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1503      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.0
HLA B*4002      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0803      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*1501      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2402      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1509      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2402      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*4801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4601      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*3201      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA A*2602      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA B*3801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*3101      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*0702      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*1501      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*2301      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*2602      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*1517      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6901      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*6901      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*6802      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*3501      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*5701      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*2501      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2602      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0802      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0250      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*2705      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4403      1:26-34 9       DGSLDTATA       1.310371        -0.499466       -4.6
HLA A*2601      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
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HLA A*6802      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*2301      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2301      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3301      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*0250      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*4501      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*5301      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*0801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*2403      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1509      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1501      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.1
HLA B*4801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*2403      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1502      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*0803      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2603      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
HLA B*0802      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3301      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA B*0801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA B*5701      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3201      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
HLA A*0201      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*5801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*3901      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0216      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3301      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA A*1101      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*3901      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*0206      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4601      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2601      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*6802      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*4402      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1517      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4403      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA A*3301      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
HLA B*5801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2603      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2902      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*0203      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2402      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA B*4001      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*6801      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2602      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*2705      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*2705      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*6901      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0219      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0201      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*8001      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*1501      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5401      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*0702      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*0803      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4402      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*5101      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
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HLA A*3001      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -3.9
HLA A*3101      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0803      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4001      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4002      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0219      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4403      1:230-238       9       SGDIATARK       0.777647        0.020034
HLA B*4801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*6801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4403      1:131-139       9       VADATELPM       0.607375        0.172412
HLA B*4501      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*1503      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*2705      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0301      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0201      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1509      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.1
HLA B*5701      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*4402      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*4501      1:207-215       9       TGFISVIAH       0.983515        -0.240948
HLA B*4402      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*8001      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*2602      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA A*0301      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2601      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3101      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*0219      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4403      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA B*3901      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*2402      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*6801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.0
HLA B*5801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -3.9
HLA B*3801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*3801      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4001      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.3
HLA B*1517      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0802      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0206      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0216      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4501      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.6
HLA B*3501      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.0
HLA A*6801      1:24-32 9       SGDGSLDTA       1.230248        -0.446258       -4.6
HLA B*1501      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3101      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*0201      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4001      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*0702      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4403      1:173-181       9       KADLHSGAQ       0.776480        0.012646
HLA A*8001      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*4403      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*1517      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*4402      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*6901      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*0101      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA A*2601      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*3301      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA B*0801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*5401      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0101      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
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HLA A*0211      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*0212      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*1501      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*3201      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*5301      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*3901      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*3201      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*1509      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4001      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2501      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4601      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3301      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0301      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*5101      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0211      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4601      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*7301      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0203      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0101      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*1101      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0803      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*4601      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4601      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1501      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA B*1503      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*2501      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*1509      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*5401      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*0702      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1502      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*2301      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*3501      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*6802      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*3501      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*0801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*2705      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0201      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*0202      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*5101      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*2301      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*3901      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0202      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.1
HLA B*4001      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1503      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*3501      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.1
HLA A*2403      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*5401      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3201      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1501      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -3.9
HLA A*0301      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2402      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*0202      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*5101      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0202      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*6802      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4402      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1501      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0216      1:282-290       9       PEQIDALAA       1.082927        -0.508857
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HLA B*5101      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*2705      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*1502      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*3002      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*7301      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*5101      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA B*0803      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*0801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA A*0219      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*4001      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA B*0702      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*2705      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0301      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*1503      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*2705      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*1101      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5101      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0203      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*2601      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*2501      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*6801      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*3101      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*5701      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*3901      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*2601      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*6801      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA A*2402      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5301      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*2705      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6802      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA B*0802      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*2902      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.3
HLA A*0201      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4402      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2902      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*6801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.2
HLA A*3002      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*0801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4403      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.6
HLA A*0201      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*3301      1:126-134       9       AHFTAVADA       0.878182        -0.138289
HLA B*5301      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2403      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4002      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*0801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA B*1801      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*2601      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*2403      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA A*6901      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0216      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*6802      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5101      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.4
HLA A*2403      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*1101      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1517      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2403      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0101      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*8001      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3201      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
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HLA A*0211      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*4002      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0206      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0216      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*8001      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*0802      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*8001      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*2301      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*6801      1:118-126       9       KPPQRGLQA       1.091777        -0.300206
HLA B*5401      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0101      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1503      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.3
HLA A*0212      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4501      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*0802      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4601      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*1502      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4402      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*6802      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*5101      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3101      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.3
HLA B*2705      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2902      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0101      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0203      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2602      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.1
HLA A*2603      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*3801      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*7301      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0201      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA A*1101      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2601      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3101      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2501      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*6802      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2603      1:279-287       9       AATPEQIDA       0.906204        -0.141272
HLA A*0216      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4501      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA B*4501      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0101      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6901      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*1501      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.1
HLA A*3201      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*6901      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*0702      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*3301      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0250      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.5
HLA A*3301      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*4801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*5701      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*5701      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2602      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4001      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*1503      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*6802      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0203      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*5101      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0201      1:97-105        9       LAKACAAEG       1.019107        -0.524160
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HLA A*2601      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*6801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*0802      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA B*4402      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*0802      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4001      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*0802      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*6802      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*7301      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*4001      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2602      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*0301      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*6901      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*3002      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*3002      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*0702      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*7301      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*8001      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1503      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0101      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2403      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*1101      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0201      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*7301      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*2603      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA B*3501      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.1
HLA B*3901      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*0801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1503      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2602      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2402      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2902      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*0211      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*5801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0206      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*3301      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2501      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*2403      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0803      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*2602      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0101      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4601      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*0702      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*6801      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA A*0203      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*3201      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*0212      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0203      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4001      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA B*3501      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1501      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.1
HLA A*0212      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4001      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0202      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA B*2705      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0250      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*6901      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.0
HLA A*3301      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
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HLA B*3901      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0250      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2601      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4002      1:90-98 9       DTAHSIRLA       1.126103        -0.393235       -4.6
HLA B*1801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*4403      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA B*1501      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0219      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0212      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*0801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*6901      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*5101      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4601      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*5301      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0702      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*0802      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1502      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*3801      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*1101      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*4402      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*1509      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA A*0212      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*0803      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*0801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2402      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*2403      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3001      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*3501      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*0803      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0212      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*6801      1:78-86 9       GDRRVIAGA       1.161693        -0.401657       -4.6
HLA A*0212      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*3801      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*1502      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*1502      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*1101      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA B*4402      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2601      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.3
HLA B*0702      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2902      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*5301      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3301      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*4403      1:274-282       9       RLPQVAATP       0.674151        0.089466
HLA A*3002      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*4402      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*3201      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*8001      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*1101      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*1101      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*0201      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0211      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA A*0212      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*3002      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA B*4403      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA B*3901      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.0
HLA A*3002      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4601      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*3801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*0211      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*4801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
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HLA B*1509      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*2603      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*3201      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1503      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0301      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*1101      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*0206      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0250      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA A*1101      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0250      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4601      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2301      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*6801      1:64-72 9       GEKIELLRA       1.198451        -0.429578       -4.6
HLA A*2602      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*1517      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*2705      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*3801      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*7301      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*0802      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*0212      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4002      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*2501      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*0803      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0219      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0250      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.4
HLA B*5101      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0216      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*0702      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*0803      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3201      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0219      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3101      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*3201      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.2
HLA A*0219      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*5701      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*8001      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*3301      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0212      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*3001      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*1503      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*5301      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*7301      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA B*4002      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.1
HLA B*1502      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*0801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*4801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*6802      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0219      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*3201      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA B*0702      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*7301      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3101      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*3501      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.0
HLA A*0201      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0211      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2603      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA A*0203      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0216      1:265-273       9       LQGIDVGDP       0.433298        0.065250
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HLA A*3001      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2403      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*2402      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA B*1517      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*4801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2501      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2902      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1509      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*3001      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*8001      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0250      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4002      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*5301      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*2603      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0203      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.2
HLA B*1801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*0803      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4402      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2601      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.2
HLA A*3101      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1509      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0203      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0203      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4402      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4402      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*2402      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4403      1:105-113       9       GAHGLLVVT       1.117598        -0.421962
HLA B*1517      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*2402      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*8001      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2403      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4403      1:272-280       9       DPRLPQVAA       1.237603        -0.492822
HLA B*1503      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*3501      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2301      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA B*5401      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA A*3201      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4501      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA B*0801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.2
HLA A*0216      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*3201      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0216      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*1509      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2403      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0219      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.1
HLA A*2301      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0219      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*8001      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0206      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*6801      1:146-154       9       GRSAVPIEP       0.740088        -0.009387
HLA A*0301      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5701      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0301      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*5401      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*1502      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0219      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
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HLA B*4403      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*1501      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*5301      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0216      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0702      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*0201      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*3101      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*0802      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0212      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0201      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4501      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*2902      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1503      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2602      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*0206      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*5401      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA A*0203      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA A*0250      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.2
HLA A*0219      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*1509      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1503      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1517      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5401      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2402      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*6802      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*5701      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4001      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*1101      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1517      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0219      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2902      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.1
HLA B*4801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2601      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*0702      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2501      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*6901      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.2
HLA A*6802      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4501      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*1101      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0802      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*6802      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.2
HLA B*1503      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA A*3002      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4501      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4002      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*0101      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*6802      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0206      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2902      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2501      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*0206      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*2602      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*2301      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2603      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA A*2402      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4002      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA B*2705      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*0801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*0803      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
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HLA B*7301      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4402      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0202      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*8001      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*1101      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*3001      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0211      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4403      1:212-220       9       VIAHLAAGQ       0.643649        0.066167
HLA A*6802      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0216      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0216      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4501      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA A*0212      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4001      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*2705      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3301      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*0211      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*3001      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*3301      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0202      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.0
HLA A*2402      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*0202      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0212      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.0
HLA A*3002      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*3901      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*0216      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1517      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0803      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.4
HLA A*3201      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*4002      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA A*0202      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0219      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0212      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*6802      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.2
HLA B*0802      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0219      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*5401      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*0803      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0206      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*5101      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*2902      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*0803      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*5101      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0250      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*3001      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*6901      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.2
HLA A*0250      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0203      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1509      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.4
HLA B*3901      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA B*3501      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*3901      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*1509      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*0702      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*7301      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*4002      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2902      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2602      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
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HLA B*4801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3301      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*0702      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2501      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*3801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4001      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1517      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*2705      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA B*0702      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*3901      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*4601      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0202      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.2
HLA B*1517      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*0802      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*0802      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3001      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*3901      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0202      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3101      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*5701      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0206      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA A*0216      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*5101      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*0101      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2601      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*1502      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*0203      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2902      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2301      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4002      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*0802      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA B*3901      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*5101      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*2501      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1509      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3101      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2602      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*3901      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA B*1503      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*7301      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2603      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*4801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*6802      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6802      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.2
HLA A*6801      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA A*2902      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*2705      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*5301      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3002      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2403      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0250      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*4002      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*4501      1:169-177       9       VKDAKADLH       0.964088        -0.272574
HLA B*7301      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*3301      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*5401      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4601      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0211      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
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HLA A*6802      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1503      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*0801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3001      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.2
HLA B*5401      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*2603      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*2602      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*3901      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*2902      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*3001      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA B*2705      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.4
HLA A*0202      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*7301      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*3801      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2301      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*3001      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.2
HLA A*3201      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5701      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2402      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*4403      1:58-66 9       SPTTTDGEK       0.695904        0.004857        -4.6
HLA A*1101      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.4
HLA A*2403      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2301      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*2705      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3201      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2402      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2601      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6901      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.2
HLA B*4403      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2301      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0216      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2602      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0202      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0211      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA B*0702      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*0802      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0201      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6802      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -3.9
HLA A*0203      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.1
HLA A*2501      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*7301      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*2603      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*1101      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*4402      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2603      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*1101      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*1101      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*0802      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0301      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.2
HLA B*5101      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*1101      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*3501      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2403      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.4
HLA A*2301      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1509      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1509      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0206      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*1509      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*3001      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
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HLA A*8001      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*4501      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA A*6801      1:227-235       9       AFGSGDIAT       0.910914        -0.218563
HLA A*6801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*0216      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3001      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.2
HLA B*1503      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA B*7301      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*2403      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*5701      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*1517      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2301      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*3201      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*2603      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*0201      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*6801      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3501      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2403      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*0206      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*8001      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3002      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0203      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.2
HLA A*2602      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3201      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA B*4402      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2301      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0219      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4501      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*2705      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4501      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3901      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*0802      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*3001      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*2705      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*4501      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*5101      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*7301      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*3001      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.2
HLA A*8001      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0203      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*3801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*2705      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2601      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*7301      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA B*3801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*2301      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*0206      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*2301      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*2301      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*2602      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*7301      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*1517      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1501      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*3801      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*1801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0301      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*3501      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.1
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HLA A*2601      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA B*0802      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*0803      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA B*4001      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3001      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*3501      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4501      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3901      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0301      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA B*5101      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*5401      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*8001      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA A*0250      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*0211      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4002      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA A*0216      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3001      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*0803      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*7301      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2603      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*6801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA B*7301      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4002      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA B*4601      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*1509      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0803      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0250      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4002      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA A*3002      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2603      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA A*3001      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4002      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*6802      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA A*3001      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*0250      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0212      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.0
HLA B*5801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0702      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*1502      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*7301      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*3201      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*5301      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.5
HLA A*2402      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA B*0802      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA A*0211      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3101      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*1501      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.2
HLA B*2705      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4501      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*1517      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2501      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1501      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*1801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0203      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5401      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.4
HLA B*3801      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*3901      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0301      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*4402      1:160-168       9       LASHPNIVG       0.939536        -0.515513
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HLA B*1517      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0206      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*4403      1:240-248       9       NIAVAPLCN       1.155344        -0.485890
HLA B*5301      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*2402      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*3002      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0301      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*1501      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*6801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*2402      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*0101      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*3002      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2602      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*0802      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*3501      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*5101      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*3501      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*2705      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1502      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*3002      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*1501      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0206      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0212      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*3301      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3001      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.2
HLA A*2603      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*5301      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA A*1101      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*3101      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*7301      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.6
HLA A*1101      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2501      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*1503      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0211      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*3901      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*4403      1:188-196       9       LAYYSGDDA       0.772228        -0.138483
HLA B*5801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3301      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0216      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0201      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0702      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA A*2402      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*0211      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*5401      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0250      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3201      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1503      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2501      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4001      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5401      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA B*1502      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*2501      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0301      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5301      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA B*3801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0206      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5101      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*0301      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*3002      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
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HLA B*3901      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5701      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3001      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0202      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*4403      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.6
HLA A*2602      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*3002      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0250      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*2301      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*6901      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2603      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*0801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2402      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2301      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA B*5801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0203      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*0803      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*0216      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0216      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4402      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -3.7
HLA A*2902      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0212      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*0803      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2603      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA A*0211      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*2705      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0206      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2402      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*2402      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*3801      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*0211      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*1501      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4002      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*0802      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*3801      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*0202      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*1509      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*2402      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*1101      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2501      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*0803      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*0219      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0219      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*8001      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*8001      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6901      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*2501      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA B*4403      1:151-159       9       PIEPDTIRA       1.099381        -0.426599
HLA B*3801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA B*1509      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3101      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*1101      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0212      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*5401      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*0211      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
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HLA A*3002      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*0201      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*0250      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA B*5301      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*3901      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.4
HLA A*2601      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0206      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0212      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*0219      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0101      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2902      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2402      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA B*0801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2402      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0206      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3301      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3002      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1501      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2902      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0206      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*3001      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3301      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*3001      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.2
HLA B*4403      1:127-135       9       HFTAVADAT       0.823504        -0.222280
HLA A*2501      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*6801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3002      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0202      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2402      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*1801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*6801      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA B*3801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*4403      1:113-121       9       TPYYSKPPQ       0.723517        -0.087021
HLA A*6901      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*3901      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0212      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*0202      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0203      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*2301      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4002      1:32-40 9       ATAARLANH       0.780469        -0.166695       -4.6
HLA B*5101      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*0803      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*2301      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0803      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*0801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*3301      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*3002      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*0802      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*1509      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*0206      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2402      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5101      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3301      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.5
HLA A*0250      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*0803      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*5801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*6801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA B*1502      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*2501      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*6802      1:232-240       9       DIATARKIN       1.021962        -0.656634
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HLA B*1502      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0211      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*3001      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA A*2603      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*0803      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*1101      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2601      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*4601      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA B*0702      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2603      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0211      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3001      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.2
HLA A*0203      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0211      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5301      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*3101      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0216      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*3101      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.3
HLA A*6802      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.2
HLA B*5301      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5301      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA B*3901      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1517      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA A*0211      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*3801      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*1101      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*3001      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1503      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4403      1:253-261       9       LGGVTLSKA       1.003832        -0.358536
HLA A*3301      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4001      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*6802      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA B*4601      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0212      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0301      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0219      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*2403      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*1503      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*0201      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2301      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA B*1502      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*4001      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*3101      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*1502      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*0202      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4501      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*5801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA B*1517      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*1509      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*6901      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3301      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*0802      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2902      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA B*0803      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3201      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*3901      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0101      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5301      1:192-200       9       SGDDALNLP       0.729648        -0.147874
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HLA B*5401      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA B*1517      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4001      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*7301      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*0219      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*3501      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6901      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA B*1517      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.1
HLA B*4002      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA A*3001      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3002      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4403      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*3002      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4001      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*3002      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*0301      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4002      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA A*0202      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0101      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*1502      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*0211      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*2402      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*2403      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.1
HLA A*0216      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*1501      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0206      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0216      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2603      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*5701      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA B*4403      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*5401      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1502      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1502      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*2301      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*3801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*3501      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA B*1517      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.2
HLA B*5401      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*3101      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5301      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4402      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA A*3001      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3201      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0101      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA A*3001      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0250      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1509      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0203      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0202      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA B*1501      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.2
HLA B*1503      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.1
HLA A*2501      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.2
HLA A*2402      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0206      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0211      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*6901      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA B*5801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
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HLA A*2601      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*1509      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2603      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.6
HLA A*2402      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*3101      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*0201      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*3002      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*0801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA B*4601      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3101      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*3501      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2301      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*0250      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*3201      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4402      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*6801      1:249-257       9       AMSRLGGVT       0.737166        -0.132110
HLA B*4801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*1501      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA B*1501      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*0803      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*5401      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*6901      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2501      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2603      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0216      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0202      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*3801      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*2902      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0301      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA B*5801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0101      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*0801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*6802      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0702      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*6901      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*3201      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*0212      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA A*0301      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA B*5701      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*3801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*1517      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*0803      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*2601      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*2902      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2602      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.5
HLA B*2705      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0101      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*4403      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*3201      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*5301      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0202      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4403      1:13-21 9       GTLLTAMVT       0.942628        -0.365430       -4.6
HLA B*3801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*0802      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2301      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*1502      1:278-286       9       VAATPEQID       1.287811        -0.753085
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HLA B*1502      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0250      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*3801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*3201      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5301      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0206      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.2
HLA A*3301      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA B*7301      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*1501      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA A*3001      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*5701      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*3201      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA B*7301      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0301      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*5401      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*1502      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2603      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6802      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0206      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2403      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1501      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA B*1502      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*3101      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0212      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0216      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*7301      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*6901      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*2602      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.5
HLA A*2301      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*3801      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA B*5801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*3901      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*3301      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA B*4001      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*8001      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*1501      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*0101      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0201      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4001      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*3001      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0301      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA B*4601      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0202      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2902      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*0202      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA B*7301      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3001      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2602      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0301      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2403      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*1801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*0206      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2902      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2601      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.2
HLA A*2602      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*5401      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA B*4002      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA A*2601      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*2301      1:155-163       9       DTIRALASH       0.889608        -0.411090
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HLA A*6801      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*8001      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0250      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0206      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4501      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*4402      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*8001      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*3801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*3501      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*2403      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2402      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0301      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*0212      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2601      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*2602      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4001      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*3201      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA B*5801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*6901      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*1517      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2403      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*3501      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*6802      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*4403      1:111-119       9       VVTPYYSKP       0.481385        0.136298
HLA B*1801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0211      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.0
HLA B*4002      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2601      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0202      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4002      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0211      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*5701      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*3501      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*6901      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0202      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0203      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0211      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0202      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.2
HLA A*3301      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.6
HLA B*5301      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.6
HLA A*2301      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*5801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*1501      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*3901      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*2603      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*1502      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*5301      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4403      1:153-161       9       EPDTIRALA       1.115489        -0.524601
HLA B*5701      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0202      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA A*2301      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*3001      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*4001      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0201      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*3001      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.2
HLA B*4001      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0203      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*7301      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*4501      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
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HLA B*1509      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*0101      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0203      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3901      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2902      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0101      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0702      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*4601      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA A*2601      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2403      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*3801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0101      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*0201      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*1501      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2501      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*3301      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0219      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*7301      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*0101      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA B*1502      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*6901      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*2902      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*6901      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*0702      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4501      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.6
HLA B*1509      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4402      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3301      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*3101      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*3002      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4002      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA A*0201      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0216      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.0
HLA A*2902      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*6801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0219      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0201      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*0301      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3301      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*4501      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.5
HLA A*0211      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2402      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA B*4801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*1509      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*5801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*4001      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2601      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.3
HLA A*3101      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*1503      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0212      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*8001      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0206      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0201      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.3
HLA B*0801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0206      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*6802      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*3901      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.2
HLA A*0250      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
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HLA A*3101      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*3801      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1517      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*6801      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*0702      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0219      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0250      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5301      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*3001      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*4402      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*0203      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.0
HLA B*7301      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*8001      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*6901      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2603      1:125-133       9       QAHFTAVAD       1.310573        -0.726705
HLA A*0211      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2501      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0301      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA B*3801      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0201      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2501      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*0101      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*5401      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*5401      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2501      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*6801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2601      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1517      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0201      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2402      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*7301      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*0203      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4001      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*4501      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*1801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*2301      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*3301      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0201      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*4403      1:23-31 9       FSGDGSLDT       1.018949        -0.464235       -4.6
HLA A*0250      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*3002      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA B*0801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*3501      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*8001      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3201      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*3101      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2601      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.3
HLA A*0201      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*2602      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.6
HLA B*1501      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0206      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*4403      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*6802      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -3.9
HLA A*2602      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*3901      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1517      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*3001      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.2
HLA A*2402      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0212      1:283-291       9       EQIDALAAD       1.034490        -0.877963
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HLA A*1101      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*6802      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*6901      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2402      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0101      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*4601      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0250      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0211      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.1
HLA B*4601      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*0202      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2602      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*0203      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0211      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4601      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.3
HLA B*0801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*1501      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*0702      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*3201      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*1101      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2403      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*0201      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*0216      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.1
HLA B*5701      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*5301      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*2602      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*0801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*0216      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2501      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3301      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0212      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0216      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*5101      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0202      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA B*1502      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0301      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1517      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*3001      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3201      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0101      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0202      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*2301      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2603      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA B*1517      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5101      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0203      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4001      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2601      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*0212      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*3101      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*6801      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA A*0101      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*3002      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*0101      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5701      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*6901      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*6802      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4601      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0219      1:96-104        9       RLAKACAAE       0.864579        -0.552025
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HLA A*6802      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4403      1:192-200       9       SGDDALNLP       0.729648        -0.147874
HLA B*7301      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0250      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.5
HLA A*2902      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4402      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*6801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4001      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*2501      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*4601      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA A*0216      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*0216      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0250      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*2601      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*3002      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA B*4601      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4002      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA A*6802      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0202      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*3501      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*1502      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*3001      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0212      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*0702      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*1101      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2602      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4001      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*2402      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2902      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*8001      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*8001      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*3101      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*1801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0203      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*0219      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.3
HLA A*0202      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3101      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.3
HLA A*0219      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*2902      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*1101      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*3001      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4501      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*0803      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*8001      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*3101      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*6901      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.2
HLA B*4601      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2402      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1509      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4002      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.6
HLA B*1501      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA A*0212      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*5801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4501      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.5
HLA A*0250      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0250      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.1
HLA B*3801      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA A*3001      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
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HLA A*2403      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*1501      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.2
HLA B*4002      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*7301      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2402      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.5
HLA B*3501      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3101      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0250      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4601      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*0206      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA B*7301      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*6802      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*3901      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0702      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*6802      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*3001      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4403      1:199-207       9       LPWLAMGAT       0.875406        -0.300985
HLA B*3901      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*1501      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*2601      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1502      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.6
HLA A*2403      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4402      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2602      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.5
HLA A*6901      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0212      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*5701      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*3301      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.6
HLA A*0201      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA B*1503      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*5801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*0101      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*2705      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*4601      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA B*5301      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*5301      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*0202      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*6901      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*3901      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*4601      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*4001      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.3
HLA A*2603      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0211      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*3101      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*0702      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*3001      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.2
HLA B*1503      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2603      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.6
HLA B*0801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4501      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA A*2403      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*0801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*1501      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*2705      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*0101      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0212      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*4601      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
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HLA B*4601      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0212      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*3301      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*6801      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*5701      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*5701      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1509      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1501      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5701      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0203      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA B*2705      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*1502      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*4001      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*6801      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.6
HLA B*4402      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0301      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA A*0301      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0202      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2501      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*1501      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA B*1517      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2602      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*2403      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*0801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*3501      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5701      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA B*5401      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4001      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2403      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3002      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2601      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*6901      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0203      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*6801      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA B*4402      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0219      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2501      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0250      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*0702      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*4001      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.3
HLA B*5701      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2601      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0702      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5701      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*0219      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*4501      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*5801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0219      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*1501      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*1509      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*4403      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*2705      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*1101      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*0702      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.3
HLA A*0212      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0301      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3001      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0201      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
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HLA B*1503      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*2705      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*3501      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*5801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0202      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2501      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*3002      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.0
HLA A*0301      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2601      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*3101      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0216      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2501      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0219      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA B*3901      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*5701      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2403      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*0802      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0202      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA B*4801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*0203      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*4801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*1501      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2902      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.2
HLA B*4403      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*1503      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*0202      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0201      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5401      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA B*4501      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4601      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*1101      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*6901      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*4601      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*0801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0802      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA B*5801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*2601      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0101      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2403      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*3001      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.2
HLA B*1801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*0702      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*1501      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3101      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*7301      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4001      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2403      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*1503      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*5101      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*4002      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.6
HLA A*6802      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*6901      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*8001      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*0702      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*0801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*6802      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*2902      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
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HLA B*0803      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2902      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*4001      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*3501      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*0202      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.4
HLA A*0203      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0203      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*0301      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*1101      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*4001      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*8001      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA B*3801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*1517      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*2705      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0301      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2403      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0219      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*2301      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3301      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*6901      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*0211      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0203      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*4501      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0212      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*8001      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*2902      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*6801      1:282-290       9       PEQIDALAA       1.082927        -0.508857
HLA A*0301      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0101      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4002      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4501      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*5301      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*4601      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*7301      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2602      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*4402      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*4501      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA A*6901      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*0801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1501      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3101      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0702      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*3201      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*0301      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*3901      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*3501      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*2705      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*4601      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2602      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.6
HLA B*3501      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*0802      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA B*5701      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*0802      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*3002      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*0702      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3301      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA A*6901      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4402      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
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HLA A*2602      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0203      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.1
HLA A*2601      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*1502      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA B*4601      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*6801      1:119-127       9       PPQRGLQAH       1.106596        -0.542455
HLA B*3901      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0216      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*2705      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4402      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*3901      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*8001      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1509      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0203      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*1503      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*1517      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2603      1:197-205       9       LNLPWLAMG       1.133498        -0.594535
HLA B*4002      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0203      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2603      1:67-75 9       IELLRAVLE       1.189071        -0.675585       -4.6
HLA A*0211      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*5801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5701      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*0702      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*0802      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5701      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0101      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*3501      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*5101      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*2601      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA B*4002      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*2301      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5701      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0212      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*0216      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*4801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*1501      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0101      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*2705      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*6802      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*0212      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*0201      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*0702      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*1502      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA B*0801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*5301      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*3201      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*0101      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*1101      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*8001      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2902      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*3101      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3101      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*0802      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*4801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0211      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*4601      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1517      1:232-240       9       DIATARKIN       1.021962        -0.656634
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HLA B*1801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*3301      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA A*0219      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*4002      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*4001      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*2705      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*3101      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0216      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3201      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*0801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*1509      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3201      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*6801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0219      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*6901      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*4801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*0801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2603      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*2501      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*3001      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4403      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA B*5401      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4402      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2501      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*2601      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4403      1:83-91 9       IAGAGTYDT       0.855598        -0.324671       -4.6
HLA A*1101      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*2403      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*0201      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2902      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0702      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2602      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA B*3801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*1501      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*6801      1:35-43 9       ARLANHLVD       1.114191        -0.561626       -4.6
HLA A*0201      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2603      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA B*1502      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*2705      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1503      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*4002      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA B*4501      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA A*3101      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*1501      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.3
HLA A*8001      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0206      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*5801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1502      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*0801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4501      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA B*4501      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*3901      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4403      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0219      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*4403      1:278-286       9       VAATPEQID       1.287811        -0.753085
HLA A*0212      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*3901      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0219      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
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HLA B*1517      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*0202      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0301      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*2705      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*2902      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3101      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0201      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*5801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*5101      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*1517      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*3501      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1517      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*0219      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*0201      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA B*1801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1501      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0219      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*3002      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*2602      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA B*4002      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA B*1801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4403      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2902      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*3201      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*8001      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*2402      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4403      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*0801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3101      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4403      1:54-62 9       TTGESPTTT       0.916232        -0.409402       -4.6
HLA A*0219      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5701      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*0203      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0212      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0206      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA B*2705      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*2403      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4402      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*2501      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*0802      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0201      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4402      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*8001      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*3501      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2601      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2902      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*0301      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0301      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*1101      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0216      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0203      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.2
HLA A*0219      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0101      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0203      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*4801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1509      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*3501      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0702      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA A*0219      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*4402      1:283-291       9       EQIDALAAD       1.034490        -0.877963
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HLA A*0301      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*6801      1:268-276       9       IDVGDPRLP       0.589892        -0.059154
HLA A*0250      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*2705      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2403      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*0203      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*2705      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*3001      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.1
HLA A*1101      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA A*3002      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*1801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*5101      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA A*0201      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0101      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*4402      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*4501      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0211      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0301      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*4402      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4601      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0101      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1517      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3501      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2601      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.3
HLA A*3101      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*4402      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1501      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2601      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*8001      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*0202      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.1
HLA B*1503      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*3101      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*6901      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*6901      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0206      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*0212      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1517      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1509      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0212      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*5801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3501      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*2403      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*6901      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*8001      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*5701      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0216      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*2301      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2501      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*1501      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2601      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0219      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2402      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*3901      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0802      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*4402      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1503      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2902      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0250      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4601      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*0101      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
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HLA B*4002      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*4501      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*5101      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*3501      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0201      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*0702      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0301      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*3801      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4402      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4601      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*4403      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*5101      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*5801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*0801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*0212      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3001      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*5801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*0801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0203      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*3301      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*3301      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA B*5801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0702      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*6901      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA A*0101      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*0101      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0250      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2602      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA A*6901      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0802      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*0202      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0250      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA A*3201      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*4403      1:143-151       9       DIPGRSAVP       0.601914        -0.066395
HLA A*8001      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2603      1:71-79 9       RAVLEAVGD       1.114775        -0.605261       -4.6
HLA B*4403      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA A*2402      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*1503      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*1101      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*0802      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*6802      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2603      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*3101      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*1101      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0216      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*3002      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*3101      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0203      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5701      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2902      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*6801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA A*0219      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*4001      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*4501      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA A*1101      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*4001      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*3002      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0216      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
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HLA B*0803      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0301      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*2601      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4601      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1509      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*1101      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*1502      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0216      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*5701      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1517      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*3801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*1801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*0803      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*5401      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0216      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*0211      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*5101      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.4
HLA A*2403      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0212      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*4002      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0219      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA A*3201      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*2601      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*3002      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*6801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*0101      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*1101      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*5701      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*5801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*8001      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*4001      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*0802      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0216      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*6901      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*0802      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*2501      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*3901      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*3301      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4001      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*1502      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0216      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*0702      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*4402      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0212      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*5701      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*1517      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4402      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2403      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0301      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0802      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA B*1501      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2403      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2601      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2501      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3101      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA A*0216      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*0803      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*0803      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4403      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA A*8001      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
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HLA A*2501      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*3101      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.2
HLA A*0101      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4002      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA A*0203      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*6801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*4403      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*3501      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*3201      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*5301      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*5301      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4601      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*2705      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA A*6802      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4402      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*3901      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA B*5101      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*0803      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0206      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.2
HLA A*0212      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4001      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*3101      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5101      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*4002      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA A*0201      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*0802      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA B*4601      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*1502      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*6802      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0702      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*0801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*0219      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*2403      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1503      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.4
HLA A*2301      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*0201      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*1509      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*2501      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0216      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*1502      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*0301      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*4601      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*1503      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*3201      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*0803      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0202      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3301      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*4801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2403      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*4601      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4402      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3301      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*6901      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0101      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*0219      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0101      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0212      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*0702      1:222-230       9       RELLSAFGS       1.147038        -0.900421
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HLA B*0802      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*0201      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2403      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0250      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.3
HLA B*4001      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*6802      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4001      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*6802      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2602      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA B*5401      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*4601      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA A*2601      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2902      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4001      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*2902      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*2402      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA A*3201      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0301      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4001      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4501      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*3501      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0211      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2501      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*2601      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0301      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1502      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*4801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*0201      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0203      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0212      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*6801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*4501      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0206      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1503      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*3002      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2403      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*1801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA A*2603      1:97-105        9       LAKACAAEG       1.019107        -0.524160
HLA B*0803      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.4
HLA B*3501      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*5701      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4601      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5101      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*1503      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3001      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.2
HLA B*0802      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*5801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*4501      1:155-163       9       DTIRALASH       0.889608        -0.411090
HLA B*4801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*2902      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA A*0101      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*1501      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.3
HLA B*5701      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*5701      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2603      1:37-45 9       LANHLVDQG       1.055014        -0.563924       -4.6
HLA B*5101      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*6901      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*3001      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1509      1:112-120       9       VTPYYSKPP       0.288012        0.075481
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HLA A*8001      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0219      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1502      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*0101      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0206      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4001      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*3001      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5701      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0301      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1517      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*0803      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*3501      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*3901      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*8001      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*3301      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4001      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*6802      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*1503      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA B*4801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*2705      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*4801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*8001      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0101      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2602      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4001      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0702      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0219      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0216      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0201      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2403      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*6801      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*0216      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*4601      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*0702      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*3002      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*2501      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*1801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA A*8001      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*5301      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*1801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*3501      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*2705      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*2403      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*3501      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*3101      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2601      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0702      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0101      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*1101      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*6901      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3002      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*4501      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -3.9
HLA B*5101      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
HLA A*3101      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1501      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*6801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3901      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.4
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HLA A*2501      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0212      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*0219      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2301      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*3901      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*0203      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*3501      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2902      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*6801      1:265-273       9       LQGIDVGDP       0.433298        0.065250
HLA A*2501      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.4
HLA B*5101      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA A*1101      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0101      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1502      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.2
HLA B*0801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0206      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0202      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*4403      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*3901      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4403      1:269-277       9       DVGDPRLPQ       0.678673        -0.190982
HLA B*1509      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*5101      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5701      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*0801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1517      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.2
HLA B*5701      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*3101      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*4801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*4002      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*6802      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*0802      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*0803      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*2705      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0212      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2301      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*5701      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*3001      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2902      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2902      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA A*2403      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*6801      1:164-172       9       PNIVGVKDA       0.977638        -0.485935
HLA A*0301      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*1801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0201      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.3
HLA A*2602      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0301      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA A*1101      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1503      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*2902      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*5801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2603      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.4
HLA B*0803      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0206      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*1503      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0803      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
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HLA A*3002      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*2403      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*0803      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*3301      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*4801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*5401      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2501      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA A*0211      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2403      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0206      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*1509      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA A*6802      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*0216      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1801      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*1101      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*1517      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*3501      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*1101      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0101      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2501      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4402      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0201      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*1101      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*1517      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2902      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*3801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*0201      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0211      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*4801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3001      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5701      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*3901      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*3901      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0212      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*1503      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0301      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1517      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*4001      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*3501      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2601      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*1801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4402      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*1503      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*3901      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*4601      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*4402      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*5401      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2403      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA A*2601      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0216      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*3501      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2902      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2403      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2301      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*1517      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*1517      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*3901      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*4801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*0211      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
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HLA B*5701      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2402      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1503      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5101      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.4
HLA B*1502      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.4
HLA B*5301      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*2601      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.3
HLA B*5701      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*3002      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4601      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0803      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5401      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0216      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*2602      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4601      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*1101      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*2403      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA A*0216      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1517      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*2403      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*0802      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*0702      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0216      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0212      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*0802      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*1101      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2902      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*5301      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*1801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0202      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*6801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*6802      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3101      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1502      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*8001      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2501      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*7301      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2602      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4501      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*7301      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0219      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3002      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*4001      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*6802      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2301      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*3801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4402      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*0801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*0702      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*8001      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0212      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*0802      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0201      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5401      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*0702      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*6801      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4001      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*0802      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*1509      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
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HLA A*0219      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4601      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*1517      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3301      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA B*4403      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2602      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*1503      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0803      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.4
HLA B*1517      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.1
HLA A*6802      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*0802      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1517      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1509      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*2403      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*0702      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*7301      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*8001      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4001      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*3901      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4402      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0206      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*8001      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*1801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*2705      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*1801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5101      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1509      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*0250      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*2501      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*4402      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0219      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0211      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*7301      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*6901      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*5101      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*1503      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0702      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*5301      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*1503      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*0802      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5701      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1501      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4001      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2603      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*2403      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1501      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*0801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0203      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*5401      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA A*6802      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2601      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA A*8001      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*2301      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*1509      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0803      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*1101      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*3101      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*0803      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
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HLA B*4402      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*0203      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*0702      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.1
HLA A*6901      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5101      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0219      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*4601      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0802      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*2705      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*0203      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0203      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2501      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*5401      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*1509      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA B*1501      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*4402      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2603      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2402      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0206      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.1
HLA B*3501      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*0702      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0206      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*0101      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3002      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*6802      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*1101      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2601      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*0211      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0212      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*1101      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*2705      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*4001      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5101      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0201      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*4801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*1501      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*1502      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*3801      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*7301      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA A*3001      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*5101      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1509      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA A*2603      1:137-145       9       LPMLLYDIP       0.585002        -0.130832
HLA A*2301      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*1502      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*0802      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*4001      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*3001      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.2
HLA A*0250      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0203      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*5101      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*0801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0211      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*5701      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1501      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5401      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*4801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*3501      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
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HLA B*4501      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA A*0301      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3901      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0212      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*0212      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*5401      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2501      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*3801      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*1517      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*1517      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*1101      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*1502      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*0212      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2902      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4402      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2501      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2402      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2301      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3101      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*2705      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0201      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3501      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*0202      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0211      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*4002      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*5701      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0219      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*2705      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*6901      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2301      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*2902      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0216      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*1503      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*8001      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*8001      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2902      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA A*1101      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*7301      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA B*4601      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1503      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA A*0211      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1509      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*4001      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*3101      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1503      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0250      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA A*0216      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*5701      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0206      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*3101      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0203      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3002      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*4801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0301      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2501      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*2603      1:259-267       9       SKAGLRLQG       0.969041        -0.533028
HLA A*3201      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.5
HLA B*1502      1:112-120       9       VTPYYSKPP       0.288012        0.075481
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HLA A*0211      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*2705      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0206      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*1101      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*0803      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*5401      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*5101      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*0206      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*3201      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*1501      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*4801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*7301      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0101      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.3
HLA B*0801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*0201      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*6901      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2603      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2902      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2603      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*4402      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*4601      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*4601      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*0801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0250      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*3901      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2403      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3901      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1503      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.2
HLA A*0301      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*1101      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2402      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.6
HLA A*0301      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*0203      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*3001      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.2
HLA A*3201      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0201      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1502      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2301      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*4801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0250      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3002      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2403      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*0702      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*6901      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5401      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*0219      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*0201      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*5801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*2705      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*3901      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*3501      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA B*1801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*0802      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*0203      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*1801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*2403      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4601      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*4402      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*0802      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*2705      1:178-186       9       SGAQIMADT       0.651538        -0.402723
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HLA A*0211      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*3901      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0211      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*6901      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*2402      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*2705      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0203      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*0801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*0702      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0301      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0211      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2601      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5401      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*0201      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*0101      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0702      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2301      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0219      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*0202      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA A*3101      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*0206      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*3801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0202      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*6802      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*5401      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*1503      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*2301      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*0702      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0101      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0250      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*1509      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2301      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2301      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*1501      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0202      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3301      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*3002      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*1517      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*8001      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*7301      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*1509      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0250      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*0211      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0250      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2301      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA B*0702      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*0801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4601      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*4801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0803      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0202      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*1509      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*2501      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA A*0211      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*3901      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.4
HLA B*2705      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0803      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*0202      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*6801      1:112-120       9       VTPYYSKPP       0.288012        0.075481
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HLA A*6802      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0803      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0702      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2301      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*2301      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA B*3801      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*0219      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1509      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA B*4601      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*5101      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0101      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*1517      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*1503      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0101      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*0803      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*5101      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0803      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2601      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2602      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*2602      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*5701      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*0212      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*3002      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*7301      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*7301      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*7301      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*3801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0219      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0301      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5701      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*7301      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0202      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*1509      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*3001      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4402      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*4402      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2902      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2603      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA A*0203      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5701      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0101      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*0301      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*3801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*4801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4001      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5401      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*2601      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*8001      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*5801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2301      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*3002      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*2705      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.2
HLA A*3201      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*8001      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4601      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0206      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0212      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0216      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*5101      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2902      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
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HLA A*2402      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1517      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*4501      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*5101      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.4
HLA B*0802      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0219      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5401      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4501      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0211      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0211      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*6801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*3901      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5401      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*3801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*5701      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*3001      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0250      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4601      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*6801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*0802      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0201      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*6901      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*3101      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*2705      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*1101      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5101      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3201      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0201      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4403      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*2601      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*3101      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2403      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2501      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*0702      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*1502      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA B*4403      1:160-168       9       LASHPNIVG       0.939536        -0.515513
HLA B*1517      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2902      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0201      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2902      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*0702      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*6802      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*8001      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*4801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1517      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*3201      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*0206      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0202      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*2603      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3801      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA A*2902      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*0802      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2501      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0206      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*0101      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*4601      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2602      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5401      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0101      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5701      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
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HLA B*1517      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*3901      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*2705      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*1101      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*5301      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0301      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*0206      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*5301      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2603      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*4601      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*3801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*0803      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2402      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*0801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*5401      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*4001      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1509      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*0206      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*4402      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*5301      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*6802      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3201      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*1101      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0216      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*3101      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3301      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*0250      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA A*0201      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0202      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*3201      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3002      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0802      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0803      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA A*0219      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4601      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1509      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*1503      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2601      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0212      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4001      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*0212      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.3
HLA A*2602      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.6
HLA A*8001      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*3901      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*5701      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2902      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*7301      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*1502      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0301      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5401      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0211      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5101      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*6901      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*7301      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*0202      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3101      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5401      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*3002      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1509      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
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HLA A*0202      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA B*4001      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*2902      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*4801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4402      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA A*0202      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*3001      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.2
HLA A*3201      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2402      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.5
HLA B*1501      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*3901      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*8001      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1503      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*1502      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*3901      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*3002      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*0802      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4601      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0802      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*4801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2601      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0802      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0101      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*1503      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*3301      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*6901      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1501      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1503      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*1509      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*2402      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA A*3002      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*3101      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5101      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*7301      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA A*8001      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4402      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2402      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0702      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3201      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA B*1501      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3201      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA B*1502      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*3801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*3301      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.6
HLA A*2602      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA B*1801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*6802      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*8001      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*5701      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1517      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA B*3501      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5101      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*1101      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*4801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3101      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*1101      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0216      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
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HLA A*6802      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0250      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4002      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0250      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*2402      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA B*1503      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2403      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*2705      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2403      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*0801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0802      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*1503      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4402      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1509      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*0801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0211      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*4801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*6901      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*3301      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA B*2705      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3801      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*2705      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5101      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*0803      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2601      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*0803      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.4
HLA A*0211      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0203      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*3001      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2501      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*4501      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*0202      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*5801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2601      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5401      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.3
HLA A*3301      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4402      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3101      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*2301      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0211      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*8001      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4001      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0219      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3002      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0203      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0201      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0216      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*3801      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA A*3101      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0216      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2902      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0201      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*7301      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA B*5401      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA A*0212      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*2705      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3001      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*2705      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
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HLA B*0702      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*3901      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2603      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.6
HLA A*2402      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*5301      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*0702      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0203      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*5301      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA A*2402      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*2603      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2902      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*1801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1509      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*5401      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*8001      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*0803      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*5101      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*1101      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0212      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2603      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA B*4402      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*4402      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0301      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4001      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2402      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2601      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.3
HLA B*1509      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*1101      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA A*6801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*2602      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*6901      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0206      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*2601      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*3301      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*5701      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0803      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.4
HLA A*3002      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*6802      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*5101      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*6901      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0101      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0250      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1517      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0201      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*1509      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*0803      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*0803      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*0802      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*0801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*3801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.5
HLA A*3301      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*2403      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*1502      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.5
HLA B*3801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0211      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0216      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*3002      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.5
HLA B*1501      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5701      1:283-291       9       EQIDALAAD       1.034490        -0.877963
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HLA B*4002      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA B*5401      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*0702      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2402      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*4501      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.6
HLA A*0206      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1509      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*2501      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*6801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2601      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0212      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*1509      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*1501      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*0301      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*0803      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0250      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0250      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*4403      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA A*0250      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*6801      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA A*3002      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*3201      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*0301      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2301      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA A*8001      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*1101      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0216      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*1517      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*0206      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4601      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*2902      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0219      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*2301      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4002      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.6
HLA B*3901      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2301      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*1509      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*0801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*2603      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.6
HLA B*3801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5301      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*5301      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA A*0250      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5301      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA B*5101      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*0216      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*3002      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2301      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0216      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0101      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2301      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4402      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0803      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0206      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5101      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2601      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0702      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
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HLA A*0101      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*0802      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2402      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*1503      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*0201      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2602      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2902      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0219      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2403      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*3501      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0211      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0250      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*4001      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5401      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0212      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*1801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5301      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*7301      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*1503      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*6901      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4001      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*4601      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*1503      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*1801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5701      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*2705      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*5101      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1502      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.5
HLA B*1801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2501      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2403      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1502      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*3201      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*0203      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3301      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*3301      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*3501      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*3901      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.5
HLA A*0201      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2403      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*5401      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*3002      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.5
HLA B*3901      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*8001      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0219      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2602      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0206      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0803      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*0803      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*1503      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA B*7301      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*0203      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*8001      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*1801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5401      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*8001      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*0802      1:179-187       9       GAQIMADTG       0.852490        -0.651340
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HLA B*3801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*4001      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0202      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*3901      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.4
HLA A*3201      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4402      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5701      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0803      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0202      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*3901      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*8001      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*2705      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*7301      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*1509      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0802      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2301      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2501      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.4
HLA B*4002      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*0206      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*1501      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2301      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4601      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*1101      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4601      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4501      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*0206      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*5701      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1503      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3901      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*1501      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA B*0801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0219      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*3801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*4801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0212      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4001      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0212      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3301      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA A*2602      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.6
HLA B*5101      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0101      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*2601      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2601      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*2301      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA A*0250      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA A*6801      1:25-33 9       GDGSLDTAT       0.949152        -0.565874       -4.6
HLA A*2603      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*3801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA A*0101      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*2705      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2902      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1509      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA B*3801      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*3002      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*0803      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2602      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0301      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3301      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*3501      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
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HLA A*1101      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2602      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*2705      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*1502      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.5
HLA A*8001      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*7301      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA A*1101      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*3002      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*0803      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1509      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*0202      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*5701      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*1502      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*8001      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3301      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*7301      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*3002      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*4501      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*2602      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA A*2602      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA A*2603      1:148-156       9       SAVPIEPDT       0.514525        -0.170199
HLA B*4402      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*0801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA B*1502      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*1101      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*2301      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0211      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0250      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*2705      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4501      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*0803      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*5701      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5101      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1517      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1501      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*7301      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*4001      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*0216      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*0206      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA B*4403      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*5301      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*4001      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*1502      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA A*0250      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*3501      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*1502      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA A*2403      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*0802      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*3301      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*1517      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*6901      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA B*1509      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*0702      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*1501      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA A*3201      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA A*3301      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5701      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
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HLA B*5401      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*2705      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*1501      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0219      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*0802      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1502      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*1801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0219      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*1501      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5301      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2603      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.5
HLA B*5401      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0201      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.3
HLA A*3002      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0219      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4402      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*6802      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0301      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3201      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*1502      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*3801      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA B*1801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2602      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2602      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*1101      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*5301      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.6
HLA A*0216      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*6802      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*0702      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*6901      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA A*3301      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.6
HLA A*2403      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*7301      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4403      1:232-240       9       DIATARKIN       1.021962        -0.656634
HLA A*3201      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*1502      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*4403      1:112-120       9       VTPYYSKPP       0.288012        0.075481
HLA A*2902      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*0203      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2603      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*5401      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*4501      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*1801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA B*4002      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*5301      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA A*2402      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*1517      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*4601      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3201      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*5301      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4402      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*6801      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.6
HLA A*0211      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*3301      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA A*3201      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.6
HLA A*0212      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5301      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA A*2301      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*5301      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*5701      1:288-296       9       LAADMRAAS       0.960186        -0.877468
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HLA A*3101      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*6802      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*1101      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*7301      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5101      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*0203      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*3801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0216      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0101      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4501      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.6
HLA A*2402      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*2705      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*1509      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*0211      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.2
HLA A*0212      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA A*2402      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2402      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*4002      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA B*0802      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3002      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1517      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*5701      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*0803      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*1101      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*3501      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4403      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*0802      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2501      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2301      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0802      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA A*2403      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*1501      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1509      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0216      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2603      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*6801      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.6
HLA A*2301      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*3002      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*3801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*0702      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0202      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2602      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*4403      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.0
HLA A*3301      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA A*2403      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0211      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*3901      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.4
HLA B*0702      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2501      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2501      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*8001      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*2602      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA A*2602      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*6901      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA B*0802      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*6901      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*6802      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2402      1:171-179       9       DAKADLHSG       0.945966        -0.677091
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HLA A*0203      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0702      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0802      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0201      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*3801      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*0702      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1517      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0212      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*3201      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*4601      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0211      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5101      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*3002      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*2705      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA B*4403      1:31-39 9       TATAARLAN       0.966344        -0.631748       -4.6
HLA B*4002      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0250      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.5
HLA B*3801      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*4402      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0206      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5401      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*5401      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*1801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*5801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*3301      1:6-14  9       FDVAARLGT       0.776247        -0.460870       -4.6
HLA B*3901      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2501      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*4403      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.6
HLA B*3501      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4501      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*4501      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA B*1502      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*2705      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0301      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA B*0802      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5401      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*0801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0211      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*4002      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.6
HLA B*4801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*1801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0201      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0250      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*3301      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*3501      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*0203      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4001      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2601      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5401      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*2705      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*3801      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1502      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*8001      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0212      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0219      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0219      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2501      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*7301      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*0301      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
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HLA B*5701      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2603      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*1509      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4403      1:16-24 9       LTAMVTPFS       1.254828        -0.955699       -4.6
HLA B*4002      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4002      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*4601      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0219      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*0101      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0250      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*0802      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4501      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*6801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2902      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*2601      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*5101      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2902      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*1101      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2603      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA B*1503      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*0803      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*2501      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*0803      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0203      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*3801      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*3301      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*0801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2402      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*6801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0212      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*3002      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*3901      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1502      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*4501      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*0702      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*0211      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA B*1509      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2501      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0211      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*3101      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5101      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*2603      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA B*4001      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*2501      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*0250      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*2501      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*1101      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*1502      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*0802      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*0216      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA B*3801      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*5401      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*1517      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2603      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA B*5101      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*7301      1:178-186       9       SGAQIMADT       0.651538        -0.402723
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HLA A*0212      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2603      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.6
HLA A*2602      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.6
HLA A*2402      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA A*2602      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*6901      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*3501      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4403      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*5801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*3201      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA A*0211      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*0702      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0301      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2603      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*2301      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2301      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*0202      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0301      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*6801      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA B*0801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2301      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA B*5801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1517      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*6802      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0211      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2601      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4501      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*1503      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2501      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA B*4002      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*5301      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*3801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*3001      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*3201      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3002      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*6801      1:39-47 9       NHLVDQGCD       1.025978        -0.694560       -4.6
HLA A*0301      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*0206      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0219      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4002      1:18-26 9       AMVTPFSGD       0.939719        -0.635778       -4.6
HLA B*1509      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*0219      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*1101      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0219      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0250      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*3002      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA A*3301      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2601      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0216      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3201      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA B*5301      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*2402      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4402      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA B*4002      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.6
HLA B*3801      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*2301      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*3501      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0301      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*0201      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
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HLA B*5101      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2602      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*6802      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*2902      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4501      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.6
HLA B*7301      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*3201      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*1502      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*2603      1:221-229       9       LRELLSAFG       0.918587        -0.597836
HLA A*0202      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2301      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5301      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2402      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA B*4801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0101      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*5401      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0201      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5101      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2402      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0219      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*6901      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*0301      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*2301      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0702      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1502      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*2501      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4403      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA B*3801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA B*3901      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0250      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA A*0101      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*3002      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0301      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*5301      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*0202      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5401      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*0101      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*6801      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*6901      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1509      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2301      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2402      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*1101      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*3001      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.2
HLA B*4403      1:82-90 9       VIAGAGTYD       0.956039        -0.641407       -4.6
HLA B*1501      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*7301      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.5
HLA B*4002      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.6
HLA A*1101      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3002      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*0801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2603      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*1502      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*1801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*3001      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5301      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA A*3201      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*7301      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.5
HLA B*3501      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0101      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
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HLA B*1502      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.6
HLA B*1801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1503      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2403      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2902      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2902      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.2
HLA A*1101      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0216      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*3801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5101      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*1509      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2402      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*6801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*0250      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0250      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*8001      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5301      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4002      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*8001      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*0801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*1801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1502      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*1517      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5101      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA B*7301      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3201      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*5301      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0803      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*0803      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*4402      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*1801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*2402      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4501      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.6
HLA A*3002      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3501      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0216      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2601      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA A*0206      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0211      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*0101      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA B*5801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*2402      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3201      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*8001      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*3101      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2602      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.6
HLA B*0803      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*0206      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*4501      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0206      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0202      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*0803      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.4
HLA A*3101      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA B*4002      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*0101      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*4403      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*1509      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0216      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
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HLA B*5101      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4501      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA A*2601      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*0201      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.3
HLA A*2601      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0101      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*3501      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2603      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA A*0201      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*3201      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.6
HLA A*3201      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA A*6801      1:45-53 9       GCDGLVVSG       1.100568        -0.772490       -4.6
HLA A*2603      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA B*3801      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*2301      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*2603      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*2705      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*0216      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1502      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA A*0211      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*0803      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4501      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4501      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4601      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*1101      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*3301      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*2402      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA A*0212      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1502      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2603      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2402      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*3301      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2402      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*1801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4001      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0201      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*3801      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4601      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*3901      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*4002      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0216      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0802      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4501      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3101      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA A*3301      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.6
HLA A*0202      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2403      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*5101      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0802      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*1501      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*4403      1:96-104        9       RLAKACAAE       0.864579        -0.552025
HLA B*4001      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*3002      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0202      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA A*3101      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*1517      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0250      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*1517      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
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HLA B*7301      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*5101      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*6901      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*3801      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*6801      1:77-85 9       VGDRRVIAG       1.023853        -0.703636       -4.6
HLA B*5301      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2602      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*5101      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4403      1:47-55 9       DGLVVSGTT       0.855967        -0.555149       -4.6
HLA B*0801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3002      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*0702      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6802      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*1502      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0211      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*4402      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4601      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*0201      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*4601      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0219      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*8001      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA B*4403      1:243-251       9       VAPLCNAMS       1.168328        -0.866100
HLA B*4601      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.3
HLA B*2705      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2601      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4001      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3001      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3301      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA B*5401      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*3501      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*3201      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.4
HLA A*3301      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*0802      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*2403      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.2
HLA A*8001      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0203      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.2
HLA A*6801      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA B*4403      1:264-272       9       RLQGIDVGD       0.959637        -0.667073
HLA A*2301      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1509      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0101      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*0801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*3101      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*6901      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0201      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.3
HLA A*2501      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4501      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*0211      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*4002      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3002      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*2301      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*3801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5101      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0202      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*2301      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*3101      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0201      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
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HLA A*6801      1:46-54 9       CDGLVVSGT       0.814162        -0.542320       -4.6
HLA A*2601      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*3901      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2602      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2402      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*1801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA B*0702      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1502      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*2402      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA A*2603      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*3901      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4002      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0201      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*5301      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.5
HLA B*4002      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*5401      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*7301      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*3501      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*1101      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*6802      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4402      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4002      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0802      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2603      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*1517      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*1503      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA B*3901      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0803      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.4
HLA A*0202      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0203      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*3801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*0211      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0250      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2403      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*3002      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*8001      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*1801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*3101      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*1101      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA B*4601      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0212      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1501      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*3101      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*7301      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*4001      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1509      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*2301      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*0801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*3001      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA A*8001      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*2403      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*4001      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3002      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2403      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*3201      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*4402      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*0216      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0206      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*2402      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
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HLA A*0206      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0202      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*3002      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2402      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0206      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*3301      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA B*0802      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3201      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*3901      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3201      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*2705      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4002      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA A*0216      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4601      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4402      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0206      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2602      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*4403      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*3301      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5701      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*1503      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4002      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA A*3301      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2501      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0219      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*3002      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0301      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5701      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*1503      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4601      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1503      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0202      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA B*1509      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*0802      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*5401      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*6901      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*5401      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*3201      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*0801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*0250      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA B*4001      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*1509      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4501      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*3501      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*5301      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA A*2501      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2601      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*3301      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*3801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4001      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0212      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*7301      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4002      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*0250      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2501      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*2602      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA A*0250      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA A*3301      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*6802      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*7301      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
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HLA B*5301      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA A*2501      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2402      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5401      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0219      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*7301      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0250      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*4001      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*3901      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA B*1517      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*3801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*6901      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5301      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4001      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1503      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0301      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4403      1:185-193       9       DTGLAYYSG       1.027506        -0.755761
HLA B*1502      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.5
HLA B*0802      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*1502      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*5701      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*8001      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0301      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*5301      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*0803      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*0801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2603      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*4403      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA B*5401      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5701      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*5801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*5701      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5101      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*3101      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*0206      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3201      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0203      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*5701      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*0702      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*7301      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0216      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*0202      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0250      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*4501      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*0803      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5701      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0216      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2301      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4501      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*2902      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4402      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*1801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*4801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5401      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*3901      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6801      1:200-208       9       PWLAMGATG       0.971053        -0.678314
HLA A*6802      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0212      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
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HLA B*0802      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA A*6802      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0212      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*5401      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*4403      1:178-186       9       SGAQIMADT       0.651538        -0.402723
HLA A*2902      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*5401      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA A*2602      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.5
HLA A*2301      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2402      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5101      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*0802      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4501      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*6801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA A*0101      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0202      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2902      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*3002      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA B*0803      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1503      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*2403      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2301      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*5301      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA B*0801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*0803      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*5101      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.4
HLA B*4402      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*1101      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*2902      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*4801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0203      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*3801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*6801      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2602      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*0212      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*3301      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*4403      1:171-179       9       DAKADLHSG       0.945966        -0.677091
HLA B*4402      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*4501      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*3301      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0206      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*7301      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*4403      1:247-255       9       CNAMSRLGG       0.914644        -0.661232
HLA A*2602      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2301      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*5101      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3002      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*5401      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*0219      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*6802      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2403      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*1101      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0206      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*2403      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*2301      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA B*4002      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*3801      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*3801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2403      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
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HLA B*0803      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4402      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1502      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA A*2902      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*5401      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0211      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2403      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0203      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*3301      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*4403      1:44-52 9       QGCDGLVVS       1.399806        -1.143256       -4.6
HLA B*7301      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*3301      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.6
HLA A*0203      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*0212      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*6801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*1502      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*1801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*4801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2301      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*8001      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4402      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0211      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*8001      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*5401      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*3801      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1502      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0211      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*3801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA A*0201      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*2705      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*6801      1:222-230       9       RELLSAFGS       1.147038        -0.900421
HLA B*4002      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2301      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*6901      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*6801      1:273-281       9       PRLPQVAAT       0.746744        -0.478283
HLA A*3301      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA B*4002      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2603      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*0803      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA A*2501      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*5701      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*0702      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*3901      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*4002      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.6
HLA A*0250      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*3002      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*6802      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*3101      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.3
HLA B*7301      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1509      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0250      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*1502      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA A*0203      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0206      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2403      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*0250      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.5
HLA B*0702      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0101      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*2603      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
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HLA B*3501      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*4002      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.6
HLA B*4501      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3201      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA B*5301      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA A*0212      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4402      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*4501      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2601      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0702      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*8001      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4002      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4403      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*2602      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA A*2402      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*5801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA B*1509      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4501      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*3501      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4501      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.6
HLA B*4002      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*4002      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5401      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5301      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*1517      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4501      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*3501      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*2603      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*3201      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA A*2902      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*1517      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*0702      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*2602      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*0803      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*3301      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*5701      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*3301      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA A*0219      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0202      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*4501      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.6
HLA A*3201      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*1503      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1517      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*2602      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA B*0801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1503      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4501      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA B*4501      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA A*8001      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*1509      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*1509      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*3801      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2902      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*2705      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4403      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA A*2402      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4403      1:190-198       9       YYSGDDALN       0.627175        -0.397841
HLA B*4501      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.6
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HLA A*2402      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*5301      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA A*2603      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*4403      1:60-68 9       TTTDGEKIE       1.003009        -0.775618       -4.6
HLA B*4002      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA B*3801      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*3901      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*1502      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*5301      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*4403      1:49-57 9       LVVSGTTGE       0.830094        -0.595526       -4.6
HLA B*1517      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*4002      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.6
HLA A*0219      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*5301      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*1509      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1502      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
HLA B*4403      1:57-65 9       ESPTTTDGE       0.984407        -0.769006       -4.6
HLA B*5301      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*7301      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA A*0211      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6801      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2402      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*2603      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*0301      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA A*6801      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA B*0803      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0250      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
HLA A*2301      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA A*8001      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*4002      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*2902      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*7301      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4403      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA A*3002      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*1101      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0212      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1509      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*4801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*0802      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*8001      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0219      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1501      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*6901      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*2705      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*0219      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*3201      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*4601      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*1101      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0250      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*5801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*2603      1:163-171       9       HPNIVGVKD       1.188721        -0.977984
HLA B*5101      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*3801      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
HLA B*5801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3301      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*5101      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0301      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*0702      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4002      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
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HLA A*2602      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*3201      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA A*6801      1:100-108       9       ACAAEGAHG       0.715935        -0.483083
HLA B*5701      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2402      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4002      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA A*0101      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0212      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*2602      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*7301      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*4501      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
HLA A*2501      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*0219      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA B*3901      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*6802      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5301      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2501      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*5301      1:283-291       9       EQIDALAAD       1.034490        -0.877963
HLA B*1502      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*7301      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*3101      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3201      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0216      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*3801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*0802      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0201      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2402      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2902      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*7301      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*3901      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0101      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*0702      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4002      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*5101      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1503      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2402      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA B*4002      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5301      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*0216      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2501      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA A*0101      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA B*1503      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*1502      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1509      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*5301      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*2705      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2403      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*7301      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.5
HLA B*0803      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6801      1:263-271       9       LRLQGIDVG       0.746768        -0.519067
HLA A*0216      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*5401      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA A*2301      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0202      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1502      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4501      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*2501      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1517      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*3801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
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HLA A*0301      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3001      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.2
HLA B*4501      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*2705      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0211      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2601      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA A*3301      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA A*2301      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0219      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*5101      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*3901      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*0216      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*3801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*3801      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0101      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1503      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*4403      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA A*0101      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0206      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4403      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*5801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5401      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0219      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*0802      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3002      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2603      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA B*2705      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.4
HLA B*1801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*7301      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4403      1:211-219       9       SVIAHLAAG       0.685711        -0.488400
HLA B*4501      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.5
HLA B*1509      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*4002      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*1101      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4403      1:70-78 9       LRAVLEAVG       0.692988        -0.485706       -4.6
HLA B*4001      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4403      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA A*1101      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*2402      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0802      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*3501      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0206      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0202      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*0802      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*3201      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3001      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*1509      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*3301      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*1101      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2602      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*8001      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4002      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*2603      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*0702      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2402      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4403      1:140-148       9       LLYDIPGRS       1.070980        -0.868816
HLA B*5101      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
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HLA A*6802      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4403      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA A*2602      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*4402      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*6801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*3201      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA B*5301      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*1101      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*5801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2301      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0211      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*3901      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA B*3801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*6801      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA A*0206      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4002      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*0803      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0201      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*0802      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2601      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*1517      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4501      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA A*3301      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*4601      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2602      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.6
HLA A*0202      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.4
HLA A*0250      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*0801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3101      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*2705      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2501      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*3101      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2402      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2602      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA A*0250      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*2602      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.5
HLA A*6901      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA A*2602      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0216      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0250      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*2705      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*4601      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*2301      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0250      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*5401      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4501      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*4403      1:223-231       9       ELLSAFGSG       0.800983        -0.620040
HLA A*2301      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*0201      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.3
HLA B*2705      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*1101      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*1101      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.4
HLA A*0216      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA B*0801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*3901      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2501      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*0803      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*1517      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*7301      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
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HLA A*6901      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1503      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*1501      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2601      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0301      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*6901      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1503      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0216      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*2603      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA B*4002      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA A*6801      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*3501      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1502      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*2705      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0201      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2603      1:179-187       9       GAQIMADTG       0.852490        -0.651340
HLA B*0802      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*5101      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3002      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*5101      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA B*0803      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*1502      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*0803      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*3101      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.3
HLA A*0250      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1517      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*2601      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3002      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*5301      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5301      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2501      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1517      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*2705      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1501      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*2501      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*0802      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2403      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*8001      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*4403      1:215-223       9       HLAAGQLRE       0.828454        -0.634859
HLA A*3201      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*5301      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*0201      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1509      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*3301      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*4403      1:177-185       9       HSGAQIMAD       1.011435        -0.860878
HLA B*3801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*4001      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*2601      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2301      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*0803      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA B*0803      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2603      1:203-211       9       AMGATGFIS       1.062603        -0.911029
HLA B*0803      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*1502      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2403      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4001      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*7301      1:288-296       9       LAADMRAAS       0.960186        -0.877468
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HLA A*6801      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*3201      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*0802      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4001      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.2
HLA A*2402      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*0211      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2603      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*3901      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*4601      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*3801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3201      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*2602      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4403      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA A*0211      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*3901      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*3201      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2603      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*4501      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*1801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2402      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*1502      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*3301      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0203      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*3301      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA B*4402      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*2402      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*4403      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0803      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*2402      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*6801      1:251-259       9       SRLGGVTLS       0.984260        -0.840497
HLA B*5101      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*4501      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.6
HLA B*5701      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*2301      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2603      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*5701      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*2501      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*6801      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA B*4001      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4002      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.6
HLA A*2501      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0219      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1502      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*2902      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4601      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0211      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*6801      1:5-13  9       GFDVAARLG       0.847984        -0.666475       -4.6
HLA B*5301      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*6801      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2602      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4002      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*3801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6801      1:218-226       9       AGQLRELLS       1.148512        -0.976666
HLA B*7301      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*3201      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*0211      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*3101      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
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HLA A*2601      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2603      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.6
HLA A*2301      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*1502      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*2301      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5401      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4601      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0203      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*4002      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA B*0702      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2603      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.6
HLA A*2403      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1503      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA B*4001      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*4403      1:17-25 9       TAMVTPFSG       0.671965        -0.543000       -4.6
HLA B*4001      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*3201      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5701      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1517      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2301      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*5401      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*2501      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*2602      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2902      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*1101      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*3501      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3201      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*8001      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3501      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*4402      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0202      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*5401      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*0801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*0206      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*5701      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4501      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*8001      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2603      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*5301      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.5
HLA B*7301      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*0801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*0702      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4402      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1509      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*1101      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*4801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*3201      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA B*4002      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.6
HLA A*0212      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3301      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA A*0216      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*3501      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*5101      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*6802      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*3901      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4601      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2602      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA B*1801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0203      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
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HLA A*2602      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.4
HLA A*3301      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*1502      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*6801      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*4001      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3501      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*1502      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*3801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA B*5401      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5401      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA B*4801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1509      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA B*5301      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*6901      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4002      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0212      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*4403      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*3301      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*2301      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA B*2705      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4403      1:19-27 9       MVTPFSGDG       0.614268        -0.473517       -4.6
HLA A*0211      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2602      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*0250      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0219      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*3801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*5701      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*4403      1:115-123       9       YYSKPPQRG       0.715411        -0.564008
HLA A*2301      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4403      1:52-60 9       SGTTGESPT       0.542713        -0.395365       -4.6
HLA B*4501      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*3301      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA B*4402      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*5801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5401      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*2403      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1501      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0702      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2301      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*2402      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*0219      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*0803      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*2603      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA A*0206      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA B*4801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0250      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*5301      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*0211      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*2603      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*0250      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*3801      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*1509      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0206      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*5101      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*3201      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*3002      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*3002      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.2
HLA A*2902      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*8001      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*3801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
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HLA B*1502      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*3901      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*1101      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*6801      1:135-143       9       TELPMLLYD       0.896106        -0.782180
HLA A*2602      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA B*1509      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3201      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4501      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0219      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3002      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*2402      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3002      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4402      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3002      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*0202      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*2603      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*0702      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*0301      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0702      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*4002      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0206      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2602      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*6802      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0216      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*3002      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*5301      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3301      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1501      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.2
HLA B*1509      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*3301      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*2402      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0202      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4002      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*4402      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2402      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*3301      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2301      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*6801      1:167-175       9       VGVKDAKAD       0.974734        -0.840029
HLA B*4002      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA A*0250      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*6801      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA B*7301      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4002      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.2
HLA B*4501      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*2603      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA A*0206      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1503      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*0802      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*0803      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*3801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2601      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5301      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.5
HLA A*2603      1:184-192       9       ADTGLAYYS       1.147424        -1.047288
HLA A*3201      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*5301      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*1101      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*3801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
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HLA A*2402      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*3801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*2705      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA A*2603      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA A*3301      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA B*1502      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*2705      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*8001      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*3201      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*6801      1:261-269       9       AGLRLQGID       0.923499        -0.790235
HLA B*4501      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA B*1503      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.2
HLA A*3002      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*3801      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA B*7301      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*1801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5301      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA B*3801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA B*0802      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA A*1101      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*7301      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*1801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4501      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3002      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4002      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*3901      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2301      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*6801      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA B*1501      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.2
HLA B*1502      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*0212      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*3301      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*0250      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*0211      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0101      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4601      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*2705      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0250      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2402      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*0201      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5301      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2602      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*0250      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2402      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*0802      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*4403      1:48-56 9       GLVVSGTTG       0.796646        -0.701256       -4.6
HLA A*2602      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*3201      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0202      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*0202      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*2301      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.4
HLA B*3901      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4403      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*2602      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.5
HLA A*2402      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*3201      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*3801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*7301      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA B*4001      1:275-283       9       LPQVAATPE       0.597160        -0.764962
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HLA B*4403      1:288-296       9       LAADMRAAS       0.960186        -0.877468
HLA B*5301      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*5301      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1509      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*1101      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0250      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA A*2402      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*5701      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*6801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*1503      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*7301      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*6801      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA A*0202      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.4
HLA B*1502      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1517      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*0802      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2403      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*7301      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.5
HLA B*5401      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*0211      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1517      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*3901      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*3901      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*2501      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*5101      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*0803      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2501      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1509      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1509      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*3901      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5301      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*1502      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2402      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2602      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA B*4403      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA A*6801      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2501      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4403      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA B*3901      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3301      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3001      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA A*0203      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2603      1:147-155       9       RSAVPIEPD       0.741969        -0.671085
HLA B*0802      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5301      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*3101      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2603      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA B*0802      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2603      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA B*4501      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0803      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*3301      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*2603      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA A*2603      1:157-165       9       IRALASHPN       0.524370        -0.458448
HLA A*3301      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA A*2603      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.6
HLA A*2501      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2602      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2602      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
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HLA A*3201      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*5101      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3301      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*1517      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*8001      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4402      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*1503      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*1503      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0803      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3201      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA A*6802      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2301      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2402      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0803      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3101      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA B*4002      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*0803      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*0803      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA B*1801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*6802      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*2603      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA B*4501      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4002      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA A*0219      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*7301      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4501      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA B*5801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA B*4403      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4002      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*3002      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*0202      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*3301      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1502      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*3301      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*2603      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4501      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA A*0250      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5401      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*5101      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0211      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*0301      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA B*7301      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.5
HLA A*2602      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4002      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*5401      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA B*4002      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4501      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*2705      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5401      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*4403      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA B*4002      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.6
HLA B*0802      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5301      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*5401      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2301      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*0203      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*0250      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*1509      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*3201      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
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HLA B*4403      1:55-63 9       TGESPTTTD       1.021077        -0.972491       -4.6
HLA A*3201      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4501      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4002      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*3801      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*2902      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2501      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5401      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2603      1:187-195       9       GLAYYSGDD       0.888672        -0.846678
HLA A*2603      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*0803      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*0216      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4403      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*5801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*1502      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*4002      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA A*0101      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA B*1502      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5301      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0201      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*6801      1:79-87 9       DRRVIAGAG       0.679129        -0.645178       -4.6
HLA B*4501      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.6
HLA A*2603      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0202      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4501      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA B*4403      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*1502      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*6901      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*6801      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*0206      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*4403      1:40-48 9       HLVDQGCDG       0.565791        -0.541228       -4.6
HLA A*6801      1:145-153       9       PGRSAVPIE       1.012324        -0.977546
HLA B*4501      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*4403      1:128-136       9       FTAVADATE       0.744660        -0.731277
HLA B*3801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA A*2602      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*0801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*0250      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA B*3801      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*2402      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA A*6801      1:254-262       9       GGVTLSKAG       0.781785        -0.744635
HLA B*4601      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA B*4501      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.6
HLA B*1509      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*1502      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0301      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*4403      1:246-254       9       LCNAMSRLG       0.720530        -0.698676
HLA A*2602      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0206      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.3
HLA A*2301      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*1101      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2301      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3301      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2601      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*2402      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0250      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*4001      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3002      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*7301      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*1509      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
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HLA A*6901      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*7301      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2902      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*5301      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*4002      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.6
HLA A*0212      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*1509      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2402      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2403      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*5701      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*7301      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.5
HLA B*1503      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*4402      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3301      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA B*7301      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.5
HLA B*3801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*6801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0203      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA A*3001      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2403      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*3501      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*7301      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*3301      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA A*2603      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*3201      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0201      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA A*0250      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0206      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4601      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*3801      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2601      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA B*4403      1:50-58 9       VVSGTTGES       0.859914        -0.870337       -4.6
HLA A*0101      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.3
HLA A*2402      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*6801      1:170-178       9       KDAKADLHS       1.015012        -1.036196
HLA A*8001      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*4801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*5301      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.6
HLA A*0212      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*2603      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0219      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*1502      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*5301      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5701      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*1509      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*3201      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA B*3801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*2602      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA A*1101      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3301      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.6
HLA B*1517      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3002      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA A*0216      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3301      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2603      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*3101      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*0202      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*5301      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*2705      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
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HLA A*2902      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*7301      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*3301      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*0801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*2301      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0702      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*5301      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*4501      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*2603      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA B*0802      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA A*3201      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4002      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*4002      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.6
HLA A*2602      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*6802      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*2602      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0216      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4002      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA A*6801      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA A*0211      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2603      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4501      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*4403      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA B*4402      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*0702      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*2602      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*4501      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA B*4501      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.6
HLA A*0219      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4002      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA B*3801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*6801      1:22-30 9       PFSGDGSLD       0.856394        -0.922121       -4.6
HLA A*8001      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*0801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4403      1:186-194       9       TGLAYYSGD       0.879513        -0.966325
HLA B*5801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2501      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*4403      1:20-28 9       VTPFSGDGS       0.877156        -0.949526       -4.6
HLA B*3501      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4403      1:109-117       9       LLVVTPYYS       0.858672        -0.945214
HLA A*0301      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*1101      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4002      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*3901      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.4
HLA B*4002      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA B*4501      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*7301      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2402      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0802      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*3901      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*4501      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*2603      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*0206      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*0101      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0202      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*1517      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*3002      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2601      1:154-162       9       PDTIRALAS       1.036621        -1.406985
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HLA B*4403      1:224-232       9       LLSAFGSGD       0.750643        -0.852655
HLA A*0250      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2501      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*0201      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*6901      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*2705      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*0211      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*4403      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*5101      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA A*3101      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*0803      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.4
HLA B*0803      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*2301      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*3301      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*6801      1:138-146       9       PMLLYDIPG       0.623540        -0.732617
HLA B*1509      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA A*2602      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*6801      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*3201      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*4601      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1509      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*0203      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1501      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2902      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*5701      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4002      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*0702      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0202      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*5401      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*4801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*6802      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*3801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*4501      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*3501      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0211      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA A*8001      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0212      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2301      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*3801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*4001      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2602      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*2403      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0250      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*7301      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*5401      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*5301      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*4403      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA A*2603      1:275-283       9       LPQVAATPE       0.597160        -0.764962
HLA B*1502      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*3201      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*2402      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*4501      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA B*7301      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.5
HLA A*0219      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*6801      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.6
HLA A*1101      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*2705      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0250      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA A*0216      1:154-162       9       PDTIRALAS       1.036621        -1.406985
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HLA B*1502      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*0802      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1517      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2501      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2402      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA A*3201      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*1801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*3002      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA A*3301      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.6
HLA B*5301      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.5
HLA B*5101      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*3901      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2603      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.6
HLA B*0803      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4002      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.6
HLA B*4403      1:86-94 9       AGTYDTAHS       0.813636        -1.058354       -4.6
HLA B*1503      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*5401      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0206      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2301      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*3301      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.6
HLA A*2602      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.6
HLA A*0211      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1509      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4002      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*3801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2603      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.6
HLA A*6801      1:56-64 9       GESPTTTDG       0.464480        -0.740070       -4.6
HLA A*0202      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*5301      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2402      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*7301      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*0250      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*3002      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*1502      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4501      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA B*4403      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*3201      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2602      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*3301      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*2603      1:154-162       9       PDTIRALAS       1.036621        -1.406985
HLA A*6801      1:154-162       9       PDTIRALAS       1.036621        -1.406985
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