```
There are more than 10,000 predictions to display.
To enable speedy output, the format was set to 'text' only.
In order to see the results in an html table (which allows for sorting), limit the number of predictions generated on the previous page.

Predictions
Allele  Position        PepLength       Sequence        Proteasome      TAP     MHC     Processing      Total
HLA B*1517      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -0.632308       2.579573        1.947266        4.288521
HLA B*3501      1:36-44 9       APSPVAAAF       1.565257        1.095420        -1.187886       2.660677        1.472791        15.412941
HLA A*6802      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -0.806733       2.087388        1.280655        6.408159
HLA B*0702      1:36-44 9       APSPVAAAF       1.565257        1.095420        -1.427895       2.660677        1.232782        26.785195
HLA A*6802      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -1.024122       2.117084        1.092962        10.571137
HLA A*6901      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -1.070256       2.087388        1.017132        11.755909
HLA A*2602      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -1.599454       2.594133        0.994679        39.760717
HLA B*1517      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -0.910717       1.762358        0.851641        8.141731
HLA A*6801      1:140-148       9       GTATVVFSR       0.913054        0.630880        -0.710287       1.543934        0.833647        5.132003
HLA B*1503      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -1.769839       2.579573        0.809735        58.862521
HLA B*1503      1:202-210       9       LGASTALAF       1.310738        0.932777        -1.435150       2.243515        0.808365        27.236420
HLA B*1517      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -1.312648       2.087388        0.774740        20.542243
HLA B*4001      1:10-18 9       LELATPYAL       1.590569        0.388292        -1.233047       1.978861        0.745813        17.102016
HLA B*1517      1:91-99 9       AAFASAAAI       1.234627        0.369594        -0.879788       1.604221        0.724433        7.582076
HLA A*0211      1:74-82 9       ILDATKPEV       0.983482        0.144529        -0.409200       1.128011        0.718811        2.565668
HLA B*1517      1:191-199       9       VTPSTTATL       1.727960        0.494658        -1.511931       2.222618        0.710687        32.503579
HLA B*4001      1:2-10  9       TEHTDFELL       1.490281        0.376705        -1.163728       1.866986        0.703258        14.579013
HLA B*3501      1:8-16  9       ELLELATPY       1.168179        1.152168        -1.624551       2.320347        0.695796        42.126115
HLA B*0702      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -1.287663       1.977371        0.689707        19.393824
HLA B*1801      1:10-18 9       LELATPYAL       1.590569        0.388292        -1.289195       1.978861        0.689665        19.462352
HLA A*0250      1:74-82 9       ILDATKPEV       0.983482        0.144529        -0.482091       1.128011        0.645920        3.034526
HLA B*3901      1:10-18 9       LELATPYAL       1.590569        0.388292        -1.333178       1.978861        0.645683        21.536626
HLA A*3201      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -1.936483       2.579573        0.643090        86.393910
HLA A*2602      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -1.483700       2.087388        0.603689        30.457888
HLA A*3001      1:50-58 9       AVRETMAVV       1.181875        0.336648        -0.925147       1.518523        0.593376        8.416806
HLA B*1501      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -2.004134       2.594133        0.589999        100.956480
HLA B*4002      1:10-18 9       LELATPYAL       1.590569        0.388292        -1.415156       1.978861        0.563705        26.010931
HLA A*0206      1:93-101        9       FASAAAIAV       1.212843        0.182258        -0.852210       1.395101        0.542891        7.115573
HLA B*1517      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -1.368326       1.896327        0.528001        23.352101
HLA B*1501      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.058036       2.579573        0.521537        114.297330
HLA B*1517      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -1.202659       1.718268        0.515609        15.946269
HLA A*2603      1:8-16  9       ELLELATPY       1.168179        1.152168        -1.824939       2.320347        0.495408        66.825002
HLA A*0250      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -0.462365       0.952818        0.490453        2.899777
HLA A*0203      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -0.655713       1.123686        0.467973        4.525985
HLA A*0202      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -1.660193       2.117084        0.456891        45.729146
HLA A*0219      1:74-82 9       ILDATKPEV       0.983482        0.144529        -0.683757       1.128011        0.444254        4.827881
HLA A*0211      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -0.514020       0.952818        0.438797        3.266031
HLA A*0250      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -0.507310       0.934977        0.427667        3.215957
HLA A*0216      1:74-82 9       ILDATKPEV       0.983482        0.144529        -0.715352       1.128011        0.412659        5.192212
HLA B*1517      1:223-231       9       GTILAELPL       1.220795        0.363284        -1.212546       1.584079        0.371533        16.313446
HLA A*0219      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -0.579693       0.934977        0.355284        3.799209
HLA B*1501      1:202-210       9       LGASTALAF       1.310738        0.932777        -1.902646       2.243515        0.340869        79.918228
HLA A*0250      1:50-58 9       AVRETMAVV       1.181875        0.336648        -1.179418       1.518523        0.339105        15.115342
HLA B*1517      1:4-12  9       HTDFELLEL       1.651839        0.218398        -1.545919       1.870237        0.324318        35.149475
HLA B*3501      1:202-210       9       LGASTALAF       1.310738        0.932777        -1.921733       2.243515        0.321782        83.508958
HLA A*3101      1:140-148       9       GTATVVFSR       0.913054        0.630880        -1.225097       1.543934        0.318837        16.791777
HLA A*1101      1:140-148       9       GTATVVFSR       0.913054        0.630880        -1.265310       1.543934        0.278624        18.420883
HLA B*0801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.317950       2.579573        0.261623        207.945829
HLA A*0206      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -0.586488       0.829467        0.242979        3.859116
HLA B*1517      1:202-210       9       LGASTALAF       1.310738        0.932777        -2.006253       2.243515        0.237262        101.450324
HLA A*0203      1:50-58 9       AVRETMAVV       1.181875        0.336648        -1.284369       1.518523        0.234154        19.247285
HLA A*2603      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.380122       2.579573        0.199451        239.950847
HLA B*1503      1:36-44 9       APSPVAAAF       1.565257        1.095420        -2.475883       2.660677        0.184794        299.145584
HLA A*6801      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -1.822909       1.977177        0.154268        66.513381
HLA A*0216      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -0.817734       0.952818        0.135084        6.572545
HLA A*6802      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -0.696848       0.820380        0.123532        4.975627
HLA A*3201      1:191-199       9       VTPSTTATL       1.727960        0.494658        -2.103875       2.222618        0.118743        127.020711
HLA A*6801      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -1.497035       1.606496        0.109460        31.407651
HLA B*1501      1:138-146       9       GAGTATVVF       1.568584        0.994672        -2.466001       2.563256        0.097255        292.415684
HLA A*6802      1:13-21 9       ATPYALNAV       1.259075        0.203216        -1.373565       1.462291        0.088726        23.635529
HLA B*1502      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -2.506778       2.594133        0.087355        321.202062
HLA A*0212      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -0.876297       0.952818        0.076521        7.521368
HLA A*6901      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -2.046571       2.117084        0.070513        111.319334
HLA A*6802      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.336176       1.395101        0.058925        21.685808
HLA A*6901      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.349572       1.395101        0.045529        22.365179
HLA A*0206      1:13-21 9       ATPYALNAV       1.259075        0.203216        -1.441273       1.462291        0.021019        27.623123
HLA B*1502      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.312349       2.320347        0.007998        205.281136
HLA B*3501      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.575895       2.579573        0.003678        376.613145
HLA A*6802      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.120084       1.123686        0.003602        13.185120
HLA B*1503      1:91-99 9       AAFASAAAI       1.234627        0.369594        -1.606437       1.604221        -0.002216       40.405164
HLA A*0202      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.408986       1.395101        -0.013885       25.644023
HLA B*3901      1:36-44 9       APSPVAAAF       1.565257        1.095420        -2.711644       2.660677        -0.050967       514.806496
HLA A*0211      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -0.991252       0.934977        -0.056276       9.800595
HLA A*6802      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -1.787577       1.718268        -0.069309       61.316516
HLA A*0250      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.467319       1.395101        -0.072218       29.330480
HLA A*0212      1:74-82 9       ILDATKPEV       0.983482        0.144529        -1.208829       1.128011        -0.080818       16.174424
HLA A*0203      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -0.923240       0.829467        -0.093773       8.379913
HLA B*5301      1:36-44 9       APSPVAAAF       1.565257        1.095420        -2.772040       2.660677        -0.111363       591.615958
HLA A*6801      1:76-84 9       DATKPEVRR       0.992226        0.534734        -1.646308       1.526960        -0.119348       44.290199
HLA B*0702      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.712147       2.579573        -0.132573       515.402841
HLA B*1503      1:138-146       9       GAGTATVVF       1.568584        0.994672        -2.703162       2.563256        -0.139906       504.850020
HLA B*1503      1:10-18 9       LELATPYAL       1.590569        0.388292        -2.128657       1.978861        -0.149796       134.479754
HLA A*0206      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -2.053953       1.896327        -0.157626       113.227699
HLA A*0202      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -2.068651       1.896327        -0.172324       117.125393
HLA A*0216      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -1.119201       0.934977        -0.184224       13.158327
HLA A*0202      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -1.383471       1.194858        -0.188612       24.180805
HLA A*0203      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.588416       1.395101        -0.193315       38.762906
HLA B*5801      1:202-210       9       LGASTALAF       1.310738        0.932777        -2.441481       2.243515        -0.197966       276.363979
HLA A*0206      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -2.316442       2.117084        -0.199358       207.224855
HLA B*1501      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.524578       2.320347        -0.204231       334.640132
HLA A*6802      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -1.416176       1.194858        -0.221317       26.072074
HLA B*1517      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -2.368586       2.117084        -0.251502       233.661045
HLA A*2602      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -2.154060       1.896327        -0.257732       142.580305
HLA A*0250      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -1.529858       1.271968        -0.257890       33.873320
HLA B*3501      1:161-169       9       APPSRGTVY       1.374663        1.214283        -2.847975       2.588946        -0.259029       704.652886
HLA A*3001      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -2.864187       2.579573        -0.284613       731.453431
HLA B*1503      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.621720       2.320347        -0.301372       418.523482
HLA B*4501      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -1.550430       1.248280        -0.302150       35.516475
HLA A*0206      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.426960       1.123686        -0.303273       26.727585
HLA B*0702      1:161-169       9       APPSRGTVY       1.374663        1.214283        -2.900082       2.588946        -0.311136       794.478435
HLA A*0201      1:74-82 9       ILDATKPEV       0.983482        0.144529        -1.439774       1.128011        -0.311763       27.527946
HLA A*2902      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.641841       2.320347        -0.321493       438.369993
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HLA B*0702      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -1.354248       1.031086        -0.323162       22.607256
HLA A*0203      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -1.605018       1.271968        -0.333050       40.273353
HLA B*1517      1:194-202       9       STTATLTDL       1.210982        0.351136        -1.901701       1.562118        -0.339584       79.744613
HLA B*3501      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.738633       1.395101        -0.343532       54.781384
HLA A*0206      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -2.330863       1.986196        -0.344667       214.221465
HLA A*2602      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.666252       2.320347        -0.345905       463.715879
HLA A*0203      1:13-21 9       ATPYALNAV       1.259075        0.203216        -1.808262       1.462291        -0.345971       64.307605
HLA B*4402      1:10-18 9       LELATPYAL       1.590569        0.388292        -2.337564       1.978861        -0.358703       217.552318
HLA A*0206      1:91-99 9       AAFASAAAI       1.234627        0.369594        -1.973760       1.604221        -0.369539       94.136936
HLA A*6802      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -1.137992       0.764021        -0.373971       13.740162
HLA A*0206      1:204-212       9       ASTALAFTV       1.108485        0.186630        -1.685774       1.295115        -0.390660       48.503635
HLA B*3501      1:138-146       9       GAGTATVVF       1.568584        0.994672        -2.968443       2.563256        -0.405187       929.913878
HLA A*3001      1:71-79 9       RTAILDATK       0.821937        0.327507        -1.556031       1.149444        -0.406587       35.977504
HLA A*0206      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.012857       2.594133        -0.418724       1030.047835
HLA A*2602      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -3.003854       2.579573        -0.424281       1008.914043
HLA A*0250      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -1.324104       0.877544        -0.446560       21.091330
HLA A*0211      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -1.724456       1.271968        -0.452488       53.022012
HLA B*2705      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -1.793273       1.335319        -0.457954       62.125890
HLA A*0211      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -2.547255       2.087388        -0.459867       352.578034
HLA A*6801      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -2.021196       1.559867        -0.461329       105.001659
HLA B*0702      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -1.443030       0.967740        -0.475291       27.735129
HLA A*0212      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -1.413732       0.934977        -0.478755       25.925797
HLA B*4801      1:10-18 9       LELATPYAL       1.590569        0.388292        -2.476592       1.978861        -0.497732       299.634724
HLA A*0206      1:50-58 9       AVRETMAVV       1.181875        0.336648        -2.025444       1.518523        -0.506921       106.033728
HLA B*1517      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.102824       2.594133        -0.508691       1267.137878
HLA A*6901      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.840570       2.320347        -0.520222       692.739032
HLA A*6901      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -1.341312       0.820380        -0.520932       21.943788
HLA A*2601      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.118678       2.594133        -0.524545       1314.250643
HLA A*0250      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -2.510885       1.986196        -0.524689       324.253912
HLA B*1517      1:204-212       9       ASTALAFTV       1.108485        0.186630        -1.829304       1.295115        -0.534190       67.500086
HLA B*4002      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -1.788865       1.248280        -0.540585       61.498566
HLA A*8001      1:8-16  9       ELLELATPY       1.168179        1.152168        -2.861724       2.320347        -0.541377       727.318143
HLA A*2603      1:47-55 9       EVRAVRETM       1.250113        0.064179        -1.856615       1.314292        -0.542323       71.881104
HLA A*0211      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.941328       1.395101        -0.546227       87.363046
HLA A*6801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -2.459934       1.909325        -0.550609       288.359519
HLA B*3901      1:93-101        9       FASAAAIAV       1.212843        0.182258        -1.950223       1.395101        -0.555122       89.170853
HLA B*3901      1:200-208       9       TDLGASTAL       1.577364        0.302370        -2.436035       1.879734        -0.556301       272.919980
HLA A*3001      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.688401       1.123686        -0.564715       48.797886
HLA A*3002      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.164249       2.594133        -0.570115       1459.650261
HLA B*4002      1:200-208       9       TDLGASTAL       1.577364        0.302370        -2.451518       1.879734        -0.571784       282.825417
HLA A*6802      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -1.858537       1.271968        -0.586569       72.199903
HLA A*6901      1:4-12  9       HTDFELLEL       1.651839        0.218398        -2.458064       1.870237        -0.587827       287.120434
HLA A*1101      1:71-79 9       RTAILDATK       0.821937        0.327507        -1.741213       1.149444        -0.591769       55.107757
HLA B*1517      1:138-146       9       GAGTATVVF       1.568584        0.994672        -3.155156       2.563256        -0.591900       1429.408309
HLA B*1503      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.188707       2.594133        -0.594574       1544.212089
HLA A*0101      1:4-12  9       HTDFELLEL       1.651839        0.218398        -2.468740       1.870237        -0.598503       294.266052
HLA A*0211      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.722360       1.123686        -0.598674       52.766765
HLA A*3301      1:76-84 9       DATKPEVRR       0.992226        0.534734        -2.126712       1.526960        -0.599752       133.878714
HLA B*0702      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -1.151873       0.534755        -0.617118       14.186413
HLA B*0702      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.743139       1.123686        -0.619453       55.352764
HLA A*6802      1:191-199       9       VTPSTTATL       1.727960        0.494658        -2.849404       2.222618        -0.626786       706.974455
HLA A*6801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -2.376288       1.748241        -0.628047       237.841660
HLA A*6801      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -2.350523       1.721236        -0.629287       224.142120
HLA A*0203      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -1.587895       0.952818        -0.635077       38.716380
HLA B*3901      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -2.753127       2.117084        -0.636042       566.404279
HLA A*6801      1:71-79 9       RTAILDATK       0.821937        0.327507        -1.788729       1.149444        -0.639284       61.479272
HLA A*0203      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -1.702075       1.060336        -0.641739       50.358758
HLA A*0211      1:191-199       9       VTPSTTATL       1.727960        0.494658        -2.867913       2.222618        -0.645295       737.756365
HLA B*0702      1:50-58 9       AVRETMAVV       1.181875        0.336648        -2.173391       1.518523        -0.654868       149.070292
HLA A*2603      1:191-199       9       VTPSTTATL       1.727960        0.494658        -2.878363       2.222618        -0.655746       755.724452
HLA B*4002      1:2-10  9       TEHTDFELL       1.490281        0.376705        -2.528953       1.866986        -0.661967       338.028068
HLA A*2603      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -2.749969       2.087388        -0.662581       562.300951
HLA A*3001      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -1.264568       0.600711        -0.663857       18.389419
HLA A*0219      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -1.616732       0.952818        -0.663915       41.374458
HLA A*0211      1:50-58 9       AVRETMAVV       1.181875        0.336648        -2.184114       1.518523        -0.665591       152.796762
HLA B*3901      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -2.647066       1.977371        -0.669695       443.676140
HLA A*0202      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.796886       1.123686        -0.673200       62.644959
HLA A*6901      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.796985       1.123686        -0.673298       62.659195
HLA B*0702      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.269731       2.594133        -0.675598       1860.935359
HLA B*1503      1:161-169       9       APPSRGTVY       1.374663        1.214283        -3.266231       2.588946        -0.677284       1845.995148
HLA A*0250      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -1.801096       1.123686        -0.677410       63.255225
HLA A*3301      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -2.247019       1.559867        -0.687152       176.611615
HLA A*3001      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -1.047518       0.351592        -0.695926       11.156241
HLA A*2601      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.022598       2.320347        -0.702251       1053.412235
HLA A*3001      1:91-99 9       AAFASAAAI       1.234627        0.369594        -2.312448       1.604221        -0.708227       205.327784
HLA B*1502      1:161-169       9       APPSRGTVY       1.374663        1.214283        -3.305091       2.588946        -0.716145       2018.789499
HLA A*6802      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -2.618158       1.896327        -0.721831       415.105044
HLA A*0201      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -1.564550       0.829467        -0.735083       36.690215
HLA B*0802      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -3.320931       2.579573        -0.741358       2093.781051
HLA A*0250      1:9-17  9       LLELATPYA       0.993939        -0.356018       -1.379716       0.637921        -0.741795       23.972663
HLA A*2602      1:47-55 9       EVRAVRETM       1.250113        0.064179        -2.067561       1.314292        -0.753269       116.831755
HLA A*0206      1:49-57 9       RAVRETMAV       0.926962        0.318191        -1.999130       1.245153        -0.753977       99.799829
HLA A*0202      1:13-21 9       ATPYALNAV       1.259075        0.203216        -2.223524       1.462291        -0.761233       167.310968
HLA A*6801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -2.505947       1.742555        -0.763391       320.587516
HLA A*0206      1:74-82 9       ILDATKPEV       0.983482        0.144529        -1.896462       1.128011        -0.768451       78.788350
HLA A*3201      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.089408       2.320347        -0.769061       1228.593785
HLA A*0202      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -1.726383       0.952818        -0.773565       53.257746
HLA A*2601      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -2.670669       1.896327        -0.774342       468.456209
HLA B*1517      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -2.046801       1.271968        -0.774833       111.378368
HLA B*1503      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -1.808201       1.029850        -0.778351       64.298560
HLA A*6802      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -1.852851       1.060336        -0.792515       71.260828
HLA A*0201      1:93-101        9       FASAAAIAV       1.212843        0.182258        -2.189476       1.395101        -0.794375       154.694786
HLA A*3101      1:71-79 9       RTAILDATK       0.821937        0.327507        -1.946342       1.149444        -0.796897       88.377471
HLA A*6801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -2.433662       1.636392        -0.797270       271.432815
HLA B*2705      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -1.970551       1.160079        -0.810472       93.443837
HLA A*0203      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.035239       2.222618        -0.812621       1084.522553
HLA A*3201      1:91-99 9       AAFASAAAI       1.234627        0.369594        -2.428860       1.604221        -0.824639       268.447895
HLA B*1517      1:36-44 9       APSPVAAAF       1.565257        1.095420        -3.487947       2.660677        -0.827270       3075.719711
HLA A*0206      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.063916       2.222618        -0.841298       1158.554322
HLA B*3901      1:91-99 9       AAFASAAAI       1.234627        0.369594        -2.448262       1.604221        -0.844041       280.712693
HLA A*2501      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.449378       2.594133        -0.855244       2814.346783
HLA A*6802      1:91-99 9       AAFASAAAI       1.234627        0.369594        -2.463595       1.604221        -0.859374       290.800260
HLA B*4403      1:10-18 9       LELATPYAL       1.590569        0.388292        -2.852331       1.978861        -0.873471       711.756071
HLA B*1517      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.197428       2.320347        -0.877081       1575.535657
HLA A*0202      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -2.972249       2.087388        -0.884861       938.099479
HLA B*1517      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -1.980710       1.094281        -0.886429       95.655476
HLA A*3101      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -2.502549       1.606496        -0.896054       318.089440
HLA A*0216      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -2.021727       1.123686        -0.898041       105.130116
HLA A*0219      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -2.896450       1.986196        -0.910254       787.861375
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HLA A*0206	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-1.979657	1.060336	-0.919322	95.423923
HLA B*4601	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.520252	2.594133	-0.926119	3313.234498
HLA B*1517	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-2.912351	1.986196	-0.926155	817.242840
HLA A*0206	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-1.996729	1.070235	-0.926494	99.249568
HLA A*3201	1:138-146	9	GAGTATVVF	1.568584	0.994672	-3.500239	2.563256	-0.936983	3164.020301
HLA B*3501	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.535862	2.594133	-0.941729	3434.489184
HLA A*0203	1:91-99	9	AAFASAAAI	1.234627	0.369594	-2.546851	1.604221	-0.942630	352.250112
HLA A*0203	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-2.077156	1.128647	-0.948509	119.441760
HLA A*2403	1:138-146	9	GAGTATVVF	1.568584	0.994672	-3.515863	2.563256	-0.952607	3279.920647
HLA A*0250	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.177335	2.222618	-0.954717	1504.303412
HLA A*0202	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.178421	2.222618	-0.955803	1508.067924
HLA B*1503	1:49-57	9	RAVRETMAV	0.926962	0.318191	-2.202388	1.245153	-0.957236	159.363348
HLA A*0211	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-1.789466	0.829467	-0.959999	61.583796
HLA A*3001	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-2.089632	1.128647	-0.960985	122.922663
HLA A*2501	1:8-16	9	ELLELATPY	1.168179	1.152168	-3.283532	2.320347	-0.963185	1921.021222
HLA B*1517	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-1.800307	0.834848	-0.965458	63.140349
HLA A*3101	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-2.714722	1.748514	-0.966208	518.467865
HLA A*0202	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-2.684648	1.718268	-0.966380	483.780585
HLA A*0203	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-3.054185	2.087388	-0.966797	1132.882413
HLA A*0216	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-2.956446	1.986196	-0.970250	904.578495
HLA B*1501	1:36-44	9	APSPVAAAF	1.565257	1.095420	-3.635537	2.660677	-0.974860	4320.526813
HLA B*1517	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-2.104490	1.124732	-0.979758	127.200877
HLA A*0206	1:40-48	9	VAAAFNDEV	1.065598	0.129260	-2.181116	1.194858	-0.986258	151.745635
HLA A*2602	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.211746	2.222618	-0.989128	1628.343399
HLA A*6802	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-2.119438	1.128647	-0.990791	131.655052
HLA B*1502	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-3.577443	2.579573	-0.997870	3779.578228
HLA B*1517	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-2.133196	1.128647	-1.004549	135.892695
HLA B*5401	1:93-101	9	FASAAAIAV	1.212843	0.182258	-2.404914	1.395101	-1.009813	254.046989
HLA B*4403	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-2.744448	1.728208	-1.016239	555.197533
HLA B*1517	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-1.836005	0.809887	-1.026118	68.549621
HLA A*0206	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-2.302477	1.271968	-1.030509	200.667253
HLA A*3101	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-2.755857	1.721236	-1.034621	569.976076
HLA A*2902	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.639578	2.594133	-1.045444	4360.916980
HLA A*3001	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-2.355603	1.307494	-1.048109	226.779118
HLA A*6802	1:25-33	9	ERADIDRRV	1.311800	0.083077	-2.452411	1.394877	-1.057534	283.407436
HLA A*0202	1:91-99	9	AAFASAAAI	1.234627	0.369594	-2.666553	1.604221	-1.062332	464.037098
HLA B*4601	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-3.642374	2.579573	-1.062800	4389.082115
HLA B*5801	1:138-146	9	GAGTATVVF	1.568584	0.994672	-3.629221	2.563256	-1.065965	4258.153265
HLA A*3001	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-2.196209	1.124732	-1.071478	157.111979
HLA A*0202	1:74-82	9	ILDATKPEV	0.983482	0.144529	-2.201919	1.128011	-1.073908	159.191014
HLA A*0201	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-2.198122	1.123686	-1.074435	157.805371
HLA B*1503	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-2.837708	1.762358	-1.075350	688.189410
HLA A*2602	1:13-21	9	ATPYALNAV	1.259075	0.203216	-2.543989	1.462291	-1.081698	349.936680
HLA B*1517	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-1.439623	0.351592	-1.088031	27.518417
HLA B*3501	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-2.806375	1.718268	-1.088107	640.287839
HLA A*0201	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-2.987530	1.896327	-1.091203	971.694949
HLA A*0201	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-2.055593	0.952818	-1.102775	113.656067
HLA A*0206	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-2.823926	1.718268	-1.105658	666.693017
HLA A*6802	1:204-212	9	ASTALAFTV	1.108485	0.186630	-2.403044	1.295115	-1.107929	252.955346
HLA A*0206	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-2.144131	1.029850	-1.114280	139.357586
HLA B*1517	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-2.188682	1.072739	-1.115942	154.412178
HLA A*0206	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-2.245267	1.128647	-1.116620	175.900286
HLA A*3301	1:140-148	9	GTATVVFSR	0.913054	0.630880	-2.663433	1.543934	-1.119499	460.715248
HLA B*1502	1:202-210	9	LGASTALAF	1.310738	0.932777	-3.374269	2.243515	-1.130754	2367.387082
HLA B*4501	1:10-18	9	LELATPYAL	1.590569	0.388292	-3.110009	1.978861	-1.131148	1288.275057
HLA B*1501	1:91-99	9	AAFASAAAI	1.234627	0.369594	-2.735660	1.604221	-1.131439	544.077109
HLA A*0216	1:93-101	9	FASAAAIAV	1.212843	0.182258	-2.535823	1.395101	-1.140722	343.417686
HLA A*0202	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-1.971909	0.829467	-1.142442	93.736485
HLA A*2402	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.370167	2.222618	-1.147549	2345.130811
HLA A*2902	1:202-210	9	LGASTALAF	1.310738	0.932777	-3.397844	2.243515	-1.154329	2499.447425
HLA B*4501	1:2-10	9	TEHTDFELL	1.490281	0.376705	-3.021579	1.866986	-1.154593	1050.941839
HLA B*4402	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-2.884242	1.728208	-1.156034	766.023134
HLA A*0203	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.280783	2.117084	-1.163699	1908.900384
HLA A*3201	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.281032	2.117084	-1.163948	1909.995353
HLA B*1801	1:36-44	9	APSPVAAAF	1.565257	1.095420	-3.826592	2.660677	-1.165915	6707.985669
HLA A*2403	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.388984	2.222618	-1.166326	2448.748353
HLA B*1503	1:191-199	9	VTPSTTATL	1.727960	0.494658	-3.392732	2.222618	-1.170114	2470.196640
HLA A*0203	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-2.105679	0.934977	-1.170702	127.549554
HLA B*4601	1:138-146	9	GAGTATVVF	1.568584	0.994672	-3.739083	2.563256	-1.175827	5483.820209
HLA B*1502	1:36-44	9	APSPVAAAF	1.565257	1.095420	-3.848461	2.660677	-1.187784	7054.417072
HLA B*1501	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-2.223092	1.029850	-1.193242	167.144506
HLA B*7301	1:86-94	9	SRWRTAAFA	1.225790	-0.065711	-2.355166	1.160079	-1.195087	226.551038
HLA B*5801	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-3.287944	2.087388	-1.200556	1940.637841
HLA A*3201	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.795997	2.594133	-1.201864	6251.685649
HLA A*6801	1:8-16	9	ELLELATPY	1.168179	1.152168	-3.525031	2.320347	-1.204684	3349.893708
HLA B*0801	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-2.819612	1.612334	-1.207278	660.103829
HLA A*0203	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.805061	2.594133	-1.210928	6383.537964
HLA A*2602	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-2.033634	0.820380	-1.213254	108.052380
HLA B*5301	1:161-169	9	APPSRGTVY	1.374663	1.214283	-3.802970	2.588946	-1.214024	6352.876371
HLA A*0250	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.338313	2.117084	-1.221229	2179.278604
HLA A*3201	1:204-212	9	ASTALAFTV	1.108485	0.186630	-2.521284	1.295115	-1.226170	332.111600
HLA A*0203	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-2.297204	1.070235	-1.226970	198.245922
HLA A*0211	1:40-48	9	VAAAFNDEV	1.065598	0.129260	-2.422267	1.194858	-1.227409	264.403591
HLA B*1517	1:50-58	9	AVRETMAVV	1.181875	0.336648	-2.752934	1.518523	-1.234410	566.153071
HLA A*0211	1:91-99	9	AAFASAAAI	1.234627	0.369594	-2.839306	1.604221	-1.235084	690.725732
HLA A*3001	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-1.665738	0.427495	-1.238243	46.316729
HLA B*3901	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-3.018750	1.778264	-1.240486	1044.118767
HLA A*0202	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-2.518432	1.271968	-1.246464	329.937569
HLA A*2403	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-3.841023	2.594133	-1.246889	6934.619923
HLA A*3101	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-2.993812	1.742555	-1.251257	985.853694
HLA A*0206	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.124110	1.870237	-1.253873	1330.792079
HLA A*0206	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-2.355486	1.100579	-1.254907	226.717783
HLA A*0206	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-3.343655	2.087388	-1.256267	2206.253867
HLA B*4403	1:2-10	9	TEHTDFELL	1.490281	0.376705	-3.126666	1.866986	-1.259680	1338.648165
HLA A*3002	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-3.842047	2.579573	-1.262474	6950.995998
HLA A*6901	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-2.323617	1.060336	-1.263281	210.677023
HLA A*2501	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-3.848217	2.579573	-1.268643	7050.449173
HLA A*3002	1:161-169	9	APPSRGTVY	1.374663	1.214283	-3.862788	2.588946	-1.273842	7291.020042
HLA B*3501	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.395495	2.117084	-1.278410	2485.962202
HLA A*0211	1:8-16	9	ELLELATPY	1.168179	1.152168	-3.608052	2.320347	-1.287705	4055.574924
HLA B*1801	1:8-16	9	ELLELATPY	1.168179	1.152168	-3.610472	2.320347	-1.290125	4078.236420
HLA A*0212	1:50-58	9	AVRETMAVV	1.181875	0.336648	-2.810698	1.518523	-1.292175	646.693217
HLA A*2602	1:50-58	9	AVRETMAVV	1.181875	0.336648	-2.822883	1.518523	-1.304359	665.093549
HLA A*6901	1:91-99	9	AAFASAAAI	1.234627	0.369594	-2.908662	1.604221	-1.304441	810.330961
HLA A*0206	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-3.073986	1.762358	-1.311628	1185.731328
HLA A*0250	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-1.921841	0.603848	-1.317993	83.529742
HLA A*0301	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-2.411619	1.090544	-1.321076	257.999867
HLA A*0216	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.441521	2.117084	-1.324437	2763.891130
HLA A*0211	1:10-18	9	LELATPYAL	1.590569	0.388292	-3.303869	1.978861	-1.325009	2013.118338
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HLA A*0250      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -2.666562       1.332502        -1.334061       464.047140
HLA A*2403      1:36-44 9       APSPVAAAF       1.565257        1.095420        -3.998189       2.660677        -1.337512       9958.389592
HLA A*3001      1:49-57 9       RAVRETMAV       0.926962        0.318191        -2.587347       1.245153        -1.342194       386.675685
HLA A*0212      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.331297       1.986196        -1.345101       2144.357508
HLA B*4601      1:202-210       9       LGASTALAF       1.310738        0.932777        -3.600294       2.243515        -1.356779       3983.771586
HLA B*1501      1:161-169       9       APPSRGTVY       1.374663        1.214283        -3.947172       2.588946        -1.358226       8854.670307
HLA A*0202      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.121230       1.762358        -1.358872       1321.994775
HLA B*3501      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -3.337373       1.977371        -1.360002       2174.567841
HLA B*0801      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.123969       1.762358        -1.361611       1330.360183
HLA A*0202      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -3.958149       2.594133        -1.364016       9081.324393
HLA A*6901      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.589769       2.222618        -1.367151       3888.380324
HLA A*0250      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -2.562644       1.194858        -1.367786       365.295547
HLA A*6901      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.355784       1.986196        -1.369588       2268.733718
HLA A*0202      1:4-12  9       HTDFELLEL       1.651839        0.218398        -3.240734       1.870237        -1.370497       1740.740140
HLA A*0202      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -2.502347       1.128647        -1.373700       317.941483
HLA A*3101      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -3.353895       1.977177        -1.376718       2258.887174
HLA A*6901      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -2.578127       1.194858        -1.383269       378.553691
HLA A*0203      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.279745       1.896327        -1.383418       1904.341329
HLA B*1801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -3.965888       2.579573        -1.386315       9244.605711
HLA A*0211      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.505563       2.117084        -1.388479       3203.046137
HLA A*3201      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.049831       2.660677        -1.389154       11215.813861
HLA B*1503      1:93-101        9       FASAAAIAV       1.212843        0.182258        -2.784276       1.395101        -1.389175       608.521599
HLA A*3101      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -3.968759       2.579573        -1.389186       9305.923190
HLA A*0301      1:140-148       9       GTATVVFSR       0.913054        0.630880        -2.935569       1.543934        -1.391635       862.122014
HLA A*0212      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.288743       1.896327        -1.392416       1944.210662
HLA B*4001      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -2.644566       1.248280        -1.396286       441.129622
HLA A*0216      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -2.672309       1.271968        -1.400341       470.228492
HLA B*5801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -3.982471       2.579573        -1.402898       9604.418112
HLA B*1503      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -2.751956       1.344429        -1.407528       564.880369
HLA A*0211      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -2.855038       1.446716        -1.408322       716.205723
HLA A*0212      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.632421       2.222618        -1.409803       4289.644358
HLA A*0216      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.635593       2.222618        -1.412975       4321.087815
HLA A*2301      1:138-146       9       GAGTATVVF       1.568584        0.994672        -3.983383       2.563256        -1.420127       9624.599314
HLA B*4601      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.085223       2.660677        -1.424547       12168.118631
HLA A*0211      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.411283       1.986196        -1.425087       2578.000874
HLA B*3501      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -2.239726       0.809887        -1.429840       173.670662
HLA A*2602      1:221-229       9       PTGTILAEL       1.442456        0.106507        -2.979885       1.548963        -1.430922       954.739127
HLA A*0216      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.518889       2.087388        -1.431501       3302.854737
HLA B*5101      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.098019       2.660677        -1.437342       12531.952222
HLA A*3002      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.760135       2.320347        -1.439787       5756.183011
HLA A*3201      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.429830       1.986196        -1.443634       2690.480786
HLA A*0202      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.433349       1.986196        -1.447153       2712.373067
HLA B*2705      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -2.560769       1.111207        -1.449562       363.721932
HLA A*6802      1:47-55 9       EVRAVRETM       1.250113        0.064179        -2.775259       1.314292        -1.460967       596.017037
HLA A*2902      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.127232       2.660677        -1.466555       13403.932342
HLA A*3001      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.016104       1.546761        -1.469343       1037.777814
HLA A*0201      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.586921       2.117084        -1.469837       3862.968449
HLA A*0203      1:49-57 9       RAVRETMAV       0.926962        0.318191        -2.716761       1.245153        -1.471609       520.908203
HLA B*3801      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.137894       2.660677        -1.477217       13737.072488
HLA A*0202      1:204-212       9       ASTALAFTV       1.108485        0.186630        -2.773393       1.295115        -1.478279       593.462365
HLA B*0702      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.246001       1.762358        -1.483643       1761.982089
HLA A*0206      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -2.438939       0.952818        -1.486122       274.751008
HLA A*3002      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.709235       2.222618        -1.486617       5119.591982
HLA A*6901      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -2.768370       1.271968        -1.496402       586.637720
HLA A*6802      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -2.752436       1.254367        -1.498069       565.504125
HLA A*0202      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -2.949750       1.446716        -1.503034       890.738505
HLA B*5701      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.596639       2.087388        -1.509250       3950.377791
HLA A*2902      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.089391       2.579573        -1.509818       12285.459980
HLA B*0702      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.627798       2.117084        -1.510713       4244.216223
HLA A*0219      1:93-101        9       FASAAAIAV       1.212843        0.182258        -2.908178       1.395101        -1.513078       809.428401
HLA B*0801      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.176576       2.660677        -1.515899       15016.755545
HLA A*0206      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.837367       2.320347        -1.517019       6876.490769
HLA B*5301      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.080534       2.563256        -1.517278       12037.432452
HLA A*2402      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.100039       2.579573        -1.520466       12590.393031
HLA A*0203      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -2.398683       0.877544        -1.521139       250.428192
HLA B*5701      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.100772       2.579573        -1.521199       12611.662117
HLA B*5801      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -3.225185       1.697997        -1.527188       1679.519506
HLA A*0250      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.616684       2.087388        -1.529296       4136.989676
HLA A*0203      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -2.034381       0.502462        -1.531919       108.238427
HLA A*0301      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.853179       2.320347        -1.532832       7131.467353
HLA B*0803      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.114174       2.579573        -1.534600       13006.899642
HLA B*5701      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.102253       2.563256        -1.538996       12654.718896
HLA A*0201      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.627877       2.087388        -1.540489       4244.996960
HLA A*3101      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -3.106536       1.559867        -1.546669       1278.015319
HLA A*0212      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -2.358573       0.811766        -1.546806       228.335170
HLA A*0212      1:10-18 9       LELATPYAL       1.590569        0.388292        -3.531605       1.978861        -1.552744       3400.986329
HLA A*0212      1:93-101        9       FASAAAIAV       1.212843        0.182258        -2.948378       1.395101        -1.553277       887.928768
HLA B*1503      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -3.531610       1.977371        -1.554239       3401.023127
HLA A*6802      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.120154       1.562118        -1.558036       1318.723285
HLA B*4402      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.218895       2.660677        -1.558218       16553.698269
HLA B*1801      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -2.181924       0.623682        -1.558243       152.028297
HLA A*2602      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.121653       1.562118        -1.559535       1323.282734
HLA A*0301      1:71-79 9       RTAILDATK       0.821937        0.327507        -2.711898       1.149444        -1.562454       515.107369
HLA A*3002      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.223744       2.660677        -1.563067       16739.572857
HLA A*2601      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.143909       2.579573        -1.564335       13928.645061
HLA B*1503      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -3.391486       1.825968        -1.565518       2463.124134
HLA A*2902      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.154702       2.588946        -1.565756       14279.151639
HLA A*0203      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -2.391724       0.820380        -1.571344       246.447288
HLA A*0219      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -2.695301       1.123686        -1.571615       495.793696
HLA A*0202      1:9-17  9       LLELATPYA       0.993939        -0.356018       -2.210461       0.637921        -1.572540       162.353358
HLA A*2403      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.152766       2.579573        -1.573193       14215.640433
HLA A*2602      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.164885       2.588946        -1.575939       14617.902930
HLA B*5801      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.170557       2.594133        -1.576423       14810.057015
HLA A*3201      1:10-18 9       LELATPYAL       1.590569        0.388292        -3.555645       1.978861        -1.576784       3594.552381
HLA A*0201      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.799644       2.222618        -1.577026       6304.396702
HLA B*5801      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.238802       2.660677        -1.578125       17330.145992
HLA A*0250      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -3.024906       1.446716        -1.578190       1059.023391
HLA B*1509      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.239627       2.660677        -1.578950       17363.084969
HLA A*0203      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.341414       1.762358        -1.579056       2194.896648
HLA A*1101      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -2.670636       1.090544        -1.580092       468.420731
HLA A*0216      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.902922       2.320347        -1.582575       7996.909752
HLA A*6801      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.701191       2.117084        -1.584107       5025.632338
HLA B*1501      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.348373       1.762358        -1.586015       2230.351178
HLA B*0702      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.133428       1.546761        -1.586667       1359.653562
HLA A*1101      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -3.193970       1.606496        -1.587474       1563.038928
HLA A*3001      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -2.681824       1.094281        -1.587543       480.644918
HLA A*0212      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -2.717034       1.123686        -1.593347       521.235200
HLA A*6901      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.489784       1.896327        -1.593457       3088.759208
HLA A*2301      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.816367       2.222618        -1.593749       6551.898599
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HLA A*6901      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.254812       2.660677        -1.594135       17980.907716
HLA A*0206      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.256461       2.660677        -1.595784       18049.324400
HLA A*2902      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.492256       1.896327        -1.595929       3106.388082
HLA A*0212      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.685694       2.087388        -1.598305       4849.461441
HLA A*3201      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -2.730045       1.128647        -1.601398       537.087673
HLA B*1501      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.120036       1.518523        -1.601513       1318.366626
HLA B*1501      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.824276       2.222618        -1.601658       6672.299525
HLA B*0802      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.262732       2.660677        -1.602055       18311.829080
HLA A*2402      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.167700       2.563256        -1.604444       14712.949918
HLA A*0250      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -2.416271       0.811766        -1.604505       260.778308
HLA A*3001      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.203595       2.594133        -1.609462       15980.677547
HLA A*0250      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -2.213201       0.600711        -1.612490       163.380709
HLA B*5701      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.511963       1.896327        -1.615636       3250.597459
HLA A*0206      1:223-231       9       GTILAELPL       1.220795        0.363284        -3.200060       1.584079        -1.615981       1585.110926
HLA B*1503      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.733670       2.117084        -1.616586       5415.891987
HLA B*2705      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -3.397036       1.778264        -1.618772       2494.800275
HLA A*3001      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.279484       2.660677        -1.618807       19031.961659
HLA B*1517      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -3.317388       1.697997        -1.619391       2076.769235
HLA A*2601      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -2.441223       0.820380        -1.620843       276.199567
HLA A*2603      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.168572       1.546761        -1.621810       1474.252461
HLA A*0201      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.611525       1.986196        -1.625329       4088.132545
HLA B*3901      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.712915       2.087388        -1.625526       5163.148828
HLA A*0203      1:74-82 9       ILDATKPEV       0.983482        0.144529        -2.754001       1.128011        -1.625990       567.545303
HLA A*0250      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.948465       2.320347        -1.628117       8881.056074
HLA B*1801      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.217147       2.588946        -1.628201       16487.204244
HLA B*4001      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.291168       2.660677        -1.630491       19550.935503
HLA B*5801      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.352908       1.718268        -1.634640       2253.760463
HLA A*0219      1:8-16  9       ELLELATPY       1.168179        1.152168        -3.955880       2.320347        -1.635532       9033.989612
HLA B*1517      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.224867       2.588946        -1.635921       16782.916188
HLA A*0202      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.200027       1.562118        -1.637909       1584.990877
HLA A*6901      1:204-212       9       ASTALAFTV       1.108485        0.186630        -2.933219       1.295115        -1.638105       857.470623
HLA A*0216      1:204-212       9       ASTALAFTV       1.108485        0.186630        -2.934009       1.295115        -1.638894       859.030684
HLA B*1517      1:71-79 9       RTAILDATK       0.821937        0.327507        -2.790356       1.149444        -1.640912       617.101305
HLA A*2602      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.301804       2.660677        -1.641127       20035.660388
HLA A*2402      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.305215       2.660677        -1.644538       20193.663444
HLA B*4403      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.306775       2.660677        -1.646098       20266.332885
HLA A*6802      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -2.979344       1.332502        -1.646843       953.551908
HLA A*8001      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.241464       2.594133        -1.647331       17436.695674
HLA A*6901      1:74-82 9       ILDATKPEV       0.983482        0.144529        -2.775973       1.128011        -1.647962       596.998057
HLA B*3801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.228053       2.579573        -1.648480       16906.485152
HLA B*0801      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.237639       2.588946        -1.648693       17283.799761
HLA A*2902      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.212284       2.563256        -1.649028       16303.602720
HLA B*5101      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.238422       2.588946        -1.649475       17314.964470
HLA A*0201      1:4-12  9       HTDFELLEL       1.651839        0.218398        -3.526662       1.870237        -1.656425       3362.494400
HLA B*5701      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.317418       2.660677        -1.656741       20769.131637
HLA B*3901      1:2-10  9       TEHTDFELL       1.490281        0.376705        -3.526929       1.866986        -1.659943       3364.568782
HLA B*0702      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.223937       2.563256        -1.660681       16747.000361
HLA A*0202      1:10-18 9       LELATPYAL       1.590569        0.388292        -3.641321       1.978861        -1.662461       4378.457482
HLA B*2705      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.242651       2.579573        -1.663077       17484.397754
HLA A*2601      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.324126       2.660677        -1.663449       21092.405821
HLA A*0203      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -2.265176       0.600711        -1.664466       184.151848
HLA A*1101      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -3.387140       1.721236        -1.665904       2438.595412
HLA B*1501      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -2.790516       1.123686        -1.666830       617.328361
HLA A*6901      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.262356       2.594133        -1.668222       18295.985544
HLA A*3201      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.388455       1.718268        -1.670187       2445.994431
HLA B*0801      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.266721       2.594133        -1.672588       18480.816361
HLA A*3001      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.236378       2.563256        -1.673121       17233.661278
HLA A*3201      1:13-21 9       ATPYALNAV       1.259075        0.203216        -3.135726       1.462291        -1.673435       1366.866379
HLA B*0803      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.334144       2.660677        -1.673467       21584.615797
HLA A*0219      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.896372       2.222618        -1.673754       7877.199246
HLA A*0206      1:10-18 9       LELATPYAL       1.590569        0.388292        -3.654929       1.978861        -1.676069       4517.824476
HLA A*8001      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.265170       2.588946        -1.676224       18414.947773
HLA B*1801      1:2-10  9       TEHTDFELL       1.490281        0.376705        -3.544043       1.866986        -1.677057       3499.798654
HLA B*4601      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.000473       2.320347        -1.680125       10010.892831
HLA A*0206      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.244789       1.562118        -1.682672       1757.070369
HLA A*3201      1:4-12  9       HTDFELLEL       1.651839        0.218398        -3.553859       1.870237        -1.683622       3579.803663
HLA A*3301      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.264266       2.579573        -1.684693       18376.632900
HLA B*1502      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.250883       2.563256        -1.687627       17818.997757
HLA B*4801      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.804803       2.117084        -1.687719       6379.740329
HLA A*0206      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -2.909311       1.219814        -1.689497       811.541794
HLA A*0219      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.808586       2.117084        -1.691502       6435.550063
HLA A*2402      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.286718       2.594133        -1.692584       19351.632969
HLA A*3101      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.255911       2.563256        -1.692655       18026.489963
HLA A*0301      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.356166       2.660677        -1.695489       22707.328646
HLA A*0211      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.291586       2.594133        -1.697452       19569.771345
HLA B*4801      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.358497       2.660677        -1.697820       22829.517601
HLA A*3001      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.287674       2.588946        -1.698727       19394.288819
HLA A*0301      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.278720       2.579573        -1.699147       18998.528797
HLA B*1801      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.293954       2.594133        -1.699821       19676.780104
HLA B*4402      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.289006       2.588946        -1.700060       19453.870333
HLA A*0101      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.294309       2.594133        -1.700175       19692.860500
HLA B*4801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.280395       2.579573        -1.700822       19071.952406
HLA A*6901      1:13-21 9       ATPYALNAV       1.259075        0.203216        -3.163149       1.462291        -1.700858       1455.959351
HLA A*3001      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.925101       2.222618        -1.702483       8415.914860
HLA A*3101      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.363316       2.660677        -1.702639       23084.237214
HLA A*2601      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.291656       2.588946        -1.702710       19572.947712
HLA A*8001      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.364258       2.660677        -1.703581       23134.369721
HLA A*0203      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.366696       2.660677        -1.706020       23264.645400
HLA A*0203      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -3.692502       1.986196        -1.706306       4926.089727
HLA B*4402      1:2-10  9       TEHTDFELL       1.490281        0.376705        -3.574309       1.866986        -1.707323       3752.399985
HLA A*6901      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -2.471776       0.764021        -1.707755       296.330052
HLA A*3101      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.301980       2.594133        -1.707847       20043.791340
HLA A*0301      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.302123       2.594133        -1.707990       20050.406948
HLA A*0212      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.369175       2.660677        -1.708498       23397.806448
HLA B*5301      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -2.740566       1.031086        -1.709480       550.257764
HLA B*2705      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.370209       2.660677        -1.709532       23453.567785
HLA B*3501      1:200-208       9       TDLGASTAL       1.577364        0.302370        -3.592024       1.879734        -1.712290       3908.627133
HLA A*3301      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -3.322205       1.606496        -1.715709       2099.929361
HLA A*2501      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.305638       2.588946        -1.716692       20213.337208
HLA A*0203      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.297126       2.579573        -1.717552       19821.012572
HLA A*0219      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.381557       2.660677        -1.720880       24074.480817
HLA A*0101      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.383408       2.660677        -1.722731       24177.329217
HLA B*4601      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.312750       2.588946        -1.723804       20547.070557
HLA A*2301      1:202-210       9       LGASTALAF       1.310738        0.932777        -3.967354       2.243515        -1.723839       9275.866116
HLA A*0212      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.044958       2.320347        -1.724611       11090.674546
HLA B*2705      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.319253       2.594133        -1.725120       20857.069425
HLA B*5401      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.385936       2.660677        -1.725259       24318.476849
HLA A*6901      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.305032       2.579573        -1.725458       20185.144094
HLA A*0202      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.046415       2.320347        -1.726067       11127.936581
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HLA A*2501      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.388925       2.660677        -1.728248       24486.398608
HLA B*4402      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.307858       2.579573        -1.728285       20316.939366
HLA A*0206      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.307936       2.579573        -1.728362       20320.566798
HLA B*3501      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.332744       1.604221        -1.728523       2151.515482
HLA A*0101      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.308617       2.579573        -1.729044       20352.472103
HLA A*6802      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.389829       2.660677        -1.729153       24537.452208
HLA B*3901      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.324420       2.594133        -1.730286       21106.674092
HLA A*0202      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -2.236132       0.502462        -1.733670       172.239100
HLA A*0201      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.394655       2.660677        -1.733978       24811.630727
HLA B*3901      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -3.152069       1.417448        -1.734621       1419.283255
HLA A*0202      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -2.670443       0.934977        -1.735467       468.212980
HLA A*2301      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.396335       2.660677        -1.735658       24907.789725
HLA B*4001      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.316185       2.579573        -1.736611       20710.227010
HLA A*0201      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.330965       2.594133        -1.736832       21427.202278
HLA A*3201      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.633286       1.896327        -1.736959       4298.192857
HLA A*3101      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -3.130755       1.393369        -1.737385       1351.308632
HLA A*2403      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.328343       2.588946        -1.739397       21298.226642
HLA B*0801      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.304971       2.563256        -1.741715       20182.305110
HLA A*0211      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.638065       1.896327        -1.741738       4345.750117
HLA A*2501      1:191-199       9       VTPSTTATL       1.727960        0.494658        -3.967152       2.222618        -1.744534       9271.551518
HLA A*3301      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.066179       2.320347        -1.745831       11646.046230
HLA A*0301      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.336125       2.588946        -1.747179       21683.278032
HLA A*0212      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.019328       1.271968        -1.747360       1045.509240
HLA A*3301      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -3.496400       1.748514        -1.747886       3136.174382
HLA A*2301      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.327895       2.579573        -1.748321       21276.230789
HLA B*4402      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.311773       2.563256        -1.748516       20500.881083
HLA A*3001      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -3.310063       1.559867        -1.750195       2042.032018
HLA B*3801      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.339574       2.588946        -1.750628       21856.166100
HLA A*6901      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.269327       1.518523        -1.750804       1859.204562
HLA A*2603      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.346456       2.594133        -1.752322       22205.247802
HLA B*4001      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.346947       2.594133        -1.752813       22230.368738
HLA B*3901      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.317573       2.563256        -1.754317       20776.548636
HLA A*2301      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.349961       2.594133        -1.755828       22385.203958
HLA B*0702      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.360116       1.604221        -1.755895       2291.479498
HLA B*1801      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.000487       2.243515        -1.756972       10011.217783
HLA B*3901      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.338115       2.579573        -1.758542       21782.862613
HLA B*5801      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.348859       2.588946        -1.759913       22328.479360
HLA A*1101      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.420638       2.660677        -1.759961       26341.364233
HLA B*0802      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.349820       2.588946        -1.760874       22377.939049
HLA A*3101      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -3.056610       1.294185        -1.762424       1139.224991
HLA A*0212      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.356645       2.594133        -1.762512       22732.402683
HLA A*1101      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.356664       2.594133        -1.762531       22733.386542
HLA B*1509      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.357005       2.594133        -1.762871       22751.226378
HLA B*1509      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.342461       2.579573        -1.762888       22001.966525
HLA B*0802      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.358257       2.594133        -1.764124       22816.923550
HLA A*6802      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -2.461419       0.697019        -1.764400       289.347122
HLA A*0216      1:9-17  9       LLELATPYA       0.993939        -0.356018       -2.403110       0.637921        -1.765188       252.993666
HLA A*0216      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -2.577056       0.811766        -1.765290       377.620984
HLA B*4801      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.360193       2.594133        -1.766060       22918.862701
HLA A*0101      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.355468       2.588946        -1.766522       22670.873235
HLA B*0802      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.331146       2.563256        -1.767890       21436.129884
HLA A*8001      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.348455       2.579573        -1.768882       22307.712353
HLA A*0216      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.287996       1.518523        -1.769473       1940.868825
HLA A*0203      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.116611       1.344429        -1.772182       1308.008756
HLA A*0212      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -2.601730       0.829467        -1.772263       399.696560
HLA A*0216      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.366504       2.594133        -1.772370       23254.327238
HLA B*4801      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.336456       2.563256        -1.773200       21699.824224
HLA A*0301      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.336675       2.563256        -1.773419       21710.744580
HLA B*4402      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.371125       2.594133        -1.776992       23503.103692
HLA B*4002      1:5-13  9       TDFELLELA       1.003059        -0.335657       -2.444771       0.667402        -1.777369       278.465064
HLA A*3101      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.366346       2.588946        -1.777400       23245.899942
HLA A*6801      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -2.599212       0.820380        -1.778832       397.385268
HLA B*4001      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.342652       2.563256        -1.779396       22011.609922
HLA A*6801      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.359164       2.579573        -1.779591       22864.620025
HLA B*3901      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.024156       2.243515        -1.780641       10571.962671
HLA A*0101      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.344543       2.563256        -1.781287       22107.678656
HLA A*6802      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.376550       2.594133        -1.782417       23798.532484
HLA B*5801      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -3.899774       2.117084        -1.782690       7939.147761
HLA B*0702      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -3.389574       1.605818        -1.783755       2452.301246
HLA B*2705      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -2.720375       0.936177        -1.784198       525.260454
HLA A*3001      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -2.856941       1.072739        -1.784202       719.351030
HLA B*0702      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.027732       2.243515        -1.784216       10659.369995
HLA A*0219      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.379628       2.594133        -1.785495       23967.790662
HLA A*0206      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.348981       2.563256        -1.785725       22334.761563
HLA A*0250      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.380293       2.594133        -1.786160       24004.513420
HLA B*1801      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.352950       2.563256        -1.789694       22539.776256
HLA B*4002      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -3.097317       1.307494        -1.789822       1251.171031
HLA A*0216      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.450951       2.660677        -1.790274       28245.633461
HLA B*2705      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.379252       2.588946        -1.790306       23947.053543
HLA A*0201      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -2.985359       1.194858        -1.790501       966.849821
HLA A*3002      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.353793       2.563256        -1.790537       22583.594423
HLA A*6802      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.371614       2.579573        -1.792041       23529.565608
HLA A*6801      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.880955       2.087388        -1.793566       7602.466412
HLA A*0216      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -2.988667       1.194858        -1.793809       974.242556
HLA A*1101      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.373402       2.579573        -1.793828       23626.634756
HLA A*6901      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.383124       2.588946        -1.794178       24161.507998
HLA A*2603      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.556641       1.762358        -1.794283       3602.807004
HLA A*1101      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -3.542784       1.748241        -1.794543       3489.664985
HLA B*5701      1:98-106        9       AIAVGLGAF       1.301749        1.292384        -4.388791       2.594133        -1.794658       24478.849057
HLA B*0801      1:10-18 9       LELATPYAL       1.590569        0.388292        -3.774203       1.978861        -1.795343       5945.704342
HLA A*0206      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.040005       2.243515        -1.796490       10964.914430
HLA A*6901      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.360910       2.563256        -1.797654       22956.710411
HLA A*2601      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.361307       2.563256        -1.798051       22977.708670
HLA A*0219      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.362286       2.563256        -1.799030       23029.603142
HLA B*1509      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.388408       2.588946        -1.799462       24457.272830
HLA B*4801      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.389388       2.588946        -1.800441       24512.508854
HLA A*0211      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.461251       2.660677        -1.800575       28923.541026
HLA B*3901      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.390476       2.588946        -1.801529       24573.984222
HLA A*8001      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.367286       2.563256        -1.804030       23296.257505
HLA A*0202      1:36-44 9       APSPVAAAF       1.565257        1.095420        -4.464846       2.660677        -1.804169       29163.938474
HLA B*1503      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -3.891710       2.087388        -1.804322       7793.103649
HLA A*0211      1:13-21 9       ATPYALNAV       1.259075        0.203216        -3.266762       1.462291        -1.804470       1848.253506
HLA A*0201      1:85-93 9       QSRWRTAAF       1.378459        1.201114        -4.386808       2.579573        -1.807235       24367.334721
HLA B*0803      1:161-169       9       APPSRGTVY       1.374663        1.214283        -4.397381       2.588946        -1.808434       24967.824990
HLA B*0802      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -3.570813       1.762358        -1.808455       3722.314738
HLA A*0212      1:138-146       9       GAGTATVVF       1.568584        0.994672        -4.371940       2.563256        -1.808684       23547.265897
HLA A*2602      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -2.881648       1.072739        -1.808909       761.461683
HLA B*0801      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.053336       2.243515        -1.809821       11306.709255
HLA A*3002      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -3.706834       1.896327        -1.810507       5091.364342
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HLA A*0201	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.399949	2.588946	-1.811002	25115.897305
HLA A*6901	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-2.942612	1.128647	-1.813966	876.218646
HLA A*1101	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.377953	2.563256	-1.814697	23875.518950
HLA B*5301	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.059219	2.243515	-1.815704	11460.916150
HLA B*1801	1:200-208	9	TDLGASTAL	1.577364	0.302370	-3.695688	1.879734	-1.815954	4962.359455
HLA A*3101	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-2.906623	1.090544	-1.816079	806.534742
HLA B*4001	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.405837	2.588946	-1.816890	25458.716682
HLA A*0201	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.380349	2.563256	-1.817093	24007.630305
HLA A*0211	1:4-12  9	HTDFELLEL	1.651839	0.218398	-3.687470	1.870237	-1.817233	4869.335752
HLA A*0202	1:221-229	9	PTGTILAEL	1.442456	0.106507	-3.368006	1.548963	-1.819043	2333.487864
HLA A*0101	1:8-16  9	ELLELATPY	1.168179	1.152168	-4.139614	2.320347	-1.819267	13791.579683
HLA B*1503	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-2.948087	1.128647	-1.819440	887.333322
HLA A*2603	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.408623	2.588946	-1.819677	25622.588229
HLA B*0803	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.415328	2.594133	-1.821195	26021.266311
HLA B*5801	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.043985	2.222618	-1.821367	11065.862624
HLA B*5701	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.411480	2.588946	-1.822534	25791.700144
HLA A*2602	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.386467	2.563256	-1.823211	24348.227652
HLA A*0203	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-3.020498	1.194858	-1.825639	1048.329770
HLA A*2301	1:10-18 9	LELATPYAL	1.590569	0.388292	-3.805865	1.978861	-1.827004	6395.359604
HLA B*2705	1:8-16  9	ELLELATPY	1.168179	1.152168	-4.148091	2.320347	-1.827744	14063.420253
HLA A*6802	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-3.375608	1.546761	-1.828847	2374.698511
HLA A*0203	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.392266	1.562118	-1.830149	2467.552086
HLA A*0203	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.422158	2.588946	-1.833212	26433.725779
HLA A*0212	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.412873	2.579573	-1.833300	25874.574437
HLA A*1101	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.423906	2.588946	-1.834960	26540.334807
HLA A*0202	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-2.713002	0.877544	-1.835458	516.418772
HLA A*1101	1:8-16  9	ELLELATPY	1.168179	1.152168	-4.155830	2.320347	-1.835483	14316.279164
HLA A*6901	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-3.090903	1.254367	-1.836536	1232.828275
HLA B*3901	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.059703	2.222618	-1.837085	11473.695740
HLA A*0212	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.428302	2.588946	-1.839356	26810.337656
HLA B*1502	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-3.816738	1.977371	-1.839368	6557.501310
HLA B*5301	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-3.558892	1.718268	-1.840624	3621.527647
HLA A*3002	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.084566	2.243515	-1.841050	12149.700696
HLA B*2705	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.404702	2.563256	-1.841446	25392.280491
HLA B*5401	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.431103	2.588946	-1.842156	26983.785119
HLA B*3501	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-2.606500	0.764021	-1.842479	404.110249
HLA B*5101	1:93-101	9	FASAAAIAV	1.212843	0.182258	-3.239127	1.395101	-1.844026	1734.310671
HLA A*0203	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-2.874398	1.029850	-1.844547	748.854672
HLA A*0203	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.410836	2.563256	-1.847580	25753.497180
HLA A*0219	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.427868	2.579573	-1.848294	26783.518502
HLA A*0250	1:49-57 9	RAVRETMAV	0.926962	0.318191	-3.093703	1.245153	-1.848551	1240.803965
HLA B*3801	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.442770	2.594133	-1.848637	27718.543895
HLA B*3501	1:10-18 9	LELATPYAL	1.590569	0.388292	-3.827631	1.978861	-1.848770	6724.044802
HLA B*4001	1:200-208	9	TDLGASTAL	1.577364	0.302370	-3.730367	1.879734	-1.850633	5374.853339
HLA B*2705	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-2.880765	1.029850	-1.850914	759.914354
HLA A*0203	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-3.297836	1.446716	-1.851120	1985.344273
HLA A*0219	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.441358	2.588946	-1.852412	27628.567742
HLA A*0216	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.416111	2.563256	-1.852855	26068.185692
HLA A*6802	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.418909	2.563256	-1.855653	26236.689920
HLA B*1501	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-3.943056	2.087388	-1.855668	8771.141104
HLA A*6802	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.444688	2.588946	-1.855741	27841.177044
HLA A*3101	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-3.604340	1.748241	-1.856100	4021.057124
HLA A*0212	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-3.578670	1.718268	-1.860402	3790.266698
HLA A*0202	1:50-58 9	AVRETMAVV	1.181875	0.336648	-3.379748	1.518523	-1.861225	2397.442901
HLA A*3001	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-3.604448	1.742555	-1.861893	4022.057909
HLA B*2705	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-3.281154	1.417448	-1.863706	1910.532738
HLA B*5101	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.427348	2.563256	-1.864092	26751.515651
HLA A*3201	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-3.952976	2.087388	-1.865587	8973.784239
HLA A*6802	1:4-12  9	HTDFELLEL	1.651839	0.218398	-3.736240	1.870237	-1.866003	5448.040544
HLA B*1501	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-3.985958	2.117084	-1.868874	9681.835374
HLA A*6802	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-3.213311	1.344429	-1.868882	1634.220880
HLA A*6802	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-2.908803	1.039542	-1.869262	810.594032
HLA B*5101	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.464917	2.594133	-1.870783	29168.672069
HLA A*0203	1:4-12  9	HTDFELLEL	1.651839	0.218398	-3.741555	1.870237	-1.871318	5515.118724
HLA B*3801	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.434672	2.563256	-1.871416	27206.441253
HLA B*4501	1:36-44 9	APSPVAAAF	1.565257	1.095420	-4.533125	2.660677	-1.872448	34129.078084
HLA A*3201	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.434656	1.562118	-1.872538	2720.543892
HLA A*0216	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.462208	2.588946	-1.873261	28987.295761
HLA A*0250	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-2.935865	1.060336	-1.875529	862.709877
HLA A*0250	1:204-212	9	ASTALAFTV	1.108485	0.186630	-3.172618	1.295115	-1.877503	1488.050516
HLA B*3501	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.101129	2.222618	-1.878511	12622.036991
HLA A*3201	1:49-57 9	RAVRETMAV	0.926962	0.318191	-3.124702	1.245153	-1.879550	1332.607575
HLA A*2601	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-3.967495	2.087388	-1.880107	9278.877489
HLA A*6901	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-3.598636	1.718268	-1.880368	3968.585061
HLA B*5701	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.104663	2.222618	-1.882045	12725.154797
HLA B*1509	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-3.969450	2.087388	-1.882062	9320.736107
HLA B*3501	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-3.488919	1.605818	-1.883101	3082.616102
HLA A*2501	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.446743	2.563256	-1.883487	27973.279933
HLA A*0201	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-3.602042	1.718268	-1.883774	3999.838410
HLA A*3301	1:44-52 9	FNDEVRAVR	1.108729	0.527663	-3.521465	1.636392	-1.885072	3322.496322
HLA B*5301	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-3.862995	1.977371	-1.885624	7294.491906
HLA A*0202	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-3.516117	1.630187	-1.885930	3281.837559
HLA B*0803	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.449950	2.563256	-1.886694	28180.613166
HLA B*1509	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.450625	2.563256	-1.887369	28224.401447
HLA A*0219	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-3.159625	1.271968	-1.887657	1444.192292
HLA B*1503	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-3.012303	1.123686	-1.888617	1028.733577
HLA A*0206	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-3.233864	1.344429	-1.889436	1713.420859
HLA A*6801	1:36-44 9	APSPVAAAF	1.565257	1.095420	-4.550682	2.660677	-1.890005	35537.122425
HLA A*0216	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.787412	1.896327	-1.891085	6129.317440
HLA A*2403	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.136001	2.243515	-1.892485	13677.304161
HLA B*5101	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.472468	2.579573	-1.892895	29680.273781
HLA A*0250	1:201-209	9	DLGASTALA	1.029007	-0.426525	-2.496093	0.602482	-1.893611	313.395579
HLA A*6802	1:8-16  9	ELLELATPY	1.168179	1.152168	-4.217297	2.320347	-1.896950	16492.913645
HLA A*0250	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.459344	1.562118	-1.897227	2879.679306
HLA B*2705	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-2.726930	0.829467	-1.897463	533.248654
HLA B*4403	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.481558	2.579573	-1.901985	30308.054545
HLA A*0202	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.466904	2.563256	-1.903648	29302.476223
HLA A*0216	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.483832	2.579573	-1.904259	30467.187245
HLA A*0250	1:36-44 9	APSPVAAAF	1.565257	1.095420	-4.565721	2.660677	-1.905044	36789.281995
HLA A*0211	1:204-212	9	ASTALAFTV	1.108485	0.186630	-3.200811	1.295115	-1.905697	1587.857391
HLA B*0702	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-3.250470	1.344429	-1.906042	1780.205792
HLA B*4403	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.470581	2.563256	-1.907325	29551.618138
HLA A*0211	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.473499	2.563256	-1.910243	29750.846460
HLA B*1509	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.133397	2.222618	-1.910779	13595.565472
HLA A*2402	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.154524	2.243515	-1.911009	14273.281950
HLA A*0212	1:13-21 9	ATPYALNAV	1.259075	0.203216	-3.374542	1.462291	-1.912251	2368.873195
HLA A*0211	1:85-93 9	QSRWRTAAF	1.378459	1.201114	-4.492107	2.579573	-1.912534	31053.263453
HLA A*3201	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.156403	2.243515	-1.912888	14335.189316
HLA B*5801	1:91-99 9	AAFASAAAI	1.234627	0.369594	-3.517456	1.604221	-1.913235	3291.973174
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HLA A*0206	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.504301	2.588946	-1.915355	31937.511584
HLA A*3201	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-3.043241	1.123686	-1.919555	1104.691300
HLA A*2603	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.485282	2.563256	-1.922026	30569.053633
HLA A*2601	1:47-55	9	EVRAVRETM	1.250113	0.064179	-3.237811	1.314292	-1.923519	1729.064462
HLA A*6801	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.643835	1.718268	-1.925567	4403.876038
HLA A*0202	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.507377	2.579573	-1.927803	32164.481205
HLA B*1503	1:88-96	9	WRTAAFASA	1.223245	-0.112038	-3.040943	1.111207	-1.929736	1098.861955
HLA A*6801	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.526746	2.594133	-1.932612	33631.458763
HLA A*2603	1:36-44	9	APSPVAAAF	1.565257	1.095420	-4.595165	2.660677	-1.934488	39369.967653
HLA B*5701	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.178052	2.243515	-1.934536	15067.860389
HLA A*3101	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.157240	2.222618	-1.934622	14362.824355
HLA A*6901	1:49-57	9	RAVRETMAV	0.926962	0.318191	-3.180775	1.245153	-1.935622	1516.264918
HLA A*0201	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-2.995997	1.060336	-1.935662	990.826217
HLA A*2402	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.525663	2.588946	-1.936716	33547.687791
HLA A*2602	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-3.483732	1.546761	-1.936970	3046.013191
HLA A*0203	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.258984	2.320347	-1.938637	18154.500214
HLA A*6802	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-3.925289	1.986196	-1.939093	8419.557982
HLA B*4002	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.518992	2.579573	-1.939419	33036.376332
HLA B*5301	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.519021	2.579573	-1.939447	33038.521080
HLA B*1503	1:2-10	9	TEHTDFELL	1.490281	0.376705	-3.808943	1.866986	-1.941957	6440.844212
HLA B*4002	1:36-44	9	APSPVAAAF	1.565257	1.095420	-4.603012	2.660677	-1.942335	40087.810602
HLA A*6801	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.505661	2.563256	-1.942405	32037.707116
HLA B*3801	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.165820	2.222618	-1.943202	14649.411170
HLA B*5301	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.538058	2.594133	-1.943925	34519.021429
HLA B*7301	1:36-44	9	APSPVAAAF	1.565257	1.095420	-4.604911	2.660677	-1.944234	40263.425599
HLA A*0201	1:91-99	9	AAFASAAAI	1.234627	0.369594	-3.550523	1.604221	-1.946302	3552.408818
HLA A*3001	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.266785	2.320347	-1.946437	18483.515995
HLA A*0219	1:9-17	9	LLELATPYA	0.993939	-0.356018	-2.584368	0.637921	-1.946446	384.032268
HLA B*0801	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.064379	2.117084	-1.947295	11597.885162
HLA A*0211	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.536585	2.588946	-1.947639	34402.131249
HLA B*1503	1:50-58	9	AVRETMAVV	1.181875	0.336648	-3.466505	1.518523	-1.947982	2927.556974
HLA B*0801	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.269985	2.320347	-1.949637	18620.210496
HLA A*0211	1:9-17	9	LLELATPYA	0.993939	-0.356018	-2.587798	0.637921	-1.949877	387.077533
HLA B*3901	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.668218	1.718268	-1.949950	4658.199035
HLA A*3301	1:36-44	9	APSPVAAAF	1.565257	1.095420	-4.610855	2.660677	-1.950178	40818.300522
HLA B*5401	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-3.232544	1.282277	-1.950267	1708.219358
HLA A*2301	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.541125	2.588946	-1.952178	34763.584733
HLA A*3101	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.848875	1.896327	-1.952548	7061.137067
HLA B*4501	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.547567	2.594133	-1.953433	35283.108590
HLA A*3201	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.542642	2.588946	-1.953696	34885.288646
HLA B*5401	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.548464	2.594133	-1.954331	35356.099268
HLA A*2403	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.850886	1.896327	-1.954559	7093.912070
HLA A*3201	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.540307	1.584079	-1.956229	3469.823457
HLA A*3001	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.043816	2.087388	-1.956428	11061.553177
HLA B*4801	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.853475	1.896327	-1.957148	7136.330147
HLA A*0201	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.277529	2.320347	-1.957181	18946.490768
HLA A*0202	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.541369	1.584079	-1.957291	3478.318494
HLA A*0203	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-3.083079	1.124732	-1.958347	1210.817813
HLA B*5401	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-2.707951	0.748881	-1.959070	510.446967
HLA B*0803	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.279641	2.320347	-1.959294	19038.861283
HLA B*1501	1:10-18	9	LELATPYAL	1.590569	0.388292	-3.938197	1.978861	-1.959337	8673.559513
HLA B*4501	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.539419	2.579573	-1.959845	34627.315768
HLA B*5801	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.856689	1.896327	-1.960362	7189.340102
HLA A*0211	1:49-57	9	RAVRETMAV	0.926962	0.318191	-3.206906	1.245153	-1.961753	1610.297278
HLA B*1503	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-3.448466	1.485661	-1.962805	2808.445561
HLA A*3101	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.284829	2.320347	-1.964481	19267.644845
HLA B*5801	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.289236	2.320347	-1.968889	19464.186909
HLA B*4001	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.289387	2.320347	-1.969039	19470.927218
HLA B*3901	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.290373	2.320347	-1.970026	19515.218451
HLA B*4002	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.565952	2.594133	-1.971818	36808.791708
HLA B*5401	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.552261	2.579573	-1.972688	35666.550819
HLA B*0702	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.195988	2.222618	-1.973370	15703.178092
HLA A*0219	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.061776	2.087388	-1.974387	11528.573556
HLA A*0250	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.873009	1.896327	-1.976681	7464.634571
HLA A*2501	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.066545	2.087388	-1.979157	11655.878974
HLA A*0101	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.224111	2.243515	-1.980596	16753.706060
HLA B*4403	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.572140	2.588946	-1.983194	37337.058905
HLA B*5401	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.547416	2.563256	-1.984160	35270.894531
HLA A*0250	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.549275	2.563256	-1.986019	35422.149927
HLA B*0801	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-3.963464	1.977371	-1.986093	9193.136835
HLA B*1503	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-3.404065	1.417448	-1.986617	2535.510669
HLA A*3001	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-3.749374	1.762358	-1.987016	5615.312780
HLA B*4403	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.583042	2.594133	-1.988908	38286.151661
HLA A*0250	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.581031	2.588946	-1.992084	38109.263546
HLA B*4402	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.313304	2.320347	-1.992957	20573.320450
HLA B*5301	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-3.598885	1.605818	-1.993066	3970.861492
HLA A*3001	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.237740	2.243515	-1.994225	17287.820877
HLA A*3301	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.589815	2.594133	-1.995682	38887.970680
HLA A*8001	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.239331	2.243515	-1.995816	17351.253524
HLA A*0202	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.239820	2.243515	-1.996304	17370.789131
HLA B*7301	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.576764	2.579573	-1.997191	37736.697579
HLA A*0202	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.059946	1.060336	-1.999610	1148.010267
HLA A*0212	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.870861	1.870237	-2.000624	7427.815753
HLA A*6801	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.589947	2.588946	-2.001000	38899.753722
HLA A*0250	1:85-93	9	QSRWRTAAF	1.378459	1.201114	-4.581338	2.579573	-2.001765	38136.280981
HLA B*0801	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-3.549094	1.546761	-2.002333	3540.743386
HLA B*1501	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-3.632999	1.630187	-2.002812	4295.356958
HLA A*0212	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.124004	2.117084	-2.006920	13304.667780
HLA A*0202	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.597350	2.588946	-2.008404	39568.544834
HLA B*7301	1:98-106	9	AIAVGLGAF	1.301749	1.292384	-4.606621	2.594133	-2.012488	40422.311719
HLA A*0101	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.731555	1.718268	-2.013287	5389.586640
HLA A*3001	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.131903	2.117084	-2.014819	13548.867735
HLA B*4601	1:91-99	9	AAFASAAAI	1.234627	0.369594	-3.621332	1.604221	-2.017111	4181.496315
HLA B*3801	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-3.995342	1.977371	-2.017971	9893.308162
HLA A*0216	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-2.847566	0.829467	-2.018099	703.989894
HLA B*4002	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.582520	2.563256	-2.019264	38240.197770
HLA A*8001	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.916023	1.896327	-2.019696	8241.816164
HLA A*0211	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.081157	1.060336	-2.020821	1205.471432
HLA B*4801	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.341945	2.320347	-2.021597	21975.795898
HLA A*3001	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-3.634447	1.612334	-2.022112	4309.695077
HLA B*0801	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.245825	2.222618	-2.023207	17612.655155
HLA B*7301	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.614036	2.588946	-2.025090	41118.391902
HLA B*1503	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-3.155988	1.130830	-2.025158	1432.148393
HLA B*1509	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.008649	1.977371	-2.031278	10201.147331
HLA B*4501	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.621085	2.588946	-2.032138	41791.174479
HLA A*3301	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.621742	2.588946	-2.032796	41854.526422
HLA B*4002	1:161-169	9	APPSRGTVY	1.374663	1.214283	-4.623093	2.588946	-2.034147	41984.925432
HLA B*4001	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.151756	2.117084	-2.034672	14182.609700
HLA B*0702	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.355231	2.320347	-2.034884	22658.489280
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HLA B*4501	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.598492	2.563256	-2.035236	39672.715578
HLA A*1101	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.013465	1.977177	-2.036289	10314.910504
HLA A*0212	1:9-17	9	LLELATPYA	0.993939	-0.356018	-2.675171	0.637921	-2.037249	473.337174
HLA B*4402	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.280813	2.243515	-2.037298	19090.326784
HLA B*1503	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-3.783084	1.742555	-2.040529	6068.542012
HLA B*0802	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.361988	2.320347	-2.041641	23013.785951
HLA B*4601	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.264398	2.222618	-2.041780	18382.201014
HLA B*5101	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.023023	1.977371	-2.045652	10544.431485
HLA B*7301	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-3.381327	1.335319	-2.046008	2406.174536
HLA A*3101	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.136320	2.087388	-2.048932	13687.370871
HLA A*0206	1:200-208	9	TDLGASTAL	1.577364	0.302370	-3.928917	1.879734	-2.049183	8490.179983
HLA A*2601	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.166736	2.117084	-2.049652	14680.351958
HLA B*5701	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.370200	2.320347	-2.049852	23453.060265
HLA A*6901	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.293374	2.243515	-2.049859	19650.504711
HLA A*0211	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-2.927797	0.877544	-2.050252	846.830787
HLA A*0201	1:13-21	9	ATPYALNAV	1.259075	0.203216	-3.515314	1.462291	-2.053022	3275.771176
HLA A*0250	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-3.818999	1.762358	-2.056640	6591.717560
HLA A*3301	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.620753	2.563256	-2.057497	41759.308561
HLA B*1503	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-3.393497	1.335319	-2.058178	2474.556982
HLA B*7301	1:138-146	9	GAGTATVVF	1.568584	0.994672	-4.622100	2.563256	-2.058843	41888.957686
HLA A*6802	1:50-58	9	AVRETMAVV	1.181875	0.336648	-3.577664	1.518523	-2.059141	3781.500744
HLA A*2403	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.380086	2.320347	-2.059739	23993.088306
HLA A*8001	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.929984	1.870237	-2.059747	8511.058255
HLA A*6901	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.621877	1.562118	-2.059759	4186.747782
HLA B*5801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-3.355347	1.295115	-2.060232	2266.451977
HLA B*5301	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.381999	2.320347	-2.061651	24098.978444
HLA A*3001	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-3.763217	1.697997	-2.065220	5797.184437
HLA B*4402	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-3.891424	1.825968	-2.065455	7787.961847
HLA A*6802	1:221-229	9	PTGTILAEL	1.442456	0.106507	-3.615341	1.548963	-2.066378	4124.207727
HLA A*0211	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.785283	1.718268	-2.067015	6099.348954
HLA B*0702	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-3.460862	1.393369	-2.067493	2889.760782
HLA B*1503	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.629677	1.562118	-2.067560	4262.624621
HLA A*0216	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.939443	1.870237	-2.069206	8698.464387
HLA A*2601	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.292775	2.222618	-2.070157	19623.415103
HLA A*3001	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-3.415052	1.344429	-2.070623	2600.468720
HLA B*5701	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.187948	2.117084	-2.070864	15415.145150
HLA B*4403	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.392604	2.320347	-2.072257	24694.725812
HLA B*3901	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.945265	1.870237	-2.075028	8815.858555
HLA A*0250	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-3.146820	1.071321	-2.075499	1402.233471
HLA A*0206	1:2-10	9	TEHTDFELL	1.490281	0.376705	-3.944052	1.866986	-2.077066	8791.283378
HLA B*4801	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.301031	2.222618	-2.078413	20000.031564
HLA A*2402	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.975352	1.896327	-2.079025	9448.266150
HLA B*3801	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.400014	2.320347	-2.079667	25119.702071
HLA A*2601	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.325599	2.243515	-2.082084	21164.072751
HLA A*3001	1:13-21	9	ATPYALNAV	1.259075	0.203216	-3.545166	1.462291	-2.082875	3508.860589
HLA B*1509	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.326400	2.243515	-2.082885	21203.151678
HLA A*0101	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.305857	2.222618	-2.083239	20223.509495
HLA A*3001	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-3.981263	1.896327	-2.084936	9577.748367
HLA B*1509	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.405745	2.320347	-2.085397	25453.345824
HLA B*3501	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.173146	2.087388	-2.085758	14898.613812
HLA B*4403	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-3.913147	1.825968	-2.087179	8187.421586
HLA A*2902	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.311697	2.222618	-2.089079	20497.332351
HLA A*6802	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-3.853296	1.762358	-2.090938	7133.396636
HLA B*1503	1:86-94	9	SRWRTAAFA	1.225790	-0.065711	-3.252270	1.160079	-2.092191	1787.598227
HLA A*0250	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.810987	1.718268	-2.092719	6471.230164
HLA B*0802	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.315506	2.222618	-2.092888	20677.872739
HLA A*0250	1:13-21	9	ATPYALNAV	1.259075	0.203216	-3.556589	1.462291	-2.094298	3602.378232
HLA A*3001	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-3.816593	1.721236	-2.095357	6555.302207
HLA B*5101	1:8-16	9	ELLELATPY	1.168179	1.152168	-4.415859	2.320347	-2.095512	26053.100277
HLA A*2403	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.082883	1.986196	-2.096687	12102.730094
HLA A*0301	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.341778	2.243515	-2.098263	21967.356569
HLA B*1501	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-3.226980	1.128647	-2.098333	1686.475587
HLA B*5801	1:4-12	9	HTDFELLEL	1.651839	0.218398	-3.970385	1.870237	-2.100148	9340.826539
HLA A*0216	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.162111	1.060336	-2.101775	1452.482063
HLA B*1509	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.220577	2.117084	-2.103493	16617.943044
HLA A*0206	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-3.060021	0.955042	-2.104979	1148.209023
HLA B*2705	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.348836	2.243515	-2.105321	22327.271447
HLA B*4801	1:200-208	9	TDLGASTAL	1.577364	0.302370	-3.985539	1.879734	-2.105805	9672.516639
HLA B*1503	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-3.413905	1.307494	-2.106411	2593.612469
HLA B*4801	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.350760	2.243515	-2.107245	22426.416349
HLA A*6901	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.086769	1.978861	-2.107909	12211.510755
HLA A*2301	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-3.826418	1.718268	-2.108150	6705.300787
HLA B*5101	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.351697	2.243515	-2.108182	22474.877079
HLA A*0202	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-3.180291	1.071321	-2.108970	1514.576077
HLA B*1517	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-2.858769	0.746698	-2.112070	722.385083
HLA B*4001	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.355856	2.243515	-2.112341	22691.119010
HLA B*3501	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-3.458296	1.344429	-2.113868	2872.739561
HLA A*6801	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.336910	2.222618	-2.114292	21722.493029
HLA A*0201	1:204-212	9	ASTALAFTV	1.108485	0.186630	-3.411048	1.295115	-2.115934	2576.606581
HLA B*1501	1:47-55	9	EVRAVRETM	1.250113	0.064179	-3.430356	1.314292	-2.116064	2693.743127
HLA B*1517	1:49-57	9	RAVRETMAV	0.926962	0.318191	-3.361812	1.245153	-2.116660	2300.447381
HLA A*3001	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.103009	1.986196	-2.116813	12676.782429
HLA A*0301	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.339614	2.222618	-2.116996	21858.176263
HLA A*2402	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-3.943000	1.825968	-2.117031	8770.002356
HLA A*1101	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.361694	2.243515	-2.118179	22998.228458
HLA A*0219	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.097389	1.978861	-2.118528	12513.795933
HLA A*2403	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.236157	2.117084	-2.119073	17224.899679
HLA A*0203	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.363224	2.243515	-2.119709	23079.367284
HLA A*3002	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.207500	2.087388	-2.120112	16125.011484
HLA B*5101	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.343190	2.222618	-2.120572	22038.896225
HLA B*1501	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-2.951141	0.829467	-2.121674	893.595805
HLA A*2402	1:62-70	9	TTAEPPAHL	1.615381	0.472007	-4.209751	2.087388	-2.122363	16208.799093
HLA B*1517	1:93-101	9	FASAAAIAV	1.212843	0.182258	-3.518119	1.395101	-2.123018	3296.999204
HLA A*8001	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.347496	2.222618	-2.124878	22258.528295
HLA B*4001	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.347734	2.222618	-2.125116	22270.693651
HLA B*0802	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.368973	2.243515	-2.125458	23386.923139
HLA B*1502	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.348641	2.222618	-2.126023	22317.248288
HLA B*3501	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-2.661107	0.534755	-2.126352	458.254350
HLA A*3101	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.370792	2.243515	-2.127276	23485.055441
HLA A*6802	1:49-57	9	RAVRETMAV	0.926962	0.318191	-3.372535	1.245153	-2.127383	2357.954136
HLA A*2601	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-3.674566	1.546761	-2.127805	4726.790452
HLA A*3201	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-3.312544	1.184095	-2.128448	2053.731212
HLA A*2501	1:13-21	9	ATPYALNAV	1.259075	0.203216	-3.590793	1.462291	-2.128502	3897.562717
HLA A*0203	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.712745	1.584079	-2.128667	5161.138111
HLA B*1501	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.115020	1.986196	-2.128824	13032.256044
HLA A*2301	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.027802	1.896327	-2.131475	10661.100115
HLA A*2902	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.118008	1.986196	-2.131812	13122.245207
HLA A*6801	1:75-83	9	LDATKPEVR	1.264680	0.523618	-3.920294	1.788298	-2.131996	8323.275825
HLA B*3801	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.379179	2.243515	-2.135664	23943.037802
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HLA B*7301      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -3.247059       1.111207        -2.135851       1766.276772
HLA A*2902      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.223989       2.087388        -2.136600       16748.993667
HLA A*0219      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.380798       2.243515        -2.137283       24032.449942
HLA B*7301      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -2.933609       0.795947        -2.137663       858.241013
HLA A*6802      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.382628       2.243515        -2.139113       24133.943696
HLA A*0201      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.383679       2.243515        -2.140163       24192.375514
HLA B*5301      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.258002       2.117084        -2.140918       18113.493214
HLA A*0202      1:165-173       9               RGTVYQMWL       1.283587        0.414410        -3.839524       1.697997        -2.141526       6910.726277
HLA A*3101      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.051081       1.909325        -2.141756       11248.140154
HLA A*0201      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.661386       1.518523        -2.142862       4585.489874
HLA B*4801      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.748730       1.604221        -2.144509       5606.995314
HLA B*0702      1:100-108       9               AVGLGAFGL       1.513599        0.472597        -4.131565       1.986196        -2.145369       13538.316952
HLA A*0203      1:97-105        9               AAIAVGLGA       1.149375        -0.048796       -3.247444       1.100579        -2.146866       1767.844546
HLA B*0702      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.462173       1.314292        -2.147881       2898.497335
HLA B*2705      1:164-172       9               SRGTVYQMW       1.464059        0.361909        -3.976118       1.825968        -2.150150       9464.944040
HLA A*6901      1:200-208       9               TDLGASTAL       1.577364        0.302370        -4.031444       1.879734        -2.151710       10750.872799
HLA A*0212      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.395821       2.243515        -2.152306       24878.297304
HLA B*0702      1:127-135       9               APDVRTVSR       1.139444        0.502399        -3.797327       1.641843        -2.155484       6270.857630
HLA B*4801      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.242975       2.087388        -2.155587       17497.455862
HLA A*6802      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -3.089441       0.932462        -2.156979       1228.686840
HLA A*2602      1:223-231       9               GTILAELPL       1.220795        0.363284        -3.743641       1.584079        -2.159562       5541.676994
HLA B*4402      1:200-208       9               TDLGASTAL       1.577364        0.302370        -4.039658       1.879734        -2.159923       10956.138736
HLA A*3001      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.878379       1.718268        -2.160111       7557.522948
HLA A*0201      1:9-17  9       LLELATPYA       0.993939        -0.356018       -2.798457       0.637921        -2.160536       628.720309
HLA B*1503      1:122-130       9               EQVLTAPDV       1.040047        0.179767        -3.382760       1.219814        -2.162946       2414.128106
HLA A*2601      1:146-154       9               FSRDRNTGL       1.328162        0.434196        -3.926046       1.762358        -2.163688       8434.237502
HLA B*0803      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.408748       2.243515        -2.165232       25629.935896
HLA B*3901      1:100-108       9               AVGLGAFGL       1.513599        0.472597        -4.151620       1.986196        -2.165424       14178.160270
HLA A*0206      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -3.612296       1.446716        -2.165580       4095.393146
HLA A*0202      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.510070       1.344429        -2.165641       3236.454506
HLA B*4402      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.391481       2.222618        -2.168863       24630.949549
HLA B*2705      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.286194       2.117084        -2.169110       19328.301134
HLA B*1509      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.148716       1.978861        -2.169855       14083.672512
HLA A*0202      1:92-100        9               AFASAAAIA       1.132156        -0.021408       -3.280943       1.110748        -2.170195       1909.602745
HLA B*1503      1:147-155       9               SRDRNTGLL       1.371307        0.406957        -3.948883       1.778264        -2.170619       8889.612297
HLA B*2705      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.396143       2.222618        -2.173525       24896.742808
HLA B*0803      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.396664       2.222618        -2.174046       24926.661644
HLA A*0206      1:189-197       9               AAVTPSTTA       1.238891        -0.108061       -3.305058       1.130830        -2.174228       2018.636605
HLA A*2403      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.045019       1.870237        -2.174782       11092.234638
HLA B*3801      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.292316       2.117084        -2.175232       19602.724720
HLA A*2501      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -2.996792       0.820380        -2.176412       992.639642
HLA A*8001      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.293975       2.117084        -2.176891       19677.738170
HLA B*1501      1:223-231       9               GTILAELPL       1.220795        0.363284        -3.761079       1.584079        -2.177000       5768.715038
HLA A*3301      1:142-150       9               ATVVFSRDR       0.986082        0.735154        -3.898350       1.721236        -2.177114       7913.162734
HLA B*0802      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.295039       2.117084        -2.177955       19726.021144
HLA A*0203      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -2.942528       0.764021        -2.178507       876.048014
HLA B*1503      1:165-173       9               RGTVYQMWL       1.283587        0.414410        -3.878502       1.697997        -2.180504       7559.649285
HLA A*0219      1:169-177       9               YQMWLLGGA       0.988610        -0.159143       -3.010015       0.829467        -2.180548       1023.327197
HLA A*3101      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.298944       2.117084        -2.181860       19904.182195
HLA A*2602      1:100-108       9               AVGLGAFGL       1.513599        0.472597        -4.171614       1.986196        -2.185418       14846.155282
HLA A*1101      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.408860       2.222618        -2.186242       25636.592206
HLA A*0216      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.165200       1.978861        -2.186339       14628.503658
HLA A*3301      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.273767       2.087388        -2.186379       18783.099413
HLA B*1502      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.274425       2.087388        -2.187037       18811.573029
HLA A*6802      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.054877       1.866986        -2.187892       11346.906778
HLA B*0702      1:93-101        9               FASAAAIAV       1.212843        0.182258        -3.583529       1.395101        -2.188428       3832.908967
HLA A*3002      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.306822       2.117084        -2.189738       20268.525776
HLA A*2402      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.510370       2.320347        -2.190022       32386.930906
HLA A*0301      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.278325       2.087388        -2.190937       18981.269613
HLA B*1509      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.058110       1.866986        -2.191124       11431.688403
HLA B*4002      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -3.349050       1.157030        -2.192020       2233.828880
HLA A*0216      1:194-202       9               STTATLTDL       1.210982        0.351136        -3.754454       1.562118        -2.192336       5681.376082
HLA A*0211      1:156-164       9               VMNNVAPPS       0.722767        -0.916838       -1.998979       -0.194071       -2.193051       99.765281
HLA A*2301      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.513847       2.320347        -2.193500       32647.282148
HLA A*0216      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.437378       2.243515        -2.193863       27376.526478
HLA B*0702      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.440097       1.245153        -2.194945       2754.844846
HLA A*6901      1:122-130       9               EQVLTAPDV       1.040047        0.179767        -3.416790       1.219814        -2.196976       2610.900089
HLA B*1801      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.420201       2.222618        -2.197583       26314.871847
HLA A*1101      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.315358       2.117084        -2.198274       20670.826445
HLA A*0101      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.286149       2.087388        -2.198761       19326.314520
HLA B*3501      1:129-137       9               DVRTVSRPL       1.249474        0.297287        -3.747523       1.546761        -2.200761       5591.425695
HLA A*0301      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.319805       2.117084        -2.202721       20883.602379
HLA A*3001      1:223-231       9               GTILAELPL       1.220795        0.363284        -3.786806       1.584079        -2.202727       6120.768404
HLA B*7301      1:164-172       9               SRGTVYQMW       1.464059        0.361909        -4.029799       1.825968        -2.203831       10710.237069
HLA A*3101      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.922517       1.718268        -2.204249       8365.981498
HLA B*4601      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.323132       2.117084        -2.206048       21044.193501
HLA A*0250      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.076690       1.870237        -2.206453       11931.364284
HLA A*1101      1:166-174       9               GTVYQMWLL       1.476128        0.420199        -4.103192       1.896327        -2.206865       12682.132797
HLA A*0211      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.453461       2.243515        -2.209945       28409.302363
HLA B*1501      1:93-101        9               FASAAAIAV       1.212843        0.182258        -3.605435       1.395101        -2.210334       4031.207031
HLA B*4402      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.327422       2.117084        -2.210338       21253.107851
HLA B*0702      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.299179       2.087388        -2.211791       19914.953050
HLA B*3901      1:112-120       9               TRPSPPPTV       1.255605        0.230056        -3.698057       1.485661        -2.212395       4989.493953
HLA B*0702      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -3.341987       1.128647        -2.213340       2197.795853
HLA A*0250      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.817608       1.604221        -2.213386       6570.640337
HLA A*2501      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.457704       2.243515        -2.214189       28688.229001
HLA A*6802      1:195-203       9               TTATLTDLG       0.805893        -0.593490       -2.428780       0.212403        -2.216377       268.398523
HLA B*3501      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.193751       1.977177        -2.216574       15622.511261
HLA B*5301      1:191-199       9               VTPSTTATL       1.727960        0.494658        -4.439606       2.222618        -2.216988       27517.289694
HLA A*3001      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -3.090625       0.872785        -2.217840       1232.041529
HLA B*1503      1:200-208       9               TDLGASTAL       1.577364        0.302370        -4.099353       1.879734        -2.219619       12570.519844
HLA A*0206      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.040196       0.820380        -2.219816       1096.973158
HLA A*6801      1:105-113       9               AFGLGVLTR       1.052600        0.695914        -3.969399       1.748514        -2.220884       9319.626842
HLA B*5401      1:113-121       9               RPSPPPTVA       1.222805        -0.255065       -3.191207       0.967740        -2.223467       1553.126394
HLA B*5401      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.543878       2.320347        -2.223531       34984.699657
HLA A*0212      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.827795       1.604221        -2.223574       6726.591628
HLA A*2602      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.094593       1.870237        -2.224356       12433.493778
HLA A*3001      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.094626       1.870237        -2.224389       12434.435507
HLA A*3301      1:123-131       9               QVLTAPDVR       1.103297        0.644944        -3.972848       1.748241        -2.224607       9393.935361
HLA A*0216      1:13-21 9       ATPYALNAV       1.259075        0.203216        -3.687756       1.462291        -2.225465       4872.550606
HLA A*0201      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.204911       1.978861        -2.226050       16029.165026
HLA B*4403      1:202-210       9               LGASTALAF       1.310738        0.932777        -4.469923       2.243515        -2.226408       29506.888151
HLA A*0202      1:200-208       9               TDLGASTAL       1.577364        0.302370        -4.106181       1.879734        -2.226447       12769.704320
HLA B*1502      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.343608       2.117084        -2.226524       22060.129028
HLA B*5401      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -3.338346       1.111207        -2.227138       2179.443666
HLA A*6901      1:146-154       9               FSRDRNTGL       1.328162        0.434196        -3.990304       1.762358        -2.227946       9779.220555
HLA B*0803      1:95-103        9               SAAAIAVGL       1.580790        0.536294        -4.345483       2.117084        -2.228399       22155.570491
HLA A*2403      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.315792       2.087388        -2.228404       20691.524774
HLA B*1502      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.209027       1.978861        -2.230167       16181.813737
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HLA A*2902      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.347360       2.117084        -2.230276       22251.545252
HLA A*1101      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.317778       2.087388        -2.230390       20786.329635
HLA A*0101      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.350544       2.117084        -2.233460       22415.257279
HLA B*3901      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.130456       1.896327        -2.234129       13503.791396
HLA A*8001      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.321610       2.087388        -2.234222       20970.549963
HLA B*1503      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.953154       1.718268        -2.234886       8977.474583
HLA A*0201      1:223-231       9       GTILAELPL       1.220795        0.363284        -3.818989       1.584079        -2.234910       6591.574920
HLA B*4501      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -3.269346       1.033072        -2.236274       1859.285029
HLA B*5101      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.353417       2.117084        -2.236333       22564.054922
HLA A*0203      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -3.867421       1.630187        -2.237234       7369.219226
HLA A*0250      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.309593       1.070235        -2.239358       2039.823780
HLA B*5801      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.065751       1.825968        -2.239782       11634.585178
HLA A*2602      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -3.800621       1.559867        -2.240753       6318.600811
HLA B*4601      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.328508       2.087388        -2.241120       21306.293643
HLA A*6901      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.523852       1.282277        -2.241575       3340.808528
HLA B*1501      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.524166       1.282277        -2.241889       3343.231243
HLA B*1517      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -3.366535       1.123686        -2.242848       2325.598662
HLA B*4501      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.563602       2.320347        -2.243255       36610.197895
HLA A*3001      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.224069       1.978861        -2.245208       16752.074697
HLA A*0201      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.517494       1.271968        -2.245526       3292.258133
HLA A*3201      1:140-148       9       GTATVVFSR       0.913054        0.630880        -3.789738       1.543934        -2.245804       6162.232844
HLA A*6801      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -3.540312       1.294185        -2.246127       3469.861000
HLA A*2603      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -3.806222       1.559867        -2.246355       6400.620692
HLA A*0203      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.226146       1.978861        -2.247285       16832.380720
HLA A*3301      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -3.541595       1.294185        -2.247410       3480.125425
HLA A*2603      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.227269       1.978861        -2.248408       16875.964356
HLA A*3002      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.234745       1.986196        -2.248549       17168.986562
HLA B*5801      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.494835       1.245153        -2.249683       3124.895120
HLA B*7301      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.570228       2.320347        -2.249880       37173.001066
HLA B*1517      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.227602       1.977371        -2.250231       16888.933524
HLA A*3101      1:127-135       9       APDVRTVSR       1.139444        0.502399        -3.892129       1.641843        -2.250286       7800.611713
HLA B*4801      1:223-231       9       GTILAELPL       1.220795        0.363284        -3.836521       1.584079        -2.252442       6863.111423
HLA A*3002      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.971006       1.718268        -2.252738       9354.176739
HLA B*1503      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.229916       1.977177        -2.252740       16979.170485
HLA B*0801      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -3.588519       1.335319        -2.253200       3877.205417
HLA B*1502      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.015810       1.762358        -2.253452       10370.752032
HLA B*4002      1:8-16  9       ELLELATPY       1.168179        1.152168        -4.573999       2.320347        -2.253651       37497.174822
HLA A*3001      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.285088       1.029850        -2.255237       1927.913399
HLA A*2602      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.499832       2.243515        -2.256317       31610.571997
HLA B*0802      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.343744       2.087388        -2.256356       22067.052000
HLA A*3101      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -3.894290       1.636392        -2.257898       7839.532899
HLA A*6801      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.502513       2.243515        -2.258998       31806.297508
HLA B*1503      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.531027       1.271968        -2.259059       3396.463195
HLA A*2902      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.977504       1.718268        -2.259236       9495.202841
HLA A*0250      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.214392       0.955042        -2.259350       1638.292783
HLA A*2403      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -3.978233       1.718268        -2.259965       9511.140280
HLA A*3301      1:191-199       9       VTPSTTATL       1.727960        0.494658        -4.483691       2.222618        -2.261073       30457.299403
HLA B*0801      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.348533       2.087388        -2.261144       22311.695222
HLA A*3001      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.238405       1.977177        -2.261228       17314.308778
HLA A*2602      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.378794       2.117084        -2.261710       23921.804437
HLA A*2501      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.132396       1.870237        -2.262160       13564.269035
HLA B*4501      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.293297       1.029850        -2.263446       1964.701707
HLA A*0212      1:223-231       9       GTILAELPL       1.220795        0.363284        -3.847836       1.584079        -2.263757       7044.272852
HLA A*2403      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.012789       1.748514        -2.264275       10298.851891
HLA B*4601      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.028676       1.762358        -2.266318       10682.576957
HLA A*0206      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.550208       1.282277        -2.267931       3549.834521
HLA A*0203      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.563140       1.295115        -2.268025       3657.123898
HLA B*5401      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.512390       2.243515        -2.268875       32537.962317
HLA B*4001      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.357099       2.087388        -2.269711       22756.150175
HLA A*0216      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.152013       0.877544        -2.274468       1419.098991
HLA A*6901      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -3.905131       1.630187        -2.274943       8037.679980
HLA A*1101      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.263035       1.986196        -2.276839       18324.612921
HLA A*6901      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.254617       1.977371        -2.277246       17972.835727
HLA B*1503      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -3.527474       1.248280        -2.279195       3368.794284
HLA A*0203      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -3.211690       0.932462        -2.279227       1628.131993
HLA A*2301      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.366906       2.087388        -2.279517       23275.849561
HLA B*1801      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.396669       2.117084        -2.279585       24926.931347
HLA A*8001      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.266491       1.986196        -2.280295       18471.020999
HLA B*5301      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.260035       1.978861        -2.281174       18198.454922
HLA B*2705      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.261475       1.978861        -2.282614       18258.905948
HLA B*4501      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.627360       1.344429        -2.282932       4239.947674
HLA B*7301      1:25-33 9       ERADIDRRV       1.311800        0.083077        -3.678189       1.394877        -2.283312       4766.386496
HLA A*3301      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.830610       1.546761        -2.283848       6770.328564
HLA B*4402      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.371602       2.087388        -2.284214       23528.929155
HLA B*3801      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.003504       1.718268        -2.285236       10081.000768
HLA B*1503      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.008109       1.721236        -2.286873       10188.462197
HLA B*5301      1:93-101        9       FASAAAIAV       1.212843        0.182258        -3.682898       1.395101        -2.287797       4818.342010
HLA A*2603      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.274296       1.986196        -2.288100       18805.976593
HLA A*3301      1:24-32 9       DERADIDRR       1.029344        0.408532        -3.726918       1.437876        -2.289041       5332.336824
HLA A*2902      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.268307       1.978861        -2.289446       18548.425667
HLA A*6802      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.169222       1.879734        -2.289488       14764.618267
HLA A*2402      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.406718       2.117084        -2.289634       25510.417420
HLA A*6901      1:221-229       9       PTGTILAEL       1.442456        0.106507        -3.839091       1.548963        -2.290129       6903.850627
HLA A*0202      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.101983       0.811766        -2.290216       1264.686136
HLA A*0206      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -2.997224       0.706535        -2.290689       993.628227
HLA B*5101      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.378460       2.087388        -2.291072       23903.434662
HLA A*2501      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.411024       2.117084        -2.293940       25764.645477
HLA B*5401      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -2.828954       0.534755        -2.294199       674.456283
HLA A*2603      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.538406       2.243515        -2.294891       34546.670620
HLA A*3002      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.165266       1.870237        -2.295029       14630.719706
HLA B*4001      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.281605       1.986196        -2.295409       19125.162728
HLA B*1503      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.193666       1.896327        -2.297339       15619.468979
HLA B*5401      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -3.329263       1.031086        -2.298177       2134.334767
HLA A*2402      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.277324       1.978861        -2.298464       18937.575505
HLA B*3501      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.612864       1.314292        -2.298572       4100.758318
HLA A*3101      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.284843       1.986196        -2.298647       19268.270270
HLA A*3201      1:71-79 9       RTAILDATK       0.821937        0.327507        -3.448151       1.149444        -2.298707       2806.410386
HLA A*2403      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.126584       1.825968        -2.300615       13383.933470
HLA A*2603      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.418566       2.117084        -2.301482       26215.975215
HLA B*5801      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.287789       1.986196        -2.301593       19399.430627
HLA B*7301      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -3.787473       1.485661        -2.301812       6130.179633
HLA B*3501      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.288470       1.986196        -2.302274       19429.889657
HLA A*3001      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.279733       1.977371        -2.302362       19042.878634
HLA A*6901      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.849128       1.546761        -2.302367       7065.263869
HLA B*0702      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -3.933602       1.630187        -2.303414       8582.262029
HLA B*1801      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.282456       1.977371        -2.305085       19162.653760
HLA A*0216      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.024165       1.718268        -2.305897       10572.191446
HLA A*0203      1:9-17  9       LLELATPYA       0.993939        -0.356018       -2.943825       0.637921        -2.305903       878.668030
HLA B*0802      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -3.918513       1.612334        -2.306179       8289.214487
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HLA B*4501      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -3.463399       1.157030        -2.306370       2906.694150
HLA B*1501      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.284225       1.977371        -2.306854       19240.874853
HLA A*3002      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -3.937671       1.630187        -2.307484       8663.055128
HLA A*2403      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.287333       1.978861        -2.308473       19379.081247
HLA B*3801      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.396347       2.087388        -2.308959       24908.463476
HLA B*0803      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.396767       2.087388        -2.309379       24932.595771
HLA B*1509      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -3.795194       1.485661        -2.309532       6240.129586
HLA B*1509      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.180331       1.870237        -2.310094       15147.138206
HLA A*0301      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.296397       1.986196        -2.310202       19787.799291
HLA A*3301      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.287970       1.977177        -2.310793       19407.513366
HLA B*2705      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.399335       2.087388        -2.311947       25080.459158
HLA B*1501      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.289138       1.977177        -2.311961       19459.764850
HLA A*0211      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.074594       1.762358        -2.312236       11873.926738
HLA B*5101      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.291905       1.978861        -2.313045       19584.175003
HLA B*4002      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -3.347043       1.033072        -2.313972       2223.532293
HLA A*0202      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -3.571621       1.254367        -2.317255       3729.248423
HLA B*5801      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.296127       1.978861        -2.317267       19775.492393
HLA A*0211      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -3.446760       1.128647        -2.318113       2797.436801
HLA B*1503      1:223-231       9       GTILAELPL       1.220795        0.363284        -3.902396       1.584079        -2.318317       7987.224845
HLA B*5401      1:191-199       9       VTPSTTATL       1.727960        0.494658        -4.543140       2.222618        -2.320522       34925.321414
HLA A*2403      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.298721       1.977371        -2.321350       19893.955278
HLA A*0250      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.565869       2.243515        -2.322354       36801.822766
HLA B*3801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.101510       1.778264        -2.323246       12633.103819
HLA A*0206      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.303582       1.977371        -2.326211       20117.880392
HLA B*4601      1:93-101        9       FASAAAIAV       1.212843        0.182258        -3.721885       1.395101        -2.326784       5270.902436
HLA B*0702      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.306244       1.978861        -2.327384       20241.569700
HLA B*1517      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.304839       1.977177        -2.327662       20176.191730
HLA B*3501      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -2.516143       0.187363        -2.328780       328.203623
HLA A*0203      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -3.662349       1.332502        -2.329847       4595.672028
HLA A*2501      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.644380       1.314292        -2.330088       4409.406787
HLA B*2705      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.226658       1.896327        -2.330331       16852.243797
HLA B*0702      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -3.943000       1.612334        -2.330665       8770.002356
HLA B*1503      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -3.267147       0.936177        -2.330970       1849.894045
HLA A*6802      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.310076       1.978861        -2.331216       20420.962054
HLA A*0206      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -3.457662       1.124732        -2.332930       2868.546499
HLA A*2902      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.203285       1.870237        -2.333048       15969.269733
HLA B*0801      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.647519       1.314292        -2.333227       4441.391716
HLA B*1801      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.421221       2.087388        -2.333833       26376.728909
HLA A*1101      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.082808       1.748514        -2.334294       12100.635094
HLA A*3201      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.214520       1.879734        -2.334786       16387.786367
HLA A*0219      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.853578       1.518523        -2.335055       7138.029046
HLA B*1801      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -3.882082       1.546761        -2.335321       7622.233747
HLA A*0206      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -3.589820       1.254367        -2.335454       3888.843137
HLA B*3501      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.206330       1.870237        -2.336093       16081.627159
HLA B*4001      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.233283       1.896327        -2.336956       17111.310855
HLA B*0802      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.316500       1.978861        -2.337639       20725.245817
HLA B*5401      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.455145       2.117084        -2.338061       28519.712933
HLA B*1501      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.235365       1.896327        -2.339038       17193.525011
HLA A*3001      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -3.675891       1.335319        -2.340572       4741.234753
HLA A*0206      1:9-17  9       LLELATPYA       0.993939        -0.356018       -2.978921       0.637921        -2.341000       952.623810
HLA B*1503      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.250759       1.909325        -2.341434       17813.889353
HLA B*1517      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -3.971706       1.630187        -2.341518       9369.269209
HLA A*0301      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.318793       1.977177        -2.341616       20834.965597
HLA A*0211      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -2.844658       0.502462        -2.342196       699.290716
HLA B*4601      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.322141       1.978861        -2.343280       20996.204970
HLA B*2705      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.329753       1.986196        -2.343557       21367.471591
HLA B*1509      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.330622       1.986196        -2.344427       21410.284817
HLA B*4403      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -3.592710       1.248280        -2.344430       3914.806422
HLA B*4001      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.063213       1.718268        -2.344945       11566.806215
HLA A*0211      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -3.830690       1.485661        -2.345028       6771.573987
HLA A*0201      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -3.280201       0.934977        -2.345224       1906.341020
HLA A*0202      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.166128       0.820380        -2.345749       1465.981187
HLA A*0202      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.416255       1.070235        -2.346020       2607.681647
HLA B*5301      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.242390       1.896327        -2.346063       17473.901565
HLA A*3001      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.094565       1.748241        -2.346324       12432.686638
HLA A*0101      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -3.093980       0.746698        -2.347282       1241.596306
HLA A*3101      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.326252       1.978861        -2.347392       21195.926388
HLA B*4002      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.592339       2.243515        -2.348824       39114.576057
HLA B*0802      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.326753       1.977371        -2.349382       21220.364666
HLA A*2501      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.912348       1.562118        -2.350231       8172.375793
HLA A*8001      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.330275       1.978861        -2.351414       21393.149242
HLA B*1501      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.232019       1.879734        -2.352285       17061.580442
HLA B*0802      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.071723       1.718268        -2.353455       11795.688476
HLA B*0803      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.332596       1.977371        -2.355225       21507.801126
HLA A*0301      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.076963       1.721236        -2.355727       11938.854128
HLA B*4001      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.333378       1.977371        -2.356008       21546.582202
HLA A*2601      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.342807       1.986196        -2.356611       22019.470630
HLA B*2705      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.335946       1.977371        -2.358576       21674.364750
HLA A*0101      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.345100       1.986196        -2.358904       22136.042056
HLA A*3001      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.107962       1.748514        -2.359448       12822.176508
HLA B*5801      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.338420       1.977371        -2.361050       21798.187575
HLA B*1517      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.705575       1.344429        -2.361146       5076.622294
HLA A*2501      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.124554       1.762358        -2.362196       13321.521011
HLA B*4001      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.234232       1.870237        -2.363996       17148.750152
HLA B*0803      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.126650       1.762358        -2.364291       13385.960980
HLA A*2603      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.231465       1.866986        -2.364479       17039.811244
HLA A*2902      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.113243       1.748514        -2.364729       12979.064578
HLA B*7301      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -3.301045       0.936177        -2.364869       2000.070130
HLA A*3001      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.660070       1.295115        -2.364955       4571.618980
HLA B*0801      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.352170       1.986196        -2.365974       22499.329276
HLA A*0202      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.233523       1.866986        -2.366537       17120.755630
HLA A*0101      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.263242       1.896327        -2.366914       18333.338801
HLA B*3901      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -3.588133       1.219814        -2.368320       3873.767001
HLA B*5801      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.345852       1.977177        -2.368675       22174.396376
HLA A*2501      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.265196       1.896327        -2.368869       18416.043656
HLA B*1502      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.249213       1.879734        -2.369479       17750.589856
HLA B*7301      1:191-199       9       VTPSTTATL       1.727960        0.494658        -4.593166       2.222618        -2.370548       39189.132166
HLA A*0212      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.616440       1.245153        -2.371287       4134.662742
HLA B*1502      1:91-99 9       AAFASAAAI       1.234627        0.369594        -3.975639       1.604221        -2.371418       9454.504126
HLA B*7301      1:202-210       9       LGASTALAF       1.310738        0.932777        -4.614976       2.243515        -2.371461       41207.466621
HLA B*5701      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.090190       1.718268        -2.371922       12308.078187
HLA B*1517      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.351180       1.978861        -2.372320       22448.143940
HLA B*0801      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.239664       1.866986        -2.372679       17364.587952
HLA B*5701      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.645362       1.271968        -2.373394       4419.389210
HLA B*0801      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.254104       1.879734        -2.374370       17951.651852
HLA A*0201      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.136931       1.762358        -2.374573       13706.636678
HLA A*2603      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.254624       1.879734        -2.374890       17973.127423
HLA A*2603      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.271939       1.896327        -2.375612       18704.209480
HLA B*5301      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.463855       2.087388        -2.376466       29097.433927
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HLA A*0203	1:221-229	9	PTGTILAEL	1.442456	0.106507	-3.925567	1.548963	-2.376604	8424.934465
HLA B*1801	1:52-60	9	RETMAVVSA	1.427872	-0.179592	-3.626172	1.248280	-2.377892	4228.357096
HLA B*3801	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.357252	1.978861	-2.378391	22764.153619
HLA B*1509	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.156972	1.778264	-2.378708	14353.969139
HLA A*3001	1:18-26	9	LNAVSDDER	1.255134	0.654191	-4.288959	1.909325	-2.379634	19451.765581
HLA A*0250	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.359361	1.978861	-2.380501	22875.012772
HLA B*4601	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.358283	1.977177	-2.381106	22818.281398
HLA A*0216	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.965541	1.584079	-2.381462	9237.206854
HLA A*3001	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.261414	1.879734	-2.381680	18256.337884
HLA A*3301	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.144130	1.762358	-2.381771	13935.729990
HLA B*1517	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.208374	1.825968	-2.382406	16157.495403
HLA A*6801	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.278870	1.896327	-2.382543	19005.107852
HLA A*6802	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.967270	1.584079	-2.383191	9274.059761
HLA A*0203	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-4.101815	1.718268	-2.383547	12641.991624
HLA B*4801	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.361006	1.977371	-2.383635	22961.802900
HLA A*0101	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.362745	1.978861	-2.383884	23053.910543
HLA B*5701	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.082559	1.697997	-2.384562	12093.697995
HLA B*1509	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.147447	1.762358	-2.385089	14042.589352
HLA A*3301	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.628918	2.243515	-2.385403	42551.782701
HLA B*4801	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.371637	1.986196	-2.385441	23530.838565
HLA A*0301	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.364732	1.978861	-2.385872	23159.664723
HLA A*6901	1:47-55	9	EVRAVRETM	1.250113	0.064179	-3.700265	1.314292	-2.385973	5014.931630
HLA B*4402	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.373383	1.986196	-2.387187	23625.612238
HLA B*0802	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.374215	1.986196	-2.388019	23670.901018
HLA A*2301	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.505222	2.117084	-2.388138	32005.312582
HLA B*3901	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.024936	1.636392	-2.388543	10590.967858
HLA B*1503	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.374920	1.986196	-2.388724	23709.349295
HLA B*1501	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-4.107299	1.718268	-2.389031	12802.630053
HLA A*0301	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.366499	1.977371	-2.389128	23254.075633
HLA A*0101	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.366504	1.977177	-2.389327	23254.327238
HLA A*2603	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.951510	1.562118	-2.389392	8943.541874
HLA A*2402	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.375883	1.986196	-2.389687	23761.996291
HLA B*5301	1:91-99	9	AAFASAAAI	1.234627	0.369594	-3.994613	1.604221	-2.390392	9876.730340
HLA B*0803	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.369370	1.978861	-2.390510	23408.314909
HLA B*1517	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.113464	1.721236	-2.392228	12985.666495
HLA A*3101	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.369669	1.977371	-2.392298	23424.403256
HLA A*3101	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.180739	1.788298	-2.392442	15161.403234
HLA B*4601	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.370037	1.977371	-2.392667	23444.307285
HLA B*5801	1:223-231	9	GTILAELPL	1.220795	0.363284	-3.976964	1.584079	-2.392885	9483.395550
HLA B*3501	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-3.675605	1.282277	-2.393328	4738.106540
HLA B*5701	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.370735	1.977371	-2.393364	23482.006401
HLA B*4801	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-3.424013	1.029850	-2.394162	2654.682396
HLA B*5701	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.380526	1.986196	-2.394330	24017.373178
HLA A*6901	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-3.224104	0.829467	-2.394637	1675.345136
HLA A*0301	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.143204	1.748514	-2.394690	13906.057667
HLA B*4501	1:202-210	9	LGASTALAF	1.310738	0.932777	-4.638370	2.243515	-2.394855	43488.030303
HLA A*2501	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.374245	1.978861	-2.395385	23672.565817
HLA B*4403	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.512684	2.117084	-2.395600	32559.973105
HLA A*0212	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.373240	1.977371	-2.395869	23617.816996
HLA A*0101	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.373301	1.977371	-2.395930	23621.139243
HLA A*0219	1:4-12	9	HTDFELLEL	1.651839	0.218398	-4.267518	1.870237	-2.397281	18514.740397
HLA B*4801	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.264520	1.866986	-2.397534	18387.372916
HLA B*5401	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.376127	1.977371	-2.398756	23775.369228
HLA A*0203	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.376809	1.977371	-2.399438	23812.698915
HLA A*1101	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.142668	1.742555	-2.400113	13888.915749
HLA A*0211	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-3.212169	0.811766	-2.400403	1629.929820
HLA A*6802	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.378106	1.977177	-2.400929	23883.916081
HLA A*2602	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.149388	1.748241	-2.401147	14105.480035
HLA A*3002	1:13-21	9	ATPYALNAV	1.259075	0.203216	-3.863470	1.462291	-2.401178	7302.467667
HLA A*3301	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.144510	1.742555	-2.401955	13947.948646
HLA A*3001	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.269440	1.866986	-2.402454	18596.855036
HLA B*4601	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.388993	1.986196	-2.402797	24490.240502
HLA A*2601	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.381226	1.977177	-2.404049	24056.123940
HLA B*1801	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.390617	1.986196	-2.404421	24581.962069
HLA A*0203	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-3.499459	1.094281	-2.405178	3158.342558
HLA B*5701	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.384167	1.978861	-2.405307	24219.213474
HLA B*4001	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.009918	1.604221	-2.405697	10230.991925
HLA A*3301	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.302896	1.896327	-2.406569	20086.125513
HLA A*0250	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.384616	1.977371	-2.407245	24244.652264
HLA A*0216	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.384773	1.977371	-2.407403	24253.441636
HLA B*4002	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.630922	2.222618	-2.408304	42748.597431
HLA B*0803	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.395151	1.986196	-2.408955	24839.969042
HLA B*1517	1:21-29	9	VSDDERADI	0.727910	0.266210	-3.403666	0.994120	-2.409546	2533.179879
HLA A*6901	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.386822	1.977177	-2.409645	24368.125681
HLA B*4501	1:95-103	9	SAAAIAVGL	1.580790	0.536294	-4.527895	2.117084	-2.410811	33720.546413
HLA B*1509	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.290644	1.879734	-2.410910	19527.363373
HLA A*0211	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-3.756789	1.344429	-2.412360	5712.009574
HLA B*1501	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.279721	1.866986	-2.412735	19042.363541
HLA B*5401	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.392320	1.978861	-2.413459	24678.566018
HLA A*0202	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-3.177495	0.764021	-2.413474	1504.856906
HLA A*6802	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.391338	1.977371	-2.413967	24622.822597
HLA A*2601	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.391350	1.977371	-2.413979	24623.488640
HLA B*4403	1:191-199	9	VTPSTTATL	1.727960	0.494658	-4.636610	2.222618	-2.413992	43312.173029
HLA B*0702	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.294168	1.879734	-2.414434	19686.469366
HLA B*2705	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-3.505192	1.090544	-2.414648	3200.309464
HLA B*0801	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.392033	1.977177	-2.414857	24662.283379
HLA B*0802	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.392367	1.977177	-2.415190	24681.236329
HLA B*3501	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.177676	1.762358	-2.415317	15054.823559
HLA A*2601	1:4-12	9	HTDFELLEL	1.651839	0.218398	-4.285928	1.870237	-2.415691	19316.489016
HLA B*5701	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.393145	1.977177	-2.415968	24725.471954
HLA A*0201	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.394012	1.977371	-2.416641	24774.879453
HLA A*8001	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.395247	1.977371	-2.417877	24845.479294
HLA A*0201	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.395337	1.977177	-2.418160	24850.587448
HLA B*4801	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.116636	1.697997	-2.418639	13080.852532
HLA A*2601	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.397590	1.978861	-2.418729	24979.849396
HLA A*3101	1:76-84	9	DATKPEVRR	0.992226	0.534734	-3.946486	1.526960	-2.419526	8840.693736
HLA B*3801	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.405916	1.986196	-2.419720	25463.399893
HLA A*2501	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.398826	1.977371	-2.421455	25051.033331
HLA B*4801	1:41-49	9	AAAFNDEVR	1.220112	0.757065	-4.400231	1.977177	-2.423054	25132.207505
HLA A*2402	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.171844	1.748514	-2.423330	14854.028342
HLA B*1502	1:100-108	9	AVGLGAFGL	1.513599	0.472597	-4.409535	1.986196	-2.423339	25676.427475
HLA A*3001	1:194-202	9	STTATLTDL	1.210982	0.351136	-3.985883	1.562118	-2.423765	9680.159434
HLA A*0211	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.303723	1.879734	-2.423989	20124.411582
HLA A*3201	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-3.548813	1.124732	-2.424081	3538.445528
HLA B*4402	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.401986	1.977371	-2.424615	25233.976956
HLA A*3101	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.122782	1.697997	-2.424785	13267.292451
HLA A*2402	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.292361	1.866986	-2.425375	19604.739747
HLA A*3201	1:221-229	9	PTGTILAEL	1.442456	0.106507	-3.974384	1.548963	-2.425421	9427.230604
HLA A*0206	1:88-96	9	WRTAAFASA	1.223245	-0.112038	-3.536849	1.111207	-2.425642	3442.301742

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HLA A*0219      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.403781       1.977371        -2.426410       25338.488735
HLA B*1503      1:13-21 9       ATPYALNAV       1.259075        0.203216        -3.888835       1.462291        -2.426543       7741.670497
HLA B*3901      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.010820       1.584079        -2.426741       10252.267852
HLA A*2403      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.293961       1.866986        -2.426975       19677.099454
HLA B*4001      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.011614       1.584079        -2.427535       10271.031710
HLA A*2902      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.405602       1.977177        -2.428425       25444.947523
HLA A*0250      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -3.914087       1.485661        -2.428426       8205.157986
HLA A*0216      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.308507       1.879734        -2.428773       20347.297844
HLA B*5101      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.034888       1.605818        -2.429070       10836.475875
HLA A*2501      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.415655       1.986196        -2.429459       26040.841001
HLA B*7301      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -3.483741       1.053156        -2.430585       3046.079106
HLA B*3501      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.060883       1.630187        -2.430695       11504.897944
HLA A*6802      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.501489       1.070235        -2.431255       3173.139661
HLA A*0219      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.327756       1.896327        -2.431429       21269.440852
HLA B*4402      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.409020       1.977177        -2.431843       25646.024937
HLA A*0212      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.409279       1.977177        -2.432102       25661.291116
HLA A*0206      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -3.503731       1.071321        -2.432409       3189.558677
HLA B*1517      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.313410       1.879734        -2.433676       20578.329532
HLA A*0301      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.181942       1.748241        -2.433702       15203.456462
HLA B*5701      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.260361       1.825968        -2.434393       18212.144845
HLA B*4501      1:191-199       9       VTPSTTATL       1.727960        0.494658        -4.657182       2.222618        -2.434564       45413.195707
HLA A*0206      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -3.199096       0.764021        -2.435075       1581.598960
HLA B*4403      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.315276       1.879734        -2.435542       20666.912875
HLA A*0206      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.135056       1.697997        -2.437059       13647.591417
HLA A*2403      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.414485       1.977177        -2.437308       25970.778147
HLA B*5801      1:194-202       9       STTATLTDL       1.210982        0.351136        -3.999702       1.562118        -2.437585       9993.144817
HLA B*2705      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.415216       1.977177        -2.438039       26014.510124
HLA B*1501      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.309049       1.870237        -2.438813       20372.741440
HLA B*4001      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.416515       1.977177        -2.439338       26092.453452
HLA A*2603      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -3.857201       1.417448        -2.439753       7197.823894
HLA B*5801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.349120       1.909325        -2.439795       22341.891587
HLA A*0203      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.319848       1.879734        -2.440114       20885.636082
HLA B*1517      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.168776       1.728208        -2.440568       14749.449824
HLA B*1801      1:24-32 9       DERADIDRR       1.029344        0.408532        -3.878450       1.437876        -2.440574       7558.749608
HLA B*3501      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.349900       1.909325        -2.440575       22382.055541
HLA A*0301      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.337175       1.896327        -2.440848       21735.776429
HLA A*0206      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.318680       0.877544        -2.441136       2082.957738
HLA B*0801      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.045945       1.604221        -2.441724       11115.902911
HLA B*1509      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.267736       1.825968        -2.441768       18524.057871
HLA A*8001      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.220201       1.778264        -2.441938       16603.565070
HLA A*0301      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.351296       1.909325        -2.441971       22454.095385
HLA A*0216      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.047416       1.604221        -2.443194       11153.611740
HLA A*0203      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.420500       1.977177        -2.443323       26332.957847
HLA B*1503      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.738726       1.295115        -2.443612       5479.312700
HLA A*2902      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.421223       1.977371        -2.443852       26376.871605
HLA A*0203      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.310985       1.866986        -2.443999       20463.760720
HLA B*0801      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.341381       1.896327        -2.445054       21947.281625
HLA A*0206      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -3.777671       1.332502        -2.445170       5993.370825
HLA A*6802      1:5-13  9       TDFELLELA       1.003059        -0.335657       -3.113274       0.667402        -2.445873       1297.999074
HLA B*0702      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.423126       1.977177        -2.445950       26492.708940
HLA A*0211      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.423432       1.977371        -2.446061       26511.347434
HLA B*1501      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.356143       1.909325        -2.446818       22706.100238
HLA A*3001      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.273868       1.825968        -2.447900       18787.469344
HLA B*1517      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -3.013031       0.565014        -2.448017       1030.460278
HLA B*3501      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -3.480381       1.031086        -2.449295       3022.605123
HLA A*0211      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.011985       1.562118        -2.449868       10279.814756
HLA B*1509      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.346200       1.896327        -2.449872       22192.157718
HLA A*1101      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.430548       1.978861        -2.451688       26949.355990
HLA A*2501      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.331572       1.879734        -2.451838       21457.130207
HLA A*8001      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.430767       1.977177        -2.453590       26962.918153
HLA B*1503      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.324020       1.870237        -2.453784       21087.271605
HLA A*0202      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.699687       1.245153        -2.454534       5008.262034
HLA B*0802      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.321706       1.866986        -2.454720       20975.201861
HLA B*1517      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.004025       1.548963        -2.455062       10093.115276
HLA A*0203      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.268063       0.811766        -2.456297       1853.801177
HLA A*2902      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -3.547121       1.090544        -2.456577       3524.689665
HLA B*1517      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -3.764716       1.307749        -2.456967       5817.228044
HLA B*3501      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.353871       1.896327        -2.457544       22587.626550
HLA A*0211      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -3.790391       1.332502        -2.457890       6171.507501
HLA A*6901      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.367218       1.909325        -2.457893       23292.602916
HLA B*3901      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.220253       1.762358        -2.457895       16605.541304
HLA A*3002      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.552379       1.094281        -2.458098       3567.623636
HLA A*6802      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.088799       1.630187        -2.458612       12268.722722
HLA A*6802      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -3.589661       1.130830        -2.458830       3887.412802
HLA A*1101      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.436345       1.977371        -2.458974       27311.438227
HLA B*5401      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.546829       2.087388        -2.459441       35223.223868
HLA B*5701      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.329915       1.870237        -2.459678       21375.449180
HLA B*5301      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.330432       1.870237        -2.460195       21400.904863
HLA A*3301      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.578023       2.117084        -2.460939       37846.281507
HLA B*1517      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -3.592908       1.130830        -2.462077       3916.585835
HLA B*4801      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.333073       1.870237        -2.462836       21531.434129
HLA B*2705      1:25-33 9       ERADIDRRV       1.311800        0.083077        -3.857906       1.394877        -2.463029       7209.515207
HLA B*5801      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.343375       1.879734        -2.463641       22048.317249
HLA B*1509      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.440846       1.977177        -2.463669       27596.003036
HLA A*3101      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.334071       1.870237        -2.463835       21580.996219
HLA B*4402      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -3.713065       1.248280        -2.464785       5164.936789
HLA A*3001      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.779523       1.314292        -2.465231       6018.975057
HLA B*5101      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.451889       1.986196        -2.465693       28306.668804
HLA B*0801      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.335956       1.870237        -2.465719       21674.833779
HLA A*2301      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.292154       1.825968        -2.466186       19595.408735
HLA A*3101      1:50-58 9       AVRETMAVV       1.181875        0.336648        -3.985192       1.518523        -2.466668       9664.775307
HLA B*4601      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.363184       1.896327        -2.466857       23077.244816
HLA B*4601      1:200-208       9       TDLGASTAL       1.577364        0.302102        -4.346745       1.879734        -2.467011       22220.028454
HLA B*4002      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.584816       2.117084        -2.467732       38442.849954
HLA B*0801      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -3.861289       1.393369        -2.467920       7265.898398
HLA A*0301      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.338223       1.870237        -2.467986       21788.284060
HLA B*1509      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.377713       1.909325        -2.468388       23862.347866
HLA A*6802      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.013245       1.543934        -2.469311       10309.666400
HLA A*3001      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -3.130726       0.660357        -2.470370       1351.220910
HLA A*0219      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.350539       1.879734        -2.470805       22415.014752
HLA A*0206      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -3.403793       0.932462        -2.471331       2533.920016
HLA B*4601      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.382281       1.909325        -2.472956       24114.628259
HLA A*6901      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.057485       1.584079        -2.473407       11415.249685
HLA A*0101      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.383577       1.909325        -2.474253       24186.748411
HLA B*7301      1:95-103        9       SAAAIAVGL       1.580790        0.536294        -4.591523       2.117084        -2.474439       39041.217818
HLA A*0206      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.298104       0.822896        -2.475207       1986.569067
HLA B*1801      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -3.893665       1.417448        -2.476217       7828.259685
HLA A*0219      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.453712       1.977177        -2.476535       28425.752079
HLA B*4402      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.386138       1.909325        -2.476814       24329.793664
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HLA B*1503      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.225300       1.748241        -2.477059       16799.630549
HLA A*3201      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.024348       1.546761        -2.477587       10576.653549
HLA B*0702      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.255949       1.778264        -2.477685       18028.050371
HLA A*6802      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.388406       1.909325        -2.479081       24457.140519
HLA A*3002      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.456940       1.977177        -2.479763       28637.833272
HLA A*0212      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -3.926953       1.446716        -2.480237       8451.868424
HLA A*6801      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.122265       1.641843        -2.480422       13251.511436
HLA B*0803      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.347738       1.866986        -2.480752       22270.934616
HLA A*0201      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.390102       1.909325        -2.480777       24552.855448
HLA A*0202      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.024922       1.543934        -2.480987       10590.624087
HLA B*1801      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.351289       1.870237        -2.481052       22453.730966
HLA A*3002      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.460006       1.978861        -2.481146       28840.729034
HLA A*0201      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.360891       1.879734        -2.481157       22955.716887
HLA A*2501      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.000355       1.518523        -2.481832       10008.185306
HLA B*5801      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.349017       1.866986        -2.482031       22336.574065
HLA A*2601      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.361831       1.879734        -2.482097       23005.445826
HLA A*0301      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.361864       1.879734        -2.482130       23007.188289
HLA B*5301      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.308845       1.825968        -2.482877       20363.155054
HLA A*2601      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.392498       1.909325        -2.483174       24688.714736
HLA B*3901      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.460803       1.977177        -2.483626       28893.670089
HLA A*2402      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.461263       1.977371        -2.483892       28924.323402
HLA B*5301      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.470360       1.986196        -2.484164       29536.594087
HLA B*4601      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.354481       1.870237        -2.484245       22619.420009
HLA A*2902      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.069985       1.584079        -2.485906       11748.560981
HLA B*3801      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.356352       1.870237        -2.486115       22717.035407
HLA B*4801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.395936       1.909325        -2.486611       24884.893031
HLA A*6901      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -3.184205       0.697019        -2.487186       1528.288463
HLA A*0202      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -2.389962       -0.098967       -2.488929       245.449375
HLA A*2603      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.360362       1.870237        -2.490125       22927.791612
HLA B*1501      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.762813       1.271968        -2.490845       5791.792661
HLA A*3001      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.269663       1.778264        -2.491399       18606.415150
HLA A*2501      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.469193       1.977177        -2.492016       29457.285273
HLA A*2301      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.469446       1.977371        -2.492076       29474.501252
HLA A*3301      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.401777       1.909325        -2.492452       25221.830222
HLA B*4402      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.389017       1.896327        -2.492689       24491.565433
HLA B*0702      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.402404       1.909325        -2.493079       25258.287977
HLA A*6901      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.360160       1.866986        -2.493174       22917.126928
HLA A*2601      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.360350       1.866986        -2.493365       22927.171437
HLA A*2301      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.360802       1.866986        -2.493816       22950.998232
HLA A*0301      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -3.788145       1.294185        -2.493960       6139.671761
HLA A*2403      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.373815       1.879734        -2.494081       23649.141344
HLA A*0201      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.057321       1.562118        -2.495203       11410.927637
HLA A*0206      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -3.242529       0.746698        -2.495831       1747.949778
HLA B*4601      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.014363       1.518523        -2.495840       10336.249109
HLA B*5701      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.405538       1.909325        -2.496213       25441.231128
HLA A*0212      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.375989       1.879734        -2.496255       23767.781734
HLA A*6801      1:24-32 9       DERADIDRR       1.029344        0.408532        -3.934325       1.437876        -2.496449       8596.574108
HLA B*1801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.224698       1.728208        -2.496490       16776.380313
HLA B*0802      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.376287       1.879734        -2.496553       23784.117140
HLA B*4501      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.483012       1.986196        -2.496816       30409.717902
HLA A*3201      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.218355       1.721236        -2.497119       16533.113733
HLA A*0101      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.376947       1.879734        -2.497213       23820.300748
HLA B*2705      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.367505       1.870237        -2.497268       23307.981260
HLA A*0301      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.365014       1.866986        -2.498028       23174.704551
HLA A*0212      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.407989       1.909325        -2.498664       25585.189401
HLA B*1801      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.476110       1.977177        -2.498933       29930.199005
HLA B*0801      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.197266       1.697997        -2.499268       15749.460296
HLA B*0803      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.476500       1.977177        -2.499323       29957.089641
HLA A*3101      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.366499       1.866986        -2.499513       23254.075633
HLA B*5101      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.103892       1.604221        -2.499671       12702.594748
HLA B*7301      1:62-70 9       TTAEPPAHL       1.615381        0.472007        -4.587320       2.087388        -2.499932       38665.188123
HLA A*0101      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.367211       1.866986        -2.500225       23292.224888
HLA A*0216      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.477618       1.977177        -2.500441       30034.331770
HLA B*0802      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.370761       1.870237        -2.500524       23483.403829
HLA B*3901      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.795757       1.295115        -2.500643       6248.236866
HLA B*2705      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.263056       1.762358        -2.500698       18325.505150
HLA A*0201      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.368233       1.866986        -2.501247       23347.103070
HLA A*8001      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.368268       1.866986        -2.501282       23348.997725
HLA A*0250      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.845961       1.344429        -2.501533       7013.927630
HLA A*0219      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -3.696393       1.194858        -2.501535       4970.419738
HLA A*3001      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.290310       1.788298        -2.502012       19512.368130
HLA A*0211      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.051513       1.548963        -2.502550       11259.342348
HLA A*3001      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.046800       1.543934        -2.502866       11137.813910
HLA B*4001      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.413214       1.909325        -2.503889       25894.879294
HLA B*1509      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.116359       1.612334        -2.504024       13072.504813
HLA A*6801      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.818872       1.314292        -2.504580       6589.792177
HLA A*3001      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -3.339619       0.834848        -2.504771       2185.843521
HLA B*2705      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.202872       1.697997        -2.504874       15954.071981
HLA B*0801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.414320       1.909325        -2.504996       25960.945077
HLA B*5301      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.372269       1.866986        -2.505283       23565.106987
HLA A*3101      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.385020       1.879734        -2.505286       24267.222435
HLA A*0206      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -3.440271       0.934977        -2.505294       2755.947919
HLA A*0206      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.135686       1.630187        -2.505498       13667.392732
HLA B*3901      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.331652       1.825968        -2.505683       21461.077313
HLA A*0203      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.415406       1.909325        -2.506081       26025.912207
HLA A*8001      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.386044       1.879734        -2.506310       24324.529374
HLA B*0702      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.403207       1.896327        -2.506880       25305.063667
HLA B*5801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.235370       1.728208        -2.507162       17193.711042
HLA B*0801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.285573       1.778264        -2.507310       19300.715950
HLA A*2403      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.205343       1.697997        -2.507346       16045.128715
HLA A*8001      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.417159       1.909325        -2.507834       26131.159227
HLA A*0301      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.068180       1.559867        -2.508313       11699.849384
HLA A*0206      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.485921       1.977177        -2.508744       30614.068797
HLA B*3501      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.375998       1.866986        -2.509012       23768.296064
HLA A*3002      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.487469       1.977371        -2.510098       30723.406317
HLA A*0301      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.252946       1.742555        -2.510391       17903.837235
HLA B*4001      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.273236       1.762358        -2.510878       18760.148573
HLA B*3501      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -3.706209       1.194858        -2.511351       5084.042982
HLA B*5101      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.488881       1.977177        -2.511705       30823.461229
HLA A*3001      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.582039       1.070235        -2.511804       3819.785108
HLA B*0802      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.408562       1.896327        -2.512235       25618.984483
HLA A*1101      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.422356       1.909325        -2.513031       26445.740805
HLA B*1517      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -3.385852       0.872785        -2.513067       2431.376611
HLA A*1101      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.383587       1.870237        -2.513350       24187.271807
HLA A*0216      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.380354       1.866986        -2.513368       24007.890063
HLA A*2301      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.384271       1.870237        -2.514034       24225.379279
HLA B*1503      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -3.708892       1.194858        -2.514034       5115.549901
HLA A*3301      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -3.605139       1.090544        -2.514595       4028.460111
HLA A*2301      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.501345       1.986196        -2.515149       31720.894306
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HLA B*4002	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.411795	1.896327	-2.515468	25810.403974
HLA A*2402	1:4-12  9	HTDFELLEL	1.651839	0.218398	-4.387332	1.870237	-2.517095	24396.749342
HLA B*0702	1:4-12  9	HTDFELLEL	1.651839	0.218398	-4.387889	1.870237	-2.517652	24428.049542
HLA B*5101	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.414525	1.896327	-2.518198	25973.166740
HLA A*0202	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.495789	1.977371	-2.518418	31317.630142
HLA A*0216	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-3.965508	1.446716	-2.518792	9236.507269
HLA B*1517	1:67-75 9	PAHLRTAIL	1.431896	0.180438	-4.131757	1.612334	-2.519423	13544.324029
HLA A*6802	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-3.801932	1.282277	-2.519655	6337.703705
HLA B*1503	1:75-83 9	LDATKPEVR	1.264680	0.523618	-4.308556	1.788298	-2.520258	20349.609585
HLA A*2902	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.430248	1.909325	-2.520923	26930.700942
HLA B*5701	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.400971	1.879734	-2.521237	25175.072192
HLA A*3002	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.040757	1.518523	-2.522234	10983.912941
HLA A*0211	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-3.455872	0.932462	-2.523409	2856.745728
HLA B*5101	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.403536	1.879734	-2.523802	25324.236589
HLA B*4001	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.302215	1.778264	-2.523951	20054.637743
HLA B*4601	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.391563	1.866986	-2.524577	24635.613766
HLA B*1501	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-3.869193	1.344429	-2.524764	7399.340078
HLA A*0216	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.287164	1.762358	-2.524806	19371.534332
HLA A*2603	1:13-21 9	ATPYALNAV	1.259075	0.203216	-3.987466	1.462291	-2.525175	9715.520292
HLA A*0219	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.393182	1.866986	-2.526196	24727.612240
HLA A*0203	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.073246	1.546761	-2.526484	11837.112103
HLA A*0212	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.289723	1.762358	-2.527364	19485.996031
HLA B*7301	1:10-18 9	LELATPYAL	1.590569	0.388292	-4.506900	1.978861	-2.528039	32129.177319
HLA B*5801	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.290545	1.762358	-2.528187	19522.926961
HLA B*0801	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-4.246748	1.718268	-2.528480	17650.141017
HLA A*2902	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.396262	1.866986	-2.529276	24903.612875
HLA A*6901	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-3.482360	0.952818	-2.529542	3036.404878
HLA B*2705	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.409304	1.879734	-2.529570	25662.818233
HLA A*2403	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.439446	1.909325	-2.530121	27507.168702
HLA B*4402	1:91-99 9	AAFASAAAI	1.234627	0.369594	-4.134408	1.604221	-2.530186	13627.229002
HLA A*2902	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.410348	1.879734	-2.530613	25724.534177
HLA A*0101	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.310140	1.778264	-2.531876	20423.945101
HLA A*2602	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.509533	1.977177	-2.532357	32324.616276
HLA A*3301	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.174941	1.641843	-2.533098	14960.319528
HLA A*3101	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.295874	1.762358	-2.533515	19763.941580
HLA A*0101	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.359486	1.825968	-2.533517	22881.572530
HLA B*2705	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.400611	1.866986	-2.533625	25154.243077
HLA B*0702	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-3.815935	1.282277	-2.533658	6545.379955
HLA B*0801	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.359700	1.825968	-2.533731	22892.839899
HLA A*0212	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.401027	1.866986	-2.534041	25178.341068
HLA B*1517	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.443494	1.909325	-2.534169	27764.768304
HLA B*0803	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.431253	1.896327	-2.534926	26993.129410
HLA B*1501	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-3.635556	1.100579	-2.534977	4320.713806
HLA B*2705	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.444305	1.909325	-2.534980	27816.637183
HLA B*5701	1:91-99 9	AAFASAAAI	1.234627	0.369594	-4.139774	1.604221	-2.535553	13796.654158
HLA B*3501	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-3.503359	0.967740	-2.535620	3186.833527
HLA A*3001	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-3.982410	1.446716	-2.535694	9603.067277
HLA A*0206	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-3.631153	1.094281	-2.536871	4277.131135
HLA B*0802	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.446370	1.909325	-2.537045	27949.228436
HLA B*1801	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.434331	1.896327	-2.538004	27185.107966
HLA B*7301	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.316756	1.778264	-2.538492	20737.470641
HLA B*1503	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-3.629386	1.090544	-2.538842	4259.766099
HLA A*0219	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.448275	1.909325	-2.538950	28072.122840
HLA A*0101	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.301411	1.762358	-2.539053	20017.567315
HLA A*2301	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.516532	1.977177	-2.539356	32849.782159
HLA B*4403	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-4.626759	2.087388	-2.539370	42340.753529
HLA A*6901	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.318725	1.778264	-2.540461	20831.697123
HLA A*0301	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.366492	1.825968	-2.540524	23253.698230
HLA A*6901	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.366741	1.825968	-2.540773	23267.036846
HLA A*2602	1:10-18 9	LELATPYAL	1.590569	0.388292	-4.520404	1.978861	-2.541544	33143.963743
HLA B*7301	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-2.868331	0.326268	-2.542063	738.467137
HLA B*4801	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-4.260450	1.718268	-2.542182	18215.889206
HLA A*8001	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.369845	1.825968	-2.543876	23433.909441
HLA A*0211	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.522669	1.977177	-2.545493	33317.265429
HLA B*5701	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.412812	1.866986	-2.545826	25870.935250
HLA B*1517	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-3.730024	1.184095	-2.545928	5370.609721
HLA B*3501	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.130235	1.584079	-2.546156	13496.926064
HLA B*4402	1:4-12  9	HTDFELLEL	1.651839	0.218398	-4.416764	1.870237	-2.546527	26107.420415
HLA A*0202	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.524483	1.977177	-2.547306	33456.703778
HLA B*4002	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-4.634815	2.087388	-2.547427	43133.526533
HLA A*2501	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.096806	1.548963	-2.547844	12497.018025
HLA A*0216	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.374248	1.825968	-2.548279	23672.693884
HLA B*3501	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.297506	1.748241	-2.549266	19838.391362
HLA A*0216	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.459424	1.909325	-2.550099	28802.060743
HLA B*0802	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.328682	1.778264	-2.550418	21314.824937
HLA A*3002	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.328759	1.778264	-2.550495	21318.630535
HLA A*0211	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.329311	1.778264	-2.551048	21345.750656
HLA B*4501	1:62-70 9	TTAEPPAHL	1.615381	0.472007	-4.638614	2.087388	-2.551226	43512.504791
HLA B*3801	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.528778	1.977177	-2.551601	33789.207803
HLA A*2501	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.460977	1.909325	-2.551652	28905.239460
HLA A*6901	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.300725	1.748241	-2.552485	19985.970775
HLA A*1101	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.432311	1.879734	-2.552576	27058.922890
HLA B*0702	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.114865	1.562118	-2.552747	13027.603673
HLA B*0702	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-4.271484	1.718268	-2.553216	18684.589363
HLA B*0803	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.433100	1.879734	-2.553366	27108.153240
HLA B*3801	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.449762	1.896327	-2.553435	28168.419485
HLA B*1501	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.379771	1.825968	-2.553803	23975.701415
HLA A*6802	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-3.625260	1.071321	-2.553939	4219.490926
HLA A*0301	1:75-83 9	LDATKPEVR	1.264680	0.523618	-4.342584	1.788298	-2.554286	22008.156862
HLA B*4801	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.316716	1.762358	-2.554358	20735.563543
HLA B*0702	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-3.649018	1.094281	-2.554737	4456.747706
HLA B*5101	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.422750	1.866986	-2.555764	26469.787243
HLA B*0702	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-3.699884	1.143950	-2.555934	5010.538459
HLA B*4001	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.382360	1.825968	-2.556392	24119.064221
HLA A*0203	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-3.687503	1.130830	-2.556672	4869.704562
HLA B*5101	1:18-26 9	LNAVSDDER	1.255134	0.654191	-4.466019	1.909325	-2.556694	29242.773899
HLA A*3002	1:91-99 9	AAFASAAAI	1.234627	0.369594	-4.160933	1.604221	-2.556712	14485.491642
HLA A*0219	1:1-9   9	MTEHTDFEL	1.355528	0.362740	-4.275945	1.718268	-2.557677	18877.532633
HLA A*0211	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.424705	1.866986	-2.557719	26589.197022
HLA B*3801	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.437529	1.879734	-2.557795	27386.006773
HLA A*2603	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.107421	1.548963	-2.558459	12806.232122
HLA A*3101	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.385755	1.825968	-2.559787	24308.348818
HLA B*0803	1:4-12  9	HTDFELLEL	1.651839	0.218398	-4.430266	1.870237	-2.560030	26931.866504
HLA B*1501	1:49-57 9	RAVRETMAV	0.926962	0.318191	-3.805249	1.245153	-2.560097	6386.301301
HLA A*6901	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-3.495258	0.934977	-2.560282	3127.939563
HLA B*0702	1:2-10  9	TEHTDFELL	1.490281	0.376705	-4.427621	1.866986	-2.560635	26768.308757
HLA B*3901	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-3.684641	1.123686	-2.560955	4837.722371
HLA A*0203	1:67-75 9	PAHLRTAIL	1.431896	0.180438	-4.173926	1.612334	-2.561591	14925.397007
HLA A*2402	1:41-49 9	AAAFNDEVR	1.220112	0.757065	-4.539083	1.977177	-2.561906	34600.537946
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HLA A*3201      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.539623       1.977177        -2.562446       34643.617309
HLA A*2601      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.080990       1.518523        -2.562466       12050.072592
HLA A*0211      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.844956       1.282277        -2.562679       6997.706140
HLA A*3201      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.540460       1.977371        -2.563089       34710.402454
HLA A*2601      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.389181       1.825968        -2.563213       24500.841955
HLA B*1801      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.390069       1.825968        -2.564101       24550.995924
HLA A*0211      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.384593       0.820380        -2.564213       2424.336558
HLA A*2301      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.444041       1.879734        -2.564307       27799.787977
HLA A*2602      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.431556       1.866986        -2.564570       27011.973834
HLA B*0702      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.148678       1.584079        -2.564600       14082.453507
HLA A*3001      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.293221       1.728208        -2.565013       19643.595968
HLA A*0301      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.171760       1.606496        -2.565264       14851.135712
HLA A*2601      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.127589       1.562118        -2.565472       13414.958970
HLA B*0803      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.475057       1.909325        -2.565732       29857.747100
HLA B*3901      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.263928       1.697997        -2.565930       18362.322636
HLA A*1101      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.432959       1.866986        -2.565973       27099.355542
HLA A*0219      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.170209       1.604221        -2.565988       14798.203887
HLA B*1501      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.113041       1.546761        -2.566280       12973.027467
HLA B*5401      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.543709       1.977177        -2.566532       34971.075350
HLA B*4801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.345217       1.778264        -2.566954       22142.030543
HLA B*5401      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.553201       1.986196        -2.567005       35743.815222
HLA B*5101      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.437942       1.870237        -2.567705       27412.094517
HLA A*6801      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.554211       1.986196        -2.568015       35827.061143
HLA A*0201      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.394928       1.825968        -2.568959       24827.206082
HLA B*1509      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.175279       1.605818        -2.569461       14971.978517
HLA B*5801      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.357822       1.788298        -2.569525       22794.099124
HLA A*0250      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.268667       1.697997        -2.570669       18563.784797
HLA B*4501      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.865988       1.295115        -2.570874       7344.940646
HLA A*2902      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.396847       1.825968        -2.570879       24937.182201
HLA B*0702      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.396885       1.825968        -2.570917       24939.340813
HLA B*1503      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.201368       1.630187        -2.571181       15898.929250
HLA A*0211      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.155464       1.584079        -2.571385       14304.202142
HLA A*0216      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.351079       1.778264        -2.572816       22442.922542
HLA B*3501      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.271025       1.697997        -2.573028       18664.888853
HLA A*0212      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.868286       1.295115        -2.573172       7383.904770
HLA B*5301      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.550398       1.977177        -2.573221       35513.867558
HLA B*4601      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.399432       1.825968        -2.573463       25086.022758
HLA A*3002      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.868671       1.295115        -2.573557       7390.458838
HLA B*3901      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.483717       1.909325        -2.574392       30459.111934
HLA B*5801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.352910       1.778264        -2.574646       22537.703410
HLA B*4403      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.471133       1.896327        -2.574806       29589.211710
HLA B*5701      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.303178       1.728208        -2.574970       20099.169392
HLA A*2602      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.552966       1.977371        -2.575595       35724.483443
HLA B*4801      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.403703       1.825968        -2.577735       25333.965551
HLA A*0101      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.366454       1.788298        -2.578157       23251.685518
HLA A*2501      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.445545       1.866986        -2.578559       27896.206811
HLA A*2403      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.357193       1.778264        -2.578929       22761.075038
HLA A*0250      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.128750       1.548963        -2.579787       13450.858199
HLA A*0206      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -3.828096       1.248280        -2.579816       6731.251176
HLA A*0206      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.490190       1.909325        -2.580865       30916.481899
HLA A*2603      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.401584       0.820380        -2.581205       2521.066991
HLA B*0803      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.407211       1.825968        -2.581243       25539.415681
HLA B*5401      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -2.768859       0.187363        -2.581496       587.298210
HLA A*0202      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.491003       1.909325        -2.581678       30974.406234
HLA B*1502      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.129079       1.546761        -2.582318       13461.049529
HLA B*1801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.491896       1.909325        -2.582571       31038.147609
HLA A*2902      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.360907       1.778264        -2.582643       22956.586219
HLA A*2602      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.855284       1.271968        -2.583316       7166.119350
HLA B*1503      1:47-55 9       EVRAVRETM       1.250113        0.064179        -3.897932       1.314292        -2.583640       7905.546340
HLA B*4001      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.282087       1.697997        -2.584089       19146.384821
HLA A*0212      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.362627       1.778264        -2.584363       23047.675431
HLA A*6801      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.454938       1.870237        -2.584702       28506.138778
HLA A*3301      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.570932       1.986196        -2.584737       37233.380595
HLA B*1501      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.328212       1.742555        -2.585656       21291.775241
HLA A*3001      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -3.696421       1.110748        -2.585673       4970.742422
HLA A*3301      1:10-18 9       LELATPYAL       1.590569        0.388292        -4.564631       1.978861        -2.585771       36697.049769
HLA A*3301      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.304733       1.718268        -2.586465       20171.280534
HLA A*0250      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.466225       1.879734        -2.586491       29256.698828
HLA A*6901      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.374995       1.788298        -2.586697       23713.454129
HLA A*0301      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.365973       1.778264        -2.587709       23225.913058
HLA B*1502      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.497854       1.909325        -2.588529       31466.909287
HLA B*1801      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.337236       1.748514        -2.588722       21738.833935
HLA A*0206      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.367314       1.778264        -2.589051       23297.769916
HLA A*0211      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -3.193368       0.603848        -2.589520       1560.875724
HLA B*5301      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.469486       1.879734        -2.589752       29477.212091
HLA B*5301      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.318154       1.728208        -2.589946       20804.329702
HLA A*0219      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.139393       1.548963        -2.590430       13784.568039
HLA B*4002      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.460796       1.870237        -2.590559       28893.201159
HLA B*4402      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.333397       1.742555        -2.590842       21547.514739
HLA A*0301      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.353786       1.762358        -2.591428       22583.227902
HLA A*0203      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.289443       1.697997        -2.591446       19473.455436
HLA A*0212      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.154608       1.562118        -2.592491       14276.062028
HLA B*5701      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.176816       1.584079        -2.592737       15025.044208
HLA B*1502      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.570987       1.977177        -2.593810       37238.013738
HLA A*3201      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.342217       1.748241        -2.593977       21989.591074
HLA B*4403      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.580779       1.986196        -2.594583       38087.210072
HLA B*0801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.224985       1.630187        -2.594798       16787.456487
HLA A*2402      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.313438       1.718268        -2.595170       20579.665493
HLA B*2705      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.337920       1.742555        -2.595364       21773.083850
HLA B*4002      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.581632       1.986196        -2.595436       38162.078834
HLA B*0801      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.237886       1.641843        -2.596043       17293.620412
HLA B*1517      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.463061       1.866986        -2.596075       29044.276646
HLA B*1503      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.142913       1.546761        -2.596151       13896.732247
HLA B*4402      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.384705       1.788298        -2.596407       24249.636890
HLA A*8001      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.315614       1.718268        -2.597346       20683.019170
HLA B*1503      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -3.702600       1.105200        -2.597400       5041.971711
HLA B*5801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.345767       1.748241        -2.597527       22170.078200
HLA B*0801      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.116119       1.518523        -2.597596       13065.293281
HLA A*3201      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.360433       1.762358        -2.598074       22931.513019
HLA A*6901      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.340652       1.742555        -2.598097       21910.505440
HLA B*3901      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.203943       1.605818        -2.598124       15993.477817
HLA B*0801      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.386669       1.788298        -2.598372       24359.558312
HLA B*5701      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.360943       1.762358        -2.598584       22958.449183
HLA A*2601      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.387008       1.788298        -2.598710       24378.542387
HLA B*1509      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.317418       1.718268        -2.599150       20769.131637
HLA B*3901      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.240994       1.641843        -2.599151       17417.839759
HLA B*4601      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.387515       1.788298        -2.599217       24407.046243
HLA B*7301      1:100-108       9       AVGLGAFGL       1.513599        0.472597        -4.585535       1.986196        -2.599339       38506.541954
HLA A*3001      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.230588       1.630187        -2.600401       17005.461471
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HLA B*1501      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.388789       1.788298        -2.600491       24478.716629
HLA A*0212      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.478079       0.877544        -2.600534       3006.622608
HLA A*0212      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.426662       1.825968        -2.600694       26709.289973
HLA A*3002      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.298848       1.697997        -2.600851       19899.767828
HLA A*0201      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.389919       1.788298        -2.601621       24542.497032
HLA B*7301      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.019085       1.417448        -2.601637       10449.257518
HLA B*5801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.344224       1.742555        -2.601668       22091.419026
HLA B*3501      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.214238       1.612334        -2.601904       16377.151086
HLA A*0211      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.299985       1.697997        -2.601988       19951.941384
HLA B*1503      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.330247       1.728208        -2.602038       21391.760472
HLA A*0250      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.579560       1.977177        -2.602383       37980.421363
HLA B*3501      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.244291       1.641843        -2.602448       17550.545446
HLA A*3201      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.632365       1.029850        -2.602514       4289.087438
HLA A*2601      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.380838       1.778264        -2.602574       24034.660262
HLA A*6802      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.106254       0.502462        -2.603792       1277.185918
HLA B*5801      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.352480       1.748514        -2.603966       22515.401906
HLA B*4402      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.352602       1.748514        -2.604088       22521.736700
HLA A*3101      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.209403       1.604221        -2.605182       16195.826492
HLA B*0801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.347753       1.742555        -2.605197       22271.657528
HLA B*1501      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.353835       1.748514        -2.605321       22585.793676
HLA A*2301      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.514705       1.909325        -2.605380       32711.811472
HLA A*0201      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.383982       1.778264        -2.605718       24209.264677
HLA B*1517      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -3.938367       1.332502        -2.605865       8676.938626
HLA B*0802      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.432520       1.825968        -2.606551       27071.954361
HLA B*1501      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.305467       1.697997        -2.607469       20205.356094
HLA A*2603      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.433840       1.825968        -2.607872       27154.388036
HLA B*3501      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.350696       1.742555        -2.608141       22423.140829
HLA A*0219      1:201-209       9       DLGASTALA       1.029007        -0.426525       -3.210853       0.602482        -2.608371       1624.999358
HLA A*3101      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.386707       1.778264        -2.608443       24361.666923
HLA B*4801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.351343       1.742555        -2.608787       22456.525000
HLA B*1502      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -3.561956       0.952818        -2.609138       3647.166024
HLA A*0203      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.388049       1.778264        -2.609785       24437.037602
HLA A*0219      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.372380       1.762358        -2.610022       23571.099525
HLA A*6802      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.389364       1.778264        -2.611100       24511.182790
HLA B*3501      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.437343       1.825968        -2.611375       27374.305009
HLA A*6802      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.437409       1.825968        -2.611440       27378.451897
HLA A*2403      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.374727       1.762358        -2.612369       23698.833902
HLA B*1501      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.706693       1.094281        -2.612412       5089.711987
HLA A*0216      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.310800       1.697997        -2.612802       20455.016761
HLA B*4002      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.590212       1.977371        -2.612841       38923.541092
HLA A*0211      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -3.713605       1.100579        -2.613027       5171.367388
HLA B*2705      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.099006       1.485661        -2.613344       12560.459115
HLA B*3801      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.522902       1.909325        -2.613577       33335.114237
HLA B*4501      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.493665       1.879734        -2.613931       31164.843934
HLA B*5401      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.523358       1.909325        -2.614033       33370.118421
HLA B*4501      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.591512       1.977177        -2.614335       39040.161789
HLA B*0801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.342600       1.728208        -2.614392       22008.990310
HLA A*2602      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.031914       1.417448        -2.614465       10762.511300
HLA A*0202      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.392907       1.778264        -2.614643       24711.965676
HLA B*4601      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.393314       1.778264        -2.615050       24735.104698
HLA A*2902      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.377680       1.762358        -2.615322       23860.540637
HLA B*1501      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.363792       1.748241        -2.615552       23109.602422
HLA B*4601      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.334530       1.718268        -2.616262       21603.774637
HLA A*0250      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -3.497598       0.880895        -2.616703       3144.839171
HLA B*1517      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.163471       1.546761        -2.616709       14570.373465
HLA A*6901      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.338012       1.721236        -2.616776       21777.678144
HLA B*3801      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.379308       1.762358        -2.616950       23950.162967
HLA B*3901      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.365242       1.748241        -2.617002       23186.868883
HLA B*5101      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.379807       1.762358        -2.617448       23977.647083
HLA A*8001      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.380253       1.762358        -2.617895       24002.305872
HLA A*0211      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -3.498853       0.880895        -2.617958       3153.937372
HLA A*2402      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.498051       1.879734        -2.618317       31481.212066
HLA A*0201      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.316453       1.697997        -2.618455       20723.003513
HLA A*0219      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.444850       1.825968        -2.618881       27851.571604
HLA B*1501      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.340157       1.721236        -2.618921       21885.509160
HLA A*2602      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.381653       1.762358        -2.619295       24079.821260
HLA B*0803      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.397759       1.778264        -2.619495       24989.581243
HLA A*0101      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.368108       1.748514        -2.619594       23340.409852
HLA A*0250      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.486774       1.866986        -2.619788       30674.247461
HLA A*0219      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.398424       1.778264        -2.620160       25027.869560
HLA A*2603      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.597543       1.977371        -2.620172       39586.101766
HLA A*1101      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.204267       1.584079        -2.620188       16005.422442
HLA B*4402      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.382649       1.762358        -2.620291       24135.118782
HLA B*4402      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.342064       1.721236        -2.620828       21981.859952
HLA A*1101      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.225333       1.604221        -2.621111       16800.902975
HLA B*4402      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.399582       1.778264        -2.621318       25094.709868
HLA B*1503      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.234439       1.612334        -2.622105       17156.916106
HLA A*2501      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.448402       1.825968        -2.622434       28080.324860
HLA B*3801      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.490021       1.866986        -2.623035       30904.441902
HLA B*5101      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.341461       1.718268        -2.623193       21951.318896
HLA B*0801      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.229092       1.605818        -2.623273       16946.959820
HLA B*5701      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.411579       1.788298        -2.623281       25797.561080
HLA A*0203      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.412070       1.788298        -2.623772       25826.746022
HLA B*0802      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.266834       1.641843        -2.624991       18485.615984
HLA B*5101      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.451130       1.825968        -2.625161       28257.249086
HLA B*4601      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.255373       1.630187        -2.625186       18004.171410
HLA B*2705      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.373681       1.748241        -2.625441       23641.849932
HLA B*1501      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.403745       1.778264        -2.625482       25336.432642
HLA B*4801      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.413837       1.788298        -2.625539       25932.029350
HLA A*3201      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.145041       1.518523        -2.626518       13965.012325
HLA A*2501      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.369443       1.742555        -2.626888       23412.240966
HLA B*5801      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.348213       1.721236        -2.626977       22295.285543
HLA B*1509      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.325247       1.697997        -2.627249       21146.905424
HLA B*7301      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.604570       1.977177        -2.627393       40231.853987
HLA A*2601      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.345817       1.718268        -2.627549       22172.597034
HLA B*5801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.257932       1.630187        -2.627744       18110.553693
HLA A*0203      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.454257       1.825968        -2.628289       28461.451476
HLA B*1501      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.091858       1.462291        -2.629567       12355.444687
HLA A*2601      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.350915       1.721236        -2.629679       22434.425191
HLA A*3301      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.500476       1.870237        -2.630239       31657.463397
HLA B*1801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.372944       1.742555        -2.630388       23601.723490
HLA A*1101      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.348845       1.718268        -2.630577       22327.754604
HLA B*5701      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.352029       1.721236        -2.630793       22492.027329
HLA A*0101      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.379198       1.748241        -2.630958       23944.074058
HLA B*3501      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.409546       1.778264        -2.631283       25677.122017
HLA A*6901      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.379917       1.748514        -2.631403       23983.744529
HLA A*0219      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.078175       1.446716        -2.631459       11972.228032
HLA A*0216      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.180645       1.548963        -2.631683       15158.122729
HLA B*0702      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.329986       1.697997        -2.631988       21378.918626
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HLA B*5701      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.410362       1.778264        -2.632098       25725.369192
HLA B*1501      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.194381       1.562118        -2.632263       15645.177991
HLA A*2402      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.360581       1.728208        -2.632373       22939.329938
HLA A*1101      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.458601       1.825968        -2.632633       28747.576756
HLA B*0801      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.381188       1.748514        -2.632674       24054.041775
HLA B*3801      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.458881       1.825968        -2.632912       28766.089738
HLA B*3901      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.151592       1.518523        -2.633068       14177.239873
HLA B*2705      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.381585       1.748514        -2.633071       24076.043751
HLA A*0201      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.445045       0.811766        -2.633279       2786.410896
HLA A*2603      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.151954       1.518523        -2.633430       14189.056178
HLA A*0211      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.543227       1.909325        -2.633902       34932.312972
HLA B*4601      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.382894       1.748241        -2.634653       24148.701707
HLA A*2403      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.382915       1.748241        -2.634674       24149.877512
HLA A*0201      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.183747       1.548963        -2.634784       15266.755110
HLA B*0702      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.423345       1.788298        -2.635047       26506.041297
HLA A*6802      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.424440       1.788298        -2.636142       26572.947549
HLA B*1502      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.503133       1.866986        -2.636147       31851.756058
HLA A*2902      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.384423       1.748241        -2.636183       24233.899457
HLA A*8001      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.334266       1.697997        -2.636269       21590.688711
HLA A*0301      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.354547       1.718268        -2.636279       22622.846588
HLA A*2601      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.379600       1.742555        -2.637044       23966.234755
HLA B*7301      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.614445       1.977371        -2.637074       41157.115719
HLA B*4001      1:204-212       9       ASTALAFTV       1.108485        0.186630        -3.932197       1.295115        -2.637082       8554.542298
HLA B*4002      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.614393       1.977177        -2.637216       41152.217591
HLA B*1801      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.355522       1.718268        -2.637254       22673.694289
HLA B*1503      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.385911       1.748514        -2.637396       24317.029729
HLA A*3001      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.244119       1.606496        -2.637623       17543.615719
HLA B*0702      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.385932       1.748241        -2.637691       24318.213730
HLA A*3002      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -3.766770       1.128647        -2.638123       5844.798441
HLA A*2601      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.386799       1.748514        -2.638284       24366.807428
HLA A*3001      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.187280       1.548963        -2.638318       15391.479374
HLA A*3301      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.615739       1.977371        -2.638369       41279.981894
HLA A*0203      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -3.893007       1.254367        -2.638641       7816.410657
HLA A*0206      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.187868       1.548963        -2.638905       15412.310007
HLA A*2403      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.188295       1.548963        -2.639333       15427.492438
HLA A*0216      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.125259       1.485661        -2.639597       13343.158951
HLA A*0201      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.388237       1.748514        -2.639722       24447.616024
HLA A*0212      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -3.859626       1.219814        -2.639812       7238.121772
HLA A*2601      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.388199       1.748241        -2.639958       24445.499973
HLA A*0301      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.368468       1.728208        -2.640260       23359.737011
HLA A*3101      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.252641       1.612334        -2.640306       17891.250151
HLA A*6802      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.338371       1.697997        -2.640374       21795.711274
HLA B*1503      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.087418       1.446716        -2.640702       12229.757740
HLA B*4801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.270938       1.630187        -2.640751       18661.153153
HLA A*2402      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.338754       1.697997        -2.640757       21814.939469
HLA B*0801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.389007       1.748241        -2.640767       24491.035452
HLA B*4801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.389080       1.748241        -2.640839       24495.143104
HLA B*5101      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.923316       1.282277        -2.641039       8381.383730
HLA B*1509      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.272134       1.630187        -2.641947       18712.609944
HLA B*4501      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.619416       1.977371        -2.642046       41630.961575
HLA B*4402      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.360327       1.718268        -2.642059       22925.931136
HLA A*0101      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.384722       1.742555        -2.642166       24250.555222
HLA B*1509      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.278570       1.636392        -2.642177       18991.952020
HLA A*2403      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.246647       1.604221        -2.642426       17646.035627
HLA A*0301      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.340594       1.697997        -2.642596       21907.542305
HLA B*1509      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.430992       1.788298        -2.642695       26976.924964
HLA A*0212      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.431079       1.788298        -2.642781       26982.325365
HLA B*4001      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.391098       1.748241        -2.642858       24609.239258
HLA A*0201      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.391152       1.748241        -2.642912       24612.301513
HLA B*5701      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.385638       1.742555        -2.643083       24301.774434
HLA B*4403      1:218-226       9       SPQPTGTIL       1.697402        0.279969        -4.620774       1.977371        -2.643404       41761.341830
HLA A*2403      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.273690       1.630187        -2.643502       18779.746434
HLA A*3002      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.552942       1.909325        -2.643618       35722.550841
HLA B*0702      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -3.977227       1.332502        -2.644725       9489.143352
HLA A*3002      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.207190       1.562118        -2.645072       16113.500637
HLA A*0201      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.387633       1.742555        -2.645077       24413.649107
HLA A*2902      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.388702       1.742555        -2.646146       24473.817315
HLA A*0250      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -3.751564       1.105200        -2.646364       5643.696777
HLA B*1509      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.388934       1.742555        -2.646379       24486.928489
HLA A*3001      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.288405       1.641843        -2.646562       19426.946701
HLA B*3901      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.389338       1.742555        -2.646783       24509.724203
HLA B*4601      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.389439       1.742555        -2.646884       24515.426446
HLA B*4601      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.395543       1.748514        -2.647029       24862.420890
HLA A*2601      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.207256       1.559867        -2.647388       16115.941645
HLA B*3901      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.210719       1.562118        -2.648601       16244.966761
HLA B*1502      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.167159       1.518523        -2.648636       14694.654355
HLA B*1501      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.718901       1.070235        -2.648667       5234.812509
HLA B*0702      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.391437       1.742555        -2.648881       24628.417916
HLA B*4001      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.397475       1.748514        -2.648961       24973.228501
HLA B*1502      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.545457       1.896327        -2.649130       35112.116094
HLA B*0801      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.894290       1.245153        -2.649138       7839.532899
HLA B*1517      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.473103       0.822896        -2.650206       2972.368907
HLA A*2602      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.371478       1.721236        -2.650242       23522.183810
HLA A*6901      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -3.994980       1.344429        -2.650551       9885.069252
HLA A*0216      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -3.722397       1.071321        -2.651076       5277.122372
HLA B*1801      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.413754       1.762358        -2.651396       25927.119686
HLA B*1503      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.257549       1.605818        -2.651730       18094.590630
HLA A*0211      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -3.756996       1.105200        -2.651796       5714.729539
HLA A*6802      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.400433       1.748241        -2.652192       25143.902997
HLA A*3001      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.289152       1.636392        -2.652759       19460.396511
HLA B*1509      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.199578       1.546761        -2.652816       15833.523435
HLA A*8001      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.441133       1.788298        -2.652835       27614.222589
HLA B*5401      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.550053       1.896327        -2.653726       35485.636250
HLA B*4002      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.381940       1.728208        -2.653732       24095.719344
HLA A*2902      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.375101       1.721236        -2.653865       23719.227754
HLA B*5701      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -3.727134       1.072739        -2.654395       5334.991441
HLA A*3001      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -3.755248       1.100579        -2.654669       5691.774224
HLA A*1101      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.432987       1.778264        -2.654723       27101.114853
HLA B*5701      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.403261       1.748514        -2.654747       25308.212508
HLA A*2602      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.535559       1.879734        -2.655825       34320.896491
HLA A*2601      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.384477       1.728208        -2.656269       24236.915007
HLA A*6901      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.262920       1.606496        -2.656424       18319.755992
HLA B*0802      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.445045       1.788298        -2.656747       27864.080347
HLA B*3501      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.901931       1.245153        -2.656778       7978.673845
HLA A*3002      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.206081       1.548963        -2.657118       16072.407821
HLA A*6802      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.399798       1.742555        -2.657243       25107.202860
HLA A*6901      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.355346       1.697997        -2.657349       22664.496492
HLA B*1501      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.385685       1.728208        -2.657477       24304.403974
HLA B*4403      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.634697       1.977177        -2.657521       43121.860731
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HLA A*8001	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.406412	1.748514	-2.657898	25492.482619
HLA A*0101	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.356190	1.697997	-2.658192	22708.557121
HLA B*4002	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.242284	1.584079	-2.658205	17469.648149
HLA B*2705	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.379489	1.721236	-2.658253	23960.141760
HLA A*2603	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-3.731335	1.072739	-2.658595	5386.846572
HLA B*3901	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-4.289243	1.630187	-2.659056	19464.502809
HLA A*3002	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.526078	1.866986	-2.659092	33579.826777
HLA B*5701	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.407455	1.748241	-2.659215	25553.788926
HLA B*5401	1:200-208	9	TDLGASTAL	1.577364	0.302370	-4.539104	1.879734	-2.659370	34602.222653
HLA B*2705	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.295852	1.636392	-2.659460	19762.979316
HLA B*4001	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.387696	1.728208	-2.659488	24417.215396
HLA B*1503	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-3.942032	1.282277	-2.659755	8750.476891
HLA A*0219	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.448240	1.788298	-2.659942	28069.844927
HLA A*2601	1:13-21	9	ATPYALNAV	1.259075	0.203216	-4.122341	1.462291	-2.660049	13253.805689
HLA A*0250	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.438365	1.778264	-2.660101	27438.800868
HLA B*3801	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.358311	1.697997	-2.660314	22819.762778
HLA B*4001	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.448646	1.788298	-2.660349	28096.128096
HLA A*2902	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.449032	1.788298	-2.660734	28121.066655
HLA A*3001	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.056452	1.395101	-2.661351	11388.109696
HLA B*4801	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.382856	1.721236	-2.661620	24146.611529
HLA B*1517	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.268472	1.606496	-2.661976	18555.451142
HLA B*0802	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.410519	1.748514	-2.662005	25734.695365
HLA A*6801	1:23-31	9	DDERADIDR	0.950475	0.333798	-3.946369	1.284273	-2.662095	8838.302701
HLA A*0211	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-3.787201	1.124732	-2.662469	6126.333863
HLA A*2603	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.246946	1.584079	-2.662867	17658.163606
HLA A*0203	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.405477	1.742555	-2.662922	25437.652889
HLA A*0219	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.405597	1.742555	-2.663041	25444.672216
HLA A*0212	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.411764	1.748514	-2.663250	25808.588830
HLA A*2402	1:18-26	9	LNAVSDDER	1.255134	0.654191	-4.572582	1.909325	-2.663257	37375.052220
HLA B*0802	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.411729	1.748241	-2.663488	25806.494591
HLA B*0801	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.225868	1.562118	-2.663751	16821.638914
HLA B*2705	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.452171	1.788298	-2.663873	28325.051083
HLA B*5301	1:18-26	9	LNAVSDDER	1.255134	0.654191	-4.573409	1.909325	-2.664084	37446.292631
HLA A*0216	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.412662	1.748514	-2.664148	25861.979432
HLA B*7301	1:18-26	9	LNAVSDDER	1.255134	0.654191	-4.573604	1.909325	-2.664279	37463.110571
HLA A*0212	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.213294	1.548963	-2.664331	16341.573161
HLA A*3201	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.490373	1.825968	-2.664405	30929.530521
HLA A*0212	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.725057	1.060336	-2.664721	5309.538598
HLA A*8001	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.392999	1.728208	-2.664791	24717.180097
HLA B*4001	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.407566	1.742555	-2.665010	25560.287181
HLA B*4801	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.413801	1.748514	-2.665287	25929.925095
HLA A*8001	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.386662	1.721236	-2.665426	24359.162968
HLA B*4801	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.277834	1.612334	-2.665500	18959.820249
HLA A*6801	1:10-18	9	LELATPYAL	1.590569	0.388292	-4.644380	1.978861	-2.665519	44094.022595
HLA B*1517	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.443790	1.778264	-2.665526	27783.700500
HLA A*2403	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.453881	1.788298	-2.665583	28436.826408
HLA A*0219	1:13-21	9	ATPYALNAV	1.259075	0.203216	-4.127970	1.462291	-2.665679	13426.721021
HLA A*0203	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.414572	1.748514	-2.666058	25975.977132
HLA A*6802	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-3.766981	1.100579	-2.666402	5847.644908
HLA B*7301	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-3.517156	0.850740	-2.666416	3289.694384
HLA A*0201	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.387959	1.721236	-2.666723	24432.014455
HLA A*0301	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.308612	1.641843	-2.666769	20352.251895
HLA A*6801	1:218-226	9	SPQPTGTIL	1.697402	0.279969	-4.644147	1.977371	-2.666776	44070.413085
HLA A*2403	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.251071	1.584079	-2.666992	17826.711331
HLA A*0219	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.415587	1.748514	-2.667073	26036.755858
HLA B*3901	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.280632	1.612334	-2.668298	19082.376146
HLA B*4501	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.272849	1.604221	-2.668627	18743.410141
HLA A*3201	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.535667	1.866986	-2.668681	34329.438477
HLA A*6901	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.305269	1.636392	-2.668877	20196.176246
HLA B*0803	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.457497	1.788298	-2.669199	28674.574639
HLA A*0201	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.397632	1.728208	-2.669424	24982.282003
HLA A*0219	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.417976	1.748241	-2.669736	26180.401168
HLA A*0212	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.418127	1.748241	-2.669886	26189.467253
HLA B*4601	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.391509	1.721236	-2.670273	24632.548610
HLA A*0212	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.413035	1.742555	-2.670480	25884.234762
HLA B*4601	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.368588	1.697997	-2.670590	23366.182953
HLA B*3501	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.459123	1.788298	-2.670825	28782.123204
HLA A*2402	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.449558	1.778264	-2.671294	28155.164846
HLA B*1509	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.088766	1.417448	-2.671318	12267.793543
HLA A*6901	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.399603	1.728208	-2.671395	25095.931734
HLA A*3101	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.255817	1.584079	-2.671738	18022.589532
HLA A*6802	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-3.481660	0.809887	-2.671773	3031.513691
HLA A*0101	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.400242	1.728208	-2.672034	25132.887326
HLA B*5401	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.314146	1.641843	-2.672303	20613.204239
HLA A*2501	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.450803	1.778264	-2.672539	28236.008340
HLA A*6901	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.158213	1.485661	-2.672551	14395.028738
HLA A*1101	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.435073	1.762358	-2.672715	27231.621333
HLA B*5101	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.461080	1.788298	-2.672782	28912.120741
HLA B*4402	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.370968	1.697997	-2.672970	23494.586240
HLA A*0101	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.395182	1.721236	-2.673946	24841.716063
HLA A*6801	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.436394	1.762358	-2.674036	27314.541192
HLA B*4601	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.402498	1.728208	-2.674290	25263.754350
HLA A*3001	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-3.956631	1.282277	-2.674354	9049.642479
HLA B*4601	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.019457	1.344429	-2.675028	10458.192970
HLA B*5401	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.019908	1.344429	-2.675479	10469.061525
HLA A*3001	1:86-94	9	SRWRTAAFA	1.225790	-0.065711	-3.835732	1.160079	-2.675653	6850.647521
HLA B*1509	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.404533	1.728208	-2.676324	25382.391818
HLA B*0803	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.424947	1.748241	-2.676707	26604.017145
HLA B*5101	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.419522	1.742555	-2.676967	26273.761796
HLA A*2501	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.223848	1.546761	-2.677086	16743.557937
HLA A*0219	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-3.497472	0.820380	-2.677092	3143.920591
HLA B*2705	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-4.395435	1.718268	-2.677167	24856.234524
HLA A*3201	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.425779	1.748514	-2.677265	26655.015336
HLA B*0802	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.419999	1.742555	-2.677444	26302.631688
HLA A*0206	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-3.180127	0.502462	-2.677665	1514.002627
HLA A*0216	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-3.897500	1.219814	-2.677686	7897.680920
HLA A*2601	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.261830	1.584079	-2.677751	18273.827619
HLA B*7301	1:166-174	9	GTVYQMWLL	1.476128	0.420199	-4.574102	1.896327	-2.677775	37506.101529
HLA A*0216	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.426101	1.748241	-2.677860	26674.778152
HLA A*0216	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.466169	1.788298	-2.677871	29252.900463
HLA A*8001	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.426611	1.748241	-2.678370	26706.111288
HLA A*0301	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.282639	1.604221	-2.678418	19170.741558
HLA B*2705	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.262541	1.584079	-2.678463	18303.806576
HLA B*0802	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.406929	1.728208	-2.678721	25522.841212
HLA B*1517	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.222800	1.543934	-2.678866	16703.207602
HLA B*2705	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.283417	1.604221	-2.679195	19205.100847
HLA B*7301	1:2-10	9	TEHTDFELL	1.490281	0.376705	-4.546613	1.866986	-2.679627	35205.697286
HLA A*0203	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-3.386557	0.706535	-2.680022	2435.325858
HLA A*6802	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-3.726335	1.045865	-2.680470	5325.187478
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HLA B*0803      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.398887       1.718268        -2.680619       25054.557185
HLA B*0801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -3.711716       1.031086        -2.680630       5148.923110
HLA A*3002      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.224581       1.543934        -2.680647       16771.843009
HLA A*3001      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.286600       1.605818        -2.680782       19346.399168
HLA A*0216      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.013771       1.332502        -2.681269       10322.167383
HLA B*1503      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -3.755163       1.072739        -2.682424       5690.665824
HLA A*6802      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.168123       1.485661        -2.682461       14727.284074
HLA A*2603      1:41-49 9       AAAFNDEVR       1.220112        0.757065        -4.659832       1.977177        -2.682656       45691.170434
HLA B*1502      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.313178       1.630187        -2.682990       20567.311161
HLA A*2501      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.401321       1.718268        -2.683053       25195.373331
HLA A*0211      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.509045       1.825968        -2.683076       32288.263234
HLA A*0203      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.431552       1.748241        -2.683311       27011.681572
HLA A*1101      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.471761       1.788298        -2.683463       29631.982445
HLA B*4001      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.405825       1.721236        -2.684589       25458.028047
HLA B*3501      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.433288       1.748514        -2.684774       27119.887948
HLA B*1801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.433140       1.748241        -2.684899       27110.646441
HLA B*4402      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.123412       1.437876        -2.685536       13286.541990
HLA B*1517      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.473929       1.788298        -2.685631       29780.314671
HLA A*2301      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.384231       1.697997        -2.686233       24223.151419
HLA A*0250      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.595938       1.909325        -2.686613       39440.102826
HLA B*3901      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.475111       1.788298        -2.686813       29861.462455
HLA B*1503      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.328733       1.641843        -2.686890       21317.361927
HLA A*2902      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.293439       1.606496        -2.686944       19653.481534
HLA A*6901      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.757404       1.070235        -2.687170       5720.111465
HLA A*0211      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.317482       1.630187        -2.687294       20772.165544
HLA A*3301      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.001883       1.314292        -2.687591       10043.440318
HLA B*4801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.415918       1.728208        -2.687710       26056.624125
HLA A*0201      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.318114       1.630187        -2.687926       20802.416455
HLA B*5401      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.555280       1.866986        -2.688294       35915.358065
HLA B*7301      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.568122       1.879734        -2.688388       36993.249843
HLA B*5401      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.558682       1.870237        -2.688445       36197.806561
HLA A*3101      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.251727       1.562118        -2.689609       17853.638555
HLA A*0206      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -3.794921       1.105200        -2.689721       6236.214839
HLA A*0201      1:49-57 9       RAVRETMAV       0.926962        0.318191        -3.934894       1.245153        -2.689741       8607.836054
HLA A*2501      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.438443       1.748241        -2.690202       27443.699855
HLA B*4402      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.438492       1.748241        -2.690251       27446.817846
HLA A*2501      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.274437       1.584079        -2.690358       18812.081879
HLA B*1501      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.107340       0.416603        -2.690736       1280.382069
HLA A*0202      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.303124       1.612334        -2.690790       20096.668659
HLA A*8001      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.434355       1.742555        -2.691799       27186.578690
HLA A*0101      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.322115       1.630187        -2.691928       20994.955549
HLA B*0702      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.440849       1.748514        -2.692334       27596.152328
HLA A*6802      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.413961       1.721236        -2.692725       25939.465755
HLA B*0702      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.413994       1.721236        -2.692758       25941.430444
HLA A*0216      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.323160       1.630187        -2.692973       21045.559707
HLA A*6802      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.305537       1.612334        -2.693203       20208.635623
HLA B*3901      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -3.804474       1.111207        -2.693267       6374.910242
HLA A*6802      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.442235       1.748514        -2.693721       27684.375403
HLA B*1801      1:7-15  9       FELLELATP       0.903395        -0.108267       -3.489112       0.795128        -2.693984       3083.983888
HLA A*2603      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.442319       1.748241        -2.694079       27689.767627
HLA A*6802      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -3.805353       1.111207        -2.694145       6387.821646
HLA B*1517      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.442846       1.748514        -2.694331       27723.342847
HLA B*0702      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.422706       1.728208        -2.694498       26467.066609
HLA B*1517      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.442853       1.748241        -2.694612       27723.792791
HLA A*2602      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.604154       1.909325        -2.694829       40193.348398
HLA A*3002      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.520858       1.825968        -2.694889       33178.587713
HLA A*2501      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.483854       1.788298        -2.695556       30468.670698
HLA A*3201      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.009918       1.314292        -2.695626       10230.991925
HLA A*3201      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -3.967622       1.271968        -2.695654       9281.588561
HLA A*0202      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -3.796838       1.100579        -2.696260       6263.805273
HLA A*3101      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.424506       1.728208        -2.696297       26576.973041
HLA B*0802      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.394834       1.697997        -2.696836       24821.834166
HLA A*2301      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.425067       1.728208        -2.696859       26611.358322
HLA A*0211      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -3.768236       1.071321        -2.696914       5864.562481
HLA A*3002      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.418202       1.721236        -2.696966       26194.001473
HLA A*2601      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.395050       1.697997        -2.697053       24834.191311
HLA B*4501      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -3.826108       1.128647        -2.697461       6700.514205
HLA B*0802      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.418702       1.721236        -2.697466       26224.202386
HLA A*3101      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.327679       1.630187        -2.697491       21265.644035
HLA B*5101      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.327866       1.630187        -2.697679       21274.849609
HLA A*0203      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.242719       1.543934        -2.698785       17487.141040
HLA B*4501      1:166-174       9       GTVYQMWLL       1.476128        0.420199        -4.595919       1.896327        -2.699592       39438.395930
HLA A*1101      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.398015       1.697997        -2.700018       25004.321393
HLA B*1502      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.525987       1.825968        -2.700018       33572.742662
HLA B*4002      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.609535       1.909325        -2.700210       40694.386754
HLA B*5101      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.478833       1.778264        -2.700569       30118.452758
HLA B*5401      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.510882       0.809887        -2.700996       3242.518245
HLA B*0803      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.220375       1.518523        -2.701852       16610.213336
HLA A*2403      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.430187       1.728208        -2.701978       26926.913214
HLA B*0803      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.444697       1.742555        -2.702142       27841.779521
HLA A*3002      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.582020       1.879734        -2.702286       38196.158724
HLA B*3501      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.120048       1.417448        -2.702599       13184.009335
HLA A*0201      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.149346       1.446716        -2.702630       14104.106538
HLA A*2902      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.400644       1.697997        -2.702647       25156.148293
HLA B*1801      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.491229       1.788298        -2.702931       30990.496950
HLA B*0803      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.451475       1.748514        -2.702961       28279.729706
HLA B*5801      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.098070       1.395101        -2.702969       12533.443834
HLA A*3002      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.445625       1.742555        -2.703070       27901.338406
HLA B*1801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.339480       1.636392        -2.703088       21851.437035
HLA B*1503      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.247068       1.543934        -2.703134       17663.131797
HLA B*1509      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.307501       1.604221        -2.703280       20300.239549
HLA A*0212      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.401793       1.697997        -2.703796       25222.785371
HLA B*0801      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.425098       1.721236        -2.703862       26613.229926
HLA A*2301      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.452854       1.748514        -2.704340       28369.677699
HLA B*1517      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.447197       1.742555        -2.704641       28002.502329
HLA B*1502      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.574999       1.870237        -2.704763       37583.690945
HLA B*1502      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.423101       1.718268        -2.704833       26491.132438
HLA B*1509      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.453329       1.748241        -2.705088       28400.696960
HLA A*8001      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.267269       1.562118        -2.705151       18504.126195
HLA A*0203      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.427012       1.721236        -2.705776       26730.828303
HLA A*2603      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.427113       1.721236        -2.705877       26737.047292
HLA A*2403      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.448743       1.742555        -2.706187       28102.360661
HLA A*1101      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.349174       1.641843        -2.707331       22344.671705
HLA A*0206      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -3.753396       1.045865        -2.707531       5667.561877
HLA A*2902      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.312015       1.604221        -2.707793       20512.307739
HLA B*0803      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.321008       1.612334        -2.708674       20941.527287
HLA A*0301      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.345283       1.636392        -2.708891       22145.384803
HLA A*2301      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.488085       1.778264        -2.709821       30766.984271
HLA B*1501      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -2.967874       0.257963        -2.709911       928.697238
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HLA A*0203      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -3.993133       1.282277        -2.710856       9843.125469
HLA A*3301      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.499184       1.788298        -2.710886       31563.408542
HLA B*1509      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.459752       1.748514        -2.711238       28823.883240
HLA B*4001      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.341479       1.630187        -2.711292       21952.268950
HLA B*5301      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.473760       1.762358        -2.711402       29768.717139
HLA B*5701      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.273998       1.562118        -2.711880       18793.060273
HLA B*4501      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -3.931797       1.219814        -2.711983       8546.678463
HLA A*6802      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.440207       1.728208        -2.711999       27555.425660
HLA A*2301      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.454729       1.742555        -2.712174       28492.416942
HLA A*0216      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.455401       1.742555        -2.712846       28536.535337
HLA A*0212      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.441264       1.728208        -2.713056       27622.589690
HLA B*5801      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.257147       1.543934        -2.713213       18077.859227
HLA A*2603      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.431676       1.718268        -2.713408       27019.427583
HLA B*5401      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.456118       1.742555        -2.713562       28583.659950
HLA A*3301      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.107238       1.393369        -2.713869       12800.829399
HLA A*0203      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.442399       1.728208        -2.714191       27694.861247
HLA A*3201      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.623754       1.909325        -2.714429       42048.798565
HLA B*5801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.351234       1.636392        -2.714842       22450.937279
HLA A*2902      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.259118       1.543934        -2.715184       18160.099266
HLA B*3901      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.463723       1.748514        -2.715209       29088.620084
HLA A*2403      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.277355       1.562118        -2.715237       18938.907404
HLA B*4402      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.162423       1.446716        -2.715707       14535.260292
HLA B*0702      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.352108       1.636392        -2.715716       22496.164808
HLA A*3002      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.478135       1.762358        -2.715777       30070.099180
HLA A*3101      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.264910       1.548963        -2.715947       18403.892959
HLA A*0212      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.437613       1.721236        -2.716377       27391.340882
HLA A*0250      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.301021       1.584079        -2.716942       19999.598777
HLA A*8001      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.301658       1.584079        -2.717579       20028.941292
HLA A*0101      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.354122       1.636392        -2.717730       22600.705366
HLA A*3101      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.748486       1.029850        -2.718635       5603.841546
HLA B*0803      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.439895       1.721236        -2.718659       27535.606242
HLA B*2705      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.026171       1.307494        -2.718677       10621.148454
HLA A*2902      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.446941       1.728208        -2.718733       27985.994739
HLA B*1501      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.331081       1.612334        -2.718746       21432.883052
HLA A*0206      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.544783       1.825968        -2.718814       35057.641982
HLA A*2403      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.440256       1.721236        -2.719020       27558.556345
HLA B*5101      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.467452       1.748241        -2.719211       29339.435405
HLA A*6901      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.361394       1.641843        -2.719551       22982.308484
HLA B*1503      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.052359       1.332502        -2.719857       11281.291961
HLA A*6801      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.324091       1.604221        -2.719870       21090.694277
HLA B*3501      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -3.850792       1.130830        -2.719962       7092.377145
HLA A*6801      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.587153       1.866986        -2.720167       38650.339593
HLA A*2501      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.441981       1.721236        -2.720745       27668.205032
HLA B*1801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.351082       1.630187        -2.720894       22443.043957
HLA A*6901      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.264893       1.543934        -2.720959       18403.196031
HLA A*0219      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.419092       1.697997        -2.721095       26247.763388
HLA B*5801      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.363238       1.641843        -2.721395       23080.116437
HLA B*4403      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.630870       1.909325        -2.721545       42743.509900
HLA A*3301      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.601337       1.879734        -2.721603       39933.479694
HLA B*4002      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.484199       1.762358        -2.721841       30492.910658
HLA B*1502      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.500718       1.778264        -2.722454       31675.108440
HLA B*0803      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.269407       1.546761        -2.722645       18595.446592
HLA B*2705      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.266890       1.543934        -2.722956       18488.016263
HLA B*3501      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.329516       1.606496        -2.723020       21355.799619
HLA A*2403      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.185420       1.462291        -2.723128       15325.673624
HLA B*0801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.359613       1.636392        -2.723220       22888.257992
HLA B*1503      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.118191       1.394877        -2.723314       13127.783587
HLA A*0206      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.533282       0.809887        -2.723396       3414.148590
HLA A*0219      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.354176       1.630187        -2.723989       22603.517689
HLA A*2301      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.354200       1.630187        -2.724012       22604.740548
HLA B*1502      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.119145       1.395101        -2.724044       13156.649337
HLA A*3101      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.019574       1.295115        -2.724460       10461.022236
HLA A*2603      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.502837       1.778264        -2.724574       31830.051833
HLA B*4601      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.308664       1.584079        -2.724585       20354.674315
HLA A*2501      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.453385       1.728208        -2.725177       28404.384671
HLA B*4001      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.287387       1.562118        -2.725270       19381.492686
HLA A*0216      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -3.980709       1.254367        -2.726342       9565.527934
HLA A*2601      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.357526       1.630187        -2.727339       22778.566911
HLA B*0801      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.122707       1.395101        -2.727606       13264.995863
HLA B*1501      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -3.492190       0.764021        -2.728169       3105.917572
HLA A*2402      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.490998       1.762358        -2.728640       30974.071099
HLA A*2402      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.277632       1.548963        -2.728669       18951.001235
HLA A*2601      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.365075       1.636392        -2.728683       23177.964467
HLA A*0301      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.359145       1.630187        -2.728958       22863.630486
HLA B*5301      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.341484       1.612334        -2.729150       21952.506470
HLA B*5701      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.335676       1.606496        -2.729180       21660.884514
HLA B*1503      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -3.661686       0.932462        -2.729224       4588.666268
HLA B*3901      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.276056       1.546761        -2.729294       18882.333135
HLA B*4501      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.638652       1.909325        -2.729327       43516.271320
HLA A*0212      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.371536       1.641843        -2.729693       23525.365335
HLA A*0219      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.542065       0.811766        -2.730298       3483.892882
HLA A*0206      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.478960       1.748514        -2.730445       30127.252668
HLA B*5401      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.361029       1.630187        -2.730842       22963.045141
HLA A*3002      1:71-79 9       RTAILDATK       0.821937        0.327507        -3.880287       1.149444        -2.730843       7590.794886
HLA A*2301      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.493376       1.762358        -2.731018       31144.113235
HLA B*5401      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.335808       1.604221        -2.731587       21667.447755
HLA B*3501      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.460478       1.728208        -2.732270       28872.107145
HLA A*2603      1:18-26 9       LNAVSDDER       1.255134        0.654191        -4.641657       1.909325        -2.732332       43818.415301
HLA A*0202      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.481173       1.748514        -2.732659       30281.176503
HLA A*0206      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.521445       1.788298        -2.733147       33223.491192
HLA A*2501      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.481720       1.748514        -2.733206       30319.370119
HLA A*0219      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.454628       1.721236        -2.733392       28485.789657
HLA B*0801      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.293317       1.559867        -2.733450       19647.953508
HLA A*0206      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.481746       1.748241        -2.733505       30321.174441
HLA B*5801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.828068       1.094281        -2.733786       6730.814206
HLA B*0801      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -3.482740       0.748881        -2.733859       3039.067156
HLA B*4501      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -2.369756       -0.364496       -2.734252       234.291406
HLA A*0250      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.016590       1.282277        -2.734313       10389.395503
HLA B*5401      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.560682       1.825968        -2.734713       36364.838787
HLA B*5801      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.347151       1.612334        -2.734817       22240.834154
HLA B*0803      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.432919       1.697997        -2.734922       27096.863380
HLA B*4001      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.347696       1.612334        -2.735362       22268.766023
HLA A*2602      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.454189       1.718268        -2.735921       28456.986601
HLA A*3301      1:2-10  9       TEHTDFELL       1.490281        0.376705        -4.602932       1.866986        -2.735946       40080.437679
HLA A*2902      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.366375       1.630187        -2.736187       23247.409084
HLA B*3801      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.478772       1.742555        -2.736216       30114.216681
HLA B*5101      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.464663       1.728208        -2.736455       29151.634724
HLA B*4403      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.607039       1.870237        -2.736803       40461.255547
HLA B*3501      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.458042       1.721236        -2.736806       28710.586529
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HLA A*0216      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.458268       1.721236        -2.737032       28725.501226
HLA B*1517      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.019381       1.282277        -2.737104       10456.382641
HLA B*7301      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.607615       1.870237        -2.737378       40514.919375
HLA B*1509      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.299633       1.562118        -2.737515       19935.757283
HLA B*4001      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.379426       1.641843        -2.737583       23956.642229
HLA A*2301      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.526419       1.788298        -2.738121       33606.178267
HLA B*4601      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.374760       1.636392        -2.738367       23700.628883
HLA A*6802      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.375634       1.636392        -2.739241       23748.373922
HLA B*4001      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.375660       1.636392        -2.739267       23749.787200
HLA A*2601      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.343655       1.604221        -2.739434       22062.516015
HLA B*1501      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -3.987997       1.248280        -2.739717       9727.406091
HLA A*3201      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.834510       1.094281        -2.740229       6831.402756
HLA A*2603      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -3.924631       1.184095        -2.740536       8406.813951
HLA B*1801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.519056       1.778264        -2.740792       33041.202209
HLA A*8001      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.371158       1.630187        -2.740971       23504.883848
HLA A*0206      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.284937       1.543934        -2.741003       19272.440289
HLA A*6901      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.353398       1.612334        -2.741064       22563.078391
HLA A*2601      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.285240       1.543934        -2.741306       19285.894751
HLA B*0803      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.469545       1.728208        -2.741337       29481.199072
HLA B*5801      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.347896       1.606496        -2.741400       22279.008460
HLA A*2402      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.490150       1.748241        -2.741910       30913.638699
HLA B*4801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.378434       1.636392        -2.742042       23902.012240
HLA A*0219      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.470276       1.728208        -2.742068       29530.842218
HLA B*3801      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.463495       1.721236        -2.742259       29073.359566
HLA A*0250      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -3.572030       0.829467        -2.742563       3732.760494
HLA B*5301      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.384527       1.641843        -2.742684       24239.668663
HLA A*2501      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.440891       1.697997        -2.742893       27598.839717
HLA A*0101      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.349411       1.606496        -2.742916       22356.884143
HLA A*2402      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.531900       1.788298        -2.743603       34033.018932
HLA B*0803      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.348901       1.604221        -2.744680       22330.653769
HLA A*0212      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.374976       1.630187        -2.744789       23712.427854
HLA B*0801      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.328870       1.584079        -2.744791       21324.051801
HLA A*6801      1:200-208       9       TDLGASTAL       1.577364        0.302370        -4.625055       1.879734        -2.745321       42175.011159
HLA A*1101      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.307508       1.562118        -2.745391       20300.569018
HLA A*0211      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.494128       1.748514        -2.745614       31198.075514
HLA B*0803      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.382154       1.636392        -2.745761       24107.584585
HLA B*5101      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.443980       1.697997        -2.745983       27795.878014
HLA A*3001      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.053783       1.307749        -2.746033       11318.337159
HLA A*0211      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.494473       1.748241        -2.746233       31222.895767
HLA A*3002      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.494739       1.748241        -2.746498       31241.988704
HLA B*5801      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.352468       1.605818        -2.746650       22514.792885
HLA A*2301      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.494931       1.748241        -2.746691       31255.851066
HLA A*0301      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.359385       1.612334        -2.747050       22876.250318
HLA A*0211      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.535495       1.788298        -2.747197       34315.883706
HLA B*3801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.475842       1.728208        -2.747634       29911.745923
HLA A*2603      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.360099       1.612334        -2.747765       22913.903697
HLA A*2902      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.310842       1.562118        -2.748725       20457.008727
HLA A*0202      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.575023       1.825968        -2.749054       37585.724236
HLA B*1501      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.386164       1.636392        -2.749772       24331.241543
HLA B*4501      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.498298       1.748514        -2.749784       31499.099682
HLA B*4801      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.391899       1.641843        -2.750056       24654.679599
HLA B*1503      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.820347       1.070235        -2.750113       6612.218479
HLA B*4601      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.312285       1.562118        -2.750167       20525.073180
HLA A*0201      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.386615       1.636392        -2.750223       24356.527503
HLA B*1502      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.498794       1.748241        -2.750553       31535.076012
HLA A*2601      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.392614       1.641843        -2.750771       24695.260201
HLA A*6801      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.561819       0.809887        -2.751933       3646.021819
HLA A*0201      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.364521       1.612334        -2.752186       23148.391258
HLA A*0216      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.480545       1.728208        -2.752337       30237.468723
HLA A*0219      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -3.813402       1.060336        -2.753066       6507.319303
HLA A*3201      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.531560       1.778264        -2.753296       34006.332745
HLA B*4001      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.360012       1.606496        -2.753516       22909.317574
HLA B*0803      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.068223       1.314292        -2.753931       11700.988747
HLA A*2902      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.303082       1.548963        -2.754119       20094.711781
HLA A*3002      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.502814       1.748514        -2.754300       31828.329909
HLA B*3901      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.360832       1.606496        -2.754336       22952.612400
HLA A*2501      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.314479       1.559867        -2.754612       20629.045474
HLA A*0201      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.396558       1.641843        -2.754715       24920.594111
HLA B*4402      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.396641       1.641843        -2.754798       24925.313176
HLA A*1101      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.483217       1.728208        -2.755009       30424.033919
HLA A*2403      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.367439       1.612334        -2.755104       23304.450906
HLA A*6802      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.361692       1.606496        -2.755196       22998.104040
HLA B*5401      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.518046       1.762358        -2.755687       32964.429367
HLA B*2705      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.397590       1.641843        -2.755747       24979.849396
HLA A*0301      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.340140       1.584079        -2.756061       21884.680389
HLA B*0803      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.397959       1.641843        -2.756116       25001.075109
HLA B*1517      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.070473       1.314292        -2.756181       11761.788572
HLA B*5101      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.504928       1.748514        -2.756414       31983.676749
HLA A*0101      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.305706       1.548963        -2.756743       20216.508662
HLA A*0101      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.398617       1.641843        -2.756774       25038.974659
HLA B*4601      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.369394       1.612334        -2.757059       23409.581307
HLA B*5401      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.545401       1.788298        -2.757103       35107.557526
HLA B*2705      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.485313       1.728208        -2.757104       30571.203586
HLA A*0219      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.341515       1.584079        -2.757436       21954.050413
HLA A*0101      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.369840       1.612334        -2.757506       23433.655893
HLA B*5701      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.387696       1.630187        -2.757509       24417.215396
HLA B*2705      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.387821       1.630187        -2.757633       24424.217405
HLA B*5101      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.090402       1.332502        -2.757900       12314.072327
HLA B*2705      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -3.609316       0.850740        -2.758576       4067.395952
HLA A*0201      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.103244       1.344429        -2.758815       12683.642283
HLA A*0212      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.395565       1.636392        -2.759172       24863.631446
HLA A*2402      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.371574       1.612334        -2.759240       23527.401737
HLA A*0101      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.343730       1.584079        -2.759651       22066.335730
HLA B*1517      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.222010       1.462291        -2.759719       16672.873380
HLA B*3801      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.548229       1.788298        -2.759932       35336.977183
HLA A*0202      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.306933       1.546761        -2.760171       20273.680004
HLA B*4801      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.322296       1.562118        -2.760178       21003.703060
HLA B*1503      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.396744       1.636392        -2.760352       24931.246982
HLA B*1801      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.458399       1.697997        -2.760402       28734.205044
HLA A*0250      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.586843       1.825968        -2.760875       38622.749031
HLA B*4501      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.586961       1.825968        -2.760992       38633.197684
HLA B*0802      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.307882       1.546761        -2.761120       20318.038519
HLA A*2601      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.373515       1.612334        -2.761180       23632.770791
HLA B*3501      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.398356       1.636392        -2.761963       25023.943326
HLA A*0202      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.550468       1.788298        -2.762171       35519.631808
HLA A*0301      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.368106       1.605818        -2.762288       23340.283583
HLA B*1509      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.484361       1.721236        -2.763125       30504.295248
HLA B*4601      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.406133       1.641843        -2.764290       25476.076431
HLA B*1501      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.211048       1.446716        -2.764332       16257.275107
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HLA B*1501      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.308354       1.543934        -2.764420       20340.144121
HLA B*1509      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.348650       1.584079        -2.764571       22317.731229
HLA B*3801      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.513107       1.748514        -2.764593       32591.694800
HLA B*0802      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.369210       1.604221        -2.764989       23399.705218
HLA B*0802      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.401481       1.636392        -2.765088       25204.643720
HLA B*5701      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.407023       1.641843        -2.765180       25528.364840
HLA B*4801      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.371583       1.605818        -2.765765       23527.910865
HLA A*1101      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.402171       1.636392        -2.765779       25244.763789
HLA B*4501      1:4-12  9       HTDFELLEL       1.651839        0.218398        -4.637446       1.870237        -2.767210       43395.669210
HLA B*4002      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.797162       1.029850        -2.767312       6268.483355
HLA A*0101      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.329781       1.562118        -2.767664       21368.858784
HLA B*3901      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.496498       1.728208        -2.768290       31368.838284
HLA A*3001      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.100829       1.332502        -2.768327       12613.299688
HLA B*5101      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -3.686079       0.917388        -2.768691       4853.765898
HLA A*3001      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.296233       1.526960        -2.769273       19780.307224
HLA B*1509      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.164270       1.394877        -2.769392       14597.198324
HLA A*2601      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.318452       1.548963        -2.769489       20818.628352
HLA A*2601      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.376498       1.606496        -2.770003       23795.700209
HLA B*1501      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.590756       0.820380        -2.770376       3897.225366
HLA B*0702      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.330465       1.559867        -2.770598       21402.525796
HLA B*3801      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.412507       1.641843        -2.770664       25852.746991
HLA B*5701      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.407169       1.636392        -2.770776       25536.928824
HLA B*4001      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.317616       1.546761        -2.770854       20778.571913
HLA A*0202      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.513730       1.742555        -2.771174       32638.452434
HLA B*5701      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.383540       1.612334        -2.771205       24184.654940
HLA B*5801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.320221       1.548963        -2.771258       20903.609058
HLA B*3901      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.016609       1.245153        -2.771456       10389.845156
HLA A*0101      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.375921       1.604221        -2.771699       23764.053176
HLA B*3901      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.493110       1.721236        -2.771874       31125.080113
HLA A*0211      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.514467       1.742555        -2.771912       32693.942660
HLA A*2602      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.597987       1.825968        -2.772018       39626.598030
HLA A*6801      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.334511       1.562118        -2.772393       21602.839665
HLA B*1801      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.494713       1.721236        -2.773477       31240.129587
HLA B*1501      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.322484       1.548963        -2.773521       21012.795244
HLA A*0250      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.403973       1.630187        -2.773786       25349.731658
HLA B*1501      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.416061       1.641843        -2.774218       26065.224314
HLA B*3801      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.522679       1.748241        -2.774438       33317.986408
HLA A*0219      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.387116       1.612334        -2.774781       24384.609862
HLA B*5101      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.416625       1.641843        -2.774782       26099.088688
HLA B*0801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.324187       1.548963        -2.775224       21095.372827
HLA A*0101      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.170430       1.395101        -2.775329       14805.731125
HLA A*0203      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.411877       1.636392        -2.775485       25815.291537
HLA B*4001      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.381665       1.605818        -2.775847       24080.472615
HLA B*4501      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.504188       1.728208        -2.775980       31929.219297
HLA A*0301      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.338178       1.562118        -2.776061       21786.044603
HLA A*0206      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.497718       1.721236        -2.776482       31457.037352
HLA B*4403      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.494819       1.718268        -2.776551       31247.735766
HLA A*0202      1:201-209       9       DLGASTALA       1.029007        -0.426525       -3.379058       0.602482        -2.776575       2393.632781
HLA B*4402      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.388960       1.612334        -2.776626       24488.385720
HLA A*2902      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.413073       1.636392        -2.776681       25886.475353
HLA B*3801      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.339405       1.562118        -2.777287       21847.654519
HLA A*0203      1:201-209       9       DLGASTALA       1.029007        -0.426525       -3.379889       0.602482        -2.777407       2398.221221
HLA A*6901      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.383319       1.605818        -2.777501       24172.359454
HLA A*0201      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.321506       1.543934        -2.777572       20965.558829
HLA A*0101      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.383582       1.605818        -2.777764       24187.010108
HLA A*0216      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.023949       1.245153        -2.778796       10566.930872
HLA A*3001      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.027398       1.248280        -2.779118       10651.184566
HLA A*3101      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.326079       1.546761        -2.779317       21187.442683
HLA B*5101      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.500608       1.721236        -2.779372       31667.055599
HLA A*0201      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.326210       1.546761        -2.779449       21193.862471
HLA B*5401      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.385542       1.605818        -2.779723       24296.384765
HLA B*4402      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.342215       1.562118        -2.780097       21989.472113
HLA B*4001      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.175209       1.395101        -2.780108       14969.548812
HLA A*0201      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.657678       0.877544        -2.780143       4546.609440
HLA A*0211      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.324375       1.543934        -2.780441       21104.504693
HLA A*2602      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.559103       1.778264        -2.780839       36232.876414
HLA A*0219      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.343016       1.562118        -2.780898       22030.075120
HLA B*5101      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.393236       1.612334        -2.780902       24730.689225
HLA B*4002      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.606948       1.825968        -2.780979       40452.719702
HLA A*3201      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.479566       1.697997        -2.781568       30169.332182
HLA A*3001      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.267379       1.485661        -2.781718       18508.831741
HLA B*4801      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.328705       1.546761        -2.781944       21315.978077
HLA A*3002      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.114498       1.332502        -2.781996       13016.613760
HLA A*0301      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.300937       1.518523        -2.782413       19995.704114
HLA B*5801      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.055413       1.271968        -2.783445       11360.911309
HLA B*4801      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.390243       1.606496        -2.783747       24560.826435
HLA B*4002      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.388056       1.604221        -2.783834       24437.434210
HLA B*4403      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.388126       1.604221        -2.783905       24441.400646
HLA A*6901      1:206-214       9       TALAFTVEP       0.912771        0.088698        -3.785415       1.001469        -2.783946       6101.197055
HLA A*8001      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.388518       1.604221        -2.784297       24463.492244
HLA B*5401      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.563144       1.778264        -2.784880       36571.597122
HLA A*2603      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.513610       1.728208        -2.785402       32629.448585
HLA B*4402      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.421907       1.636392        -2.785515       26418.428829
HLA A*2402      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.416085       1.630187        -2.785898       26066.634452
HLA B*4601      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.392419       1.606496        -2.785923       24684.174004
HLA A*2403      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.391794       1.605818        -2.785975       24648.678271
HLA A*0219      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.422950       1.636392        -2.786558       26481.961924
HLA B*4501      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.305105       1.518523        -2.786581       20188.529559
HLA B*2705      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.348753       1.562118        -2.786636       22323.044265
HLA B*1503      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.335817       1.548963        -2.786854       21667.916634
HLA A*3002      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.393605       1.606496        -2.787109       24751.703223
HLA A*0216      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.131739       1.344429        -2.787310       13543.737855
HLA A*0212      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.399892       1.612334        -2.787558       25112.636535
HLA A*6802      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.882341       1.094281        -2.788059       7626.770995
HLA A*2601      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.394005       1.605818        -2.788186       24774.477369
HLA A*2603      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.536851       1.748514        -2.788337       34423.168302
HLA A*2602      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.517115       1.728208        -2.788907       32893.884731
HLA A*0250      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.083104       1.294185        -2.788919       12108.886256
HLA A*2602      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -3.415512       0.625647        -2.789865       2603.227559
HLA B*5701      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.396965       1.605818        -2.791146       24943.928483
HLA B*0802      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.397841       1.606496        -2.791345       24994.313371
HLA B*5701      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.335385       1.543934        -2.791451       21646.358697
HLA B*0802      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.375613       1.584079        -2.791534       23747.217665
HLA B*4601      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.340549       1.548963        -2.791586       21905.290590
HLA A*2402      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.375754       1.584079        -2.791675       23754.927105
HLA A*2403      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.428173       1.636392        -2.791781       26802.361590
HLA A*3101      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.398024       1.605818        -2.792206       25004.862481
HLA B*0802      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.398081       1.605818        -2.792262       25008.109257
HLA A*0212      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.336219       1.543934        -2.792285       21687.970705
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HLA B*1501      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.398711       1.605818        -2.792892       25044.393568
HLA A*0216      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.336912       1.543934        -2.792978       21722.610546
HLA A*8001      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.405364       1.612334        -2.793030       25431.048232
HLA A*0206      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.535742       1.742555        -2.793186       34335.381982
HLA A*0216      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.429782       1.636392        -2.793390       26901.869349
HLA A*6802      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.435588       1.641843        -2.793745       27263.903545
HLA A*3002      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -3.988923       1.194858        -2.794064       9748.162134
HLA B*5401      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.512386       1.718268        -2.794118       32537.610266
HLA B*2705      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.400621       1.606496        -2.794125       25154.787410
HLA A*0202      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.542370       1.748241        -2.794129       34863.403351
HLA B*5301      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.582703       1.788298        -2.794406       38256.337443
HLA A*0201      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.400975       1.606496        -2.794480       25175.344582
HLA A*2402      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.537060       1.742555        -2.794504       34439.746365
HLA A*3001      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -3.885179       1.090544        -2.794635       7676.776275
HLA A*2902      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.436490       1.641843        -2.794647       27320.600378
HLA A*8001      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.343662       1.548963        -2.794699       22062.874085
HLA B*5801      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.354982       1.559867        -2.795114       22645.499534
HLA A*3002      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.583545       1.788298        -2.795247       38330.501830
HLA A*2602      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -2.861692       0.066377        -2.795315       727.263059
HLA B*5301      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.573634       1.778264        -2.795371       37465.745390
HLA A*2403      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.437524       1.641843        -2.795681       27385.710464
HLA A*3001      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -3.926755       1.130830        -2.795925       8448.028508
HLA A*2501      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.432571       1.636392        -2.796179       27075.176591
HLA A*0216      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.409140       1.612334        -2.796805       25653.101763
HLA B*1502      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.545417       1.748514        -2.796903       35108.887047
HLA B*4601      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.402822       1.605818        -2.797004       25282.622419
HLA A*2602      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.585614       1.788298        -2.797317       38513.625354
HLA A*2501      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.427720       1.630187        -2.797532       26774.391618
HLA A*0201      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.403536       1.605818        -2.797718       25324.236589
HLA B*1801      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.383056       1.584079        -2.798977       24157.717674
HLA A*0206      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.284749       1.485661        -2.799087       19264.101153
HLA B*4002      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.517475       1.718268        -2.799207       32921.122699
HLA A*3201      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.246227       1.446716        -2.799511       17628.956004
HLA B*4002      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.497706       1.697997        -2.799709       31456.186468
HLA B*4403      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.237771       1.437876        -2.799894       17289.036747
HLA B*3901      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.343904       1.543934        -2.799970       22075.171354
HLA B*5401      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.548523       1.748241        -2.800283       35360.881406
HLA A*0211      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.436763       1.636392        -2.800370       27337.750724
HLA B*4402      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.384701       1.584079        -2.800622       24249.374516
HLA B*5801      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.347464       1.546761        -2.800702       22256.842532
HLA B*7301      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.563125       1.762358        -2.800767       36570.014370
HLA A*8001      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.406626       1.605818        -2.800808       25505.035655
HLA B*3501      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -3.924942       1.123686        -2.801255       8412.819446
HLA A*6901      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.361640       1.559867        -2.801773       22995.367025
HLA B*0802      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.432029       1.630187        -2.801841       27041.362298
HLA A*0203      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.443839       1.641843        -2.801996       27786.857121
HLA A*0206      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.614086       0.811766        -2.802320       4112.310576
HLA B*1503      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -3.458837       0.656423        -2.802413       2876.316262
HLA A*0301      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.349693       1.546761        -2.802932       22371.402646
HLA B*1517      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.444908       1.641843        -2.803065       27855.338707
HLA A*3301      1:164-172       9       SRGTVYQMW       1.464059        0.361909        -4.629392       1.825968        -2.803424       42598.308605
HLA B*4601      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.350544       1.546761        -2.803782       22415.257279
HLA B*4402      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.410171       1.605818        -2.804353       25714.098778
HLA B*0803      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.411316       1.606496        -2.804820       25781.934876
HLA A*0250      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.553431       1.748514        -2.804917       35762.770514
HLA A*2902      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.417556       1.612334        -2.805221       26155.061120
HLA B*4002      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.593769       1.788298        -2.805472       39243.656338
HLA A*0101      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.349517       1.543934        -2.805583       22362.327477
HLA B*7301      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.534769       1.728208        -2.806561       34258.567282
HLA B*1517      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -3.907396       1.100579        -2.806817       8079.707044
HLA B*1503      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.367249       1.559867        -2.807381       23294.241109
HLA A*0250      1:75-83 9       LDATKPEVR       1.264680        0.523618        -4.595710       1.788298        -2.807412       39419.411697
HLA A*0250      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.420899       1.612334        -2.808565       26357.186912
HLA A*0219      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.450441       1.641843        -2.808598       28212.494070
HLA B*4801      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.204056       1.395101        -2.808955       15997.631458
HLA A*2301      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.530566       1.721236        -2.809330       33928.602201
HLA A*1101      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.439751       1.630187        -2.809564       27526.520902
HLA B*0702      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.271982       1.462291        -2.809690       18706.030947
HLA B*1502      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.538096       1.728208        -2.809888       34522.009463
HLA A*2501      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.451731       1.641843        -2.809888       28296.410555
HLA A*0206      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.328111       0.518215        -2.809896       2128.684467
HLA A*1101      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.105058       1.295115        -2.809943       12736.725456
HLA A*0216      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.356777       1.546761        -2.810016       22739.290594
HLA A*0202      1:5-13  9       TDFELLELA       1.003059        -0.335657       -3.477421       0.667402        -2.810019       3002.071718
HLA B*0803      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.369950       1.559867        -2.810083       23439.615004
HLA B*1503      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.117867       1.307749        -2.810118       13117.986505
HLA A*0211      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.531506       1.721236        -2.810270       34002.101687
HLA B*1801      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.414706       1.604221        -2.810485       25983.988415
HLA B*4801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.359542       1.548963        -2.810579       22884.543605
HLA A*2602      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.354599       1.543934        -2.810665       22625.539264
HLA A*2403      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.257600       1.446716        -2.810885       18096.744332
HLA B*4001      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.359892       1.548963        -2.810929       22902.997666
HLA A*0301      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.337920       1.526960        -2.810960       21773.083850
HLA A*0301      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.359982       1.548963        -2.811019       22907.706451
HLA B*1502      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.553774       1.742555        -2.811219       35791.028675
HLA B*3801      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.447841       1.636392        -2.811448       28044.041487
HLA B*0801      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.418026       1.606496        -2.811530       26183.375631
HLA B*7301      1:157-165       9       MNNVAPPSR       1.164592        0.577963        -4.554120       1.742555        -2.811564       35819.502944
HLA B*1501      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.418399       1.606496        -2.811903       26205.907537
HLA B*4402      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.442183       1.630187        -2.811996       27681.080673
HLA A*2501      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.416242       1.604221        -2.812021       26076.084344
HLA B*5301      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.510123       1.697997        -2.812126       32368.539111
HLA A*8001      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.454149       1.641843        -2.812306       28454.369586
HLA B*2705      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.372312       1.559867        -2.812444       23567.401821
HLA A*3201      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.425058       1.612334        -2.812723       26610.782470
HLA B*4402      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.419562       1.606496        -2.813066       26276.178255
HLA B*1502      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.127495       1.314292        -2.813203       13412.056347
HLA A*2603      1:91-99 9       AAFASAAAI       1.234627        0.369594        -4.417558       1.604221        -2.813337       26155.202616
HLA B*5101      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.331872       1.518523        -2.813349       21471.993681
HLA B*1509      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.362888       1.548963        -2.813925       23061.519663
HLA A*8001      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.450698       1.636392        -2.814305       28229.135261
HLA B*5401      1:105-113       9       AFGLGVLTR       1.052600        0.695914        -4.563078       1.748514        -2.814564       36566.057790
HLA A*0212      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.361812       1.546761        -2.815050       23004.450193
HLA A*6802      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -3.152689       0.337522        -2.815167       1421.311739
HLA B*2705      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.427536       1.612334        -2.815202       26763.095975
HLA A*1101      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -3.943883       1.128647        -2.815236       8787.859734
HLA A*0216      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.097535       1.282277        -2.815258       12517.993928
HLA A*2402      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.536675       1.721236        -2.815439       34409.204221
HLA A*2403      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -3.999660       1.184095        -2.815565       9992.171752
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HLA B*1502	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.377741	1.562118	-2.815624	23863.897028
HLA B*2705	1:82-90 9	VRRQSRWRT	1.037980	-0.242033	-3.611938	0.795947	-2.815992	4092.026875
HLA A*2602	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-4.446375	1.630187	-2.816187	27949.530842
HLA B*1503	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-3.940932	1.124732	-2.816200	8728.350210
HLA B*1509	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.458700	1.641843	-2.816857	28754.109389
HLA B*4001	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.036984	1.219814	-2.817170	10888.894978
HLA A*3201	1:75-83 9	LDATKPEVR	1.264680	0.523618	-4.605973	1.788298	-2.817675	40362.001014
HLA B*0803	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.380145	1.562118	-2.818027	23996.333524
HLA B*1501	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-3.770914	0.952818	-2.818096	5900.842603
HLA A*3001	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.878549	1.060336	-2.818213	7560.467267
HLA B*5301	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.560886	1.742555	-2.818331	36381.958303
HLA B*5701	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.126255	1.307749	-2.818506	13373.800524
HLA A*2402	1:91-99 9	AAFASAAAI	1.234627	0.369594	-4.422896	1.604221	-2.818675	26478.667046
HLA A*0216	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.460521	1.641843	-2.818678	28874.918790
HLA A*3201	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.561347	1.742555	-2.818791	36420.555946
HLA A*0219	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.425039	1.605818	-2.819220	26609.630804
HLA A*0206	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.366147	1.546761	-2.819385	23235.212991
HLA B*0803	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.425424	1.605818	-2.819606	26633.249925
HLA B*1502	1:75-83 9	LDATKPEVR	1.264680	0.523618	-4.608083	1.788298	-2.819785	40558.559925
HLA B*1801	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.425864	1.605818	-2.820045	26660.207066
HLA B*4801	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-3.943761	1.123686	-2.820075	8785.387932
HLA B*3801	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.426822	1.605818	-2.821004	26719.117393
HLA B*5801	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.339642	1.518523	-2.821119	21859.595313
HLA B*1801	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.339724	1.518523	-2.821201	21863.734735
HLA A*3101	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.283663	1.462291	-2.821372	19216.013180
HLA B*4403	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.599838	1.778264	-2.821574	39795.886507
HLA B*1501	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.129328	1.307749	-2.821579	13468.770958
HLA B*4002	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.600033	1.778264	-2.821769	39813.759700
HLA A*0216	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.427933	1.605818	-2.822115	26787.575894
HLA B*3501	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.130183	1.307749	-2.822434	13495.319788
HLA A*6801	1:164-172	9	SRGTVYQMW	1.464059	0.361909	-4.648484	1.825968	-2.822516	44512.734089
HLA B*3501	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.384637	1.562118	-2.822520	24245.832741
HLA B*5101	1:63-71 9	TAEPPAHLR	1.007555	0.598941	-4.429425	1.606496	-2.822930	26879.756950
HLA A*0212	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.429242	1.605818	-2.823424	26868.416856
HLA B*5401	1:80-88 9	PEVRRQSRW	1.534965	0.193243	-4.552061	1.728208	-2.823853	35650.153662
HLA B*1502	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.545215	1.721236	-2.823979	35092.556420
HLA B*4403	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.545222	1.721236	-2.823986	35093.125965
HLA A*2301	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.372998	1.548963	-2.824035	23604.660375
HLA B*5701	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.370799	1.546761	-2.824037	23485.436598
HLA B*4001	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.383998	1.559867	-2.824131	24210.181481
HLA B*3501	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-3.863737	1.039542	-2.824196	7306.972687
HLA A*0201	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-3.953004	1.128647	-2.824357	8974.366824
HLA B*1501	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.384355	1.559867	-2.824488	24230.097777
HLA B*1501	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-3.955396	1.130830	-2.824565	9023.927406
HLA B*2705	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.371412	1.546761	-2.824650	23518.621012
HLA A*0203	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.430748	1.605818	-2.824930	26961.751247
HLA A*0202	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.546589	1.721236	-2.825353	35203.792748
HLA B*1801	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.220577	1.395101	-2.825476	16617.943044
HLA B*5301	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-4.456022	1.630187	-2.825834	28577.320641
HLA A*0250	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.574149	1.748241	-2.825908	37510.159826
HLA B*4403	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.574567	1.748514	-2.826053	37546.298016
HLA A*0211	1:80-88 9	PEVRRQSRW	1.534965	0.193243	-4.554564	1.728208	-2.826356	35856.146007
HLA B*0702	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.370310	1.543934	-2.826376	23459.024311
HLA B*2705	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.345229	1.518523	-2.826706	22142.629481
HLA B*1801	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.141729	1.314292	-2.827437	13858.893247
HLA B*0803	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.411562	1.584079	-2.827483	25796.584165
HLA B*7301	1:75-83 9	LDATKPEVR	1.264680	0.523618	-4.615998	1.788298	-2.827700	41304.554419
HLA A*0219	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.374584	1.546761	-2.827822	23691.014500
HLA A*2403	1:63-71 9	TAEPPAHLR	1.007555	0.598941	-4.434416	1.606496	-2.827920	27190.402945
HLA A*2602	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.576569	1.748514	-2.828055	37719.756821
HLA A*0212	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.022915	1.194858	-2.828057	10541.807778
HLA B*0803	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.221536	1.393369	-2.828167	16654.663256
HLA B*1801	1:127-135	9	APDVRTVSR	1.139444	0.502399	-4.470130	1.641843	-2.828287	29520.938847
HLA A*0101	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.388178	1.559867	-2.828310	24444.309775
HLA B*5801	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-3.957191	1.128647	-2.828544	9061.301883
HLA A*6801	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-3.919730	1.090544	-2.829187	8312.476118
HLA A*2501	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.373815	1.543934	-2.829881	23649.141344
HLA B*1503	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-3.797924	0.967740	-2.830184	6279.480413
HLA A*3001	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.102163	1.271968	-2.830195	12652.117660
HLA A*0101	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.348744	1.518523	-2.830221	22322.561209
HLA A*6901	1:76-84 9	DATKPEVRR	0.992226	0.534734	-4.357745	1.526960	-2.830785	22790.030140
HLA A*0206	1:80-88 9	PEVRRQSRW	1.534965	0.193243	-4.559298	1.728208	-2.831090	36249.149382
HLA B*0801	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.375096	1.543934	-2.831162	23718.971118
HLA A*0101	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.377997	1.546761	-2.831236	23877.973191
HLA B*4001	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.375296	1.543934	-2.831361	23729.880572
HLA B*5701	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.380744	1.548963	-2.831781	24029.459831
HLA A*6802	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.437977	1.605818	-2.832159	27414.319053
HLA A*3101	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-4.279176	1.446716	-2.832460	19018.478572
HLA B*4002	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.575540	1.742555	-2.832984	37630.484479
HLA A*0206	1:27-35 9	ADIDRRVAA	1.371750	-0.214720	-3.990032	1.157030	-2.833002	9773.085558
HLA B*1517	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.393013	1.559867	-2.833146	24717.982413
HLA A*3101	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-3.957050	1.123686	-2.833363	9058.361122
HLA B*0803	1:103-111	9	LGAFGLGVL	1.333446	0.296741	-4.463873	1.630187	-2.833686	29098.693265
HLA B*5701	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.393765	1.559867	-2.833897	24760.810368
HLA A*0203	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.319585	1.485661	-2.833923	20872.985150
HLA A*6901	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.166713	1.332502	-2.834211	14679.557789
HLA A*6901	1:25-33 9	ERADIDRRV	1.311800	0.083077	-4.229266	1.394877	-2.834388	16953.745585
HLA B*4501	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.577149	1.742555	-2.834594	37770.193258
HLA B*4601	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.378601	1.543934	-2.834667	23911.194817
HLA B*0702	1:63-71 9	TAEPPAHLR	1.007555	0.598941	-4.441692	1.606496	-2.835196	27649.800280
HLA A*0202	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-3.790293	0.955042	-2.835251	6170.105399
HLA A*0211	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-3.905591	1.070235	-2.835357	8046.207160
HLA B*4601	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.297878	1.462291	-2.835586	19855.355724
HLA B*0802	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.395694	1.559867	-2.835826	24871.030568
HLA B*4402	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.379778	1.543934	-2.835844	23976.090536
HLA A*0219	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.118229	1.282277	-2.835952	13128.919954
HLA B*5301	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.584548	1.748241	-2.836307	38419.148506
HLA A*0101	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.299092	1.462291	-2.836801	19910.967154
HLA B*5701	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.355821	1.518523	-2.837297	22689.277738
HLA A*3002	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-3.961194	1.123686	-2.837508	9145.219251
HLA B*4601	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-4.284556	1.446716	-2.837840	19255.557283
HLA A*8001	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.384618	1.546761	-2.837857	24244.783425
HLA A*0212	1:63-71 9	TAEPPAHLR	1.007555	0.598941	-4.444652	1.606496	-2.838157	27838.917871
HLA A*0203	1:63-71 9	TAEPPAHLR	1.007555	0.598941	-4.444798	1.606496	-2.838302	27848.256975
HLA A*0219	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.058510	1.219814	-2.838696	11442.206747
HLA A*0202	1:44-52 9	FNDEVRAVR	1.108729	0.527663	-4.475193	1.636392	-2.838801	29867.117142
HLA B*4403	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.581519	1.742555	-2.838964	38152.170395
HLA A*1101	1:81-89 9	EVRRQSRWR	0.986506	0.573361	-4.399310	1.559867	-2.839442	25078.966695
HLA A*2501	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.445710	1.605818	-2.839891	27906.772889
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HLA A*3201	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.900234	1.060336	-2.839899	7947.570408
HLA A*0206	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.476467	1.636392	-2.840074	29954.820823
HLA B*5401	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.561405	1.721236	-2.840169	36425.482058
HLA A*2403	1:50-58	9	AVRETMAVV	1.181875	0.336648	-4.359223	1.518523	-2.840699	22867.712611
HLA A*3002	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.424917	1.584079	-2.840838	26602.146189
HLA A*2301	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.445195	1.604221	-2.840974	27873.729479
HLA B*4501	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.562352	1.721236	-2.841116	36504.982992
HLA A*8001	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.447690	1.606496	-2.841195	28034.333397
HLA B*5801	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-3.965028	1.123686	-2.841342	9226.319322
HLA B*3801	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.453700	1.612334	-2.841366	28424.983189
HLA A*2603	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.629702	1.788298	-2.841405	42628.739149
HLA A*6801	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.236617	1.395101	-2.841516	17243.173586
HLA A*2601	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.368595	1.526960	-2.841635	23366.562181
HLA A*0250	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.584247	1.742555	-2.841692	38392.553768
HLA B*4501	1:1-9	9	MTEHTDFEL	1.355528	0.362740	-4.560402	1.718268	-2.842134	36341.435481
HLA B*5801	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.369152	1.526960	-2.842192	23396.540687
HLA A*0206	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.455225	1.612334	-2.842891	28524.959224
HLA A*0219	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.386956	1.543934	-2.843022	24375.641085
HLA A*0216	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-3.345690	0.502462	-2.843228	2216.614337
HLA B*7301	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.448052	1.604221	-2.843831	28057.699175
HLA B*3501	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-3.904337	1.060336	-2.844001	8022.996169
HLA B*4601	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.403910	1.559867	-2.844042	25346.029169
HLA B*4403	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.632449	1.788298	-2.844151	42899.184402
HLA B*0802	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.388220	1.543934	-2.844286	24446.690229
HLA B*1517	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.450681	1.605818	-2.844863	28228.066266
HLA B*5301	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.593476	1.748514	-2.844962	39217.127330
HLA A*6901	1:43-51	9	AFNDEVRAV	1.149448	0.297268	-4.291769	1.446716	-2.845053	19578.030971
HLA B*3801	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.449286	1.604221	-2.845064	28137.501696
HLA A*0201	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.405623	1.559867	-2.845755	25446.186443
HLA B*5101	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.482195	1.636392	-2.845802	30352.521164
HLA A*2301	1:223-231	9	GTILAELPL	1.220795	0.363284	-4.430102	1.584079	-2.846023	26921.669546
HLA A*1101	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.458517	1.612334	-2.846182	28741.978538
HLA A*2501	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.452678	1.606496	-2.846182	28358.169273
HLA A*0211	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.393091	1.546761	-2.846329	24722.395618
HLA A*6901	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-3.977185	1.130830	-2.846354	9488.219363
HLA A*2403	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.390290	1.543934	-2.846356	24563.484006
HLA B*3501	1:50-58	9	AVRETMAVV	1.181875	0.336648	-4.365841	1.518523	-2.847318	23218.877746
HLA B*0802	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.409694	1.562118	-2.847577	25685.874863
HLA B*1517	1:44-52	9	FNDEVRAVR	1.108729	0.527663	-4.484100	1.636392	-2.847708	30485.982988
HLA B*1509	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.454635	1.606496	-2.848140	28486.251976
HLA A*3001	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.241962	1.393369	-2.848593	17456.705232
HLA B*0802	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.397992	1.548963	-2.849029	25002.968723
HLA B*4801	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.409210	1.559867	-2.849343	25657.265514
HLA B*4801	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.393384	1.543934	-2.849450	24739.119449
HLA A*6901	1:201-209	9	DLGASTALA	1.029007	-0.426525	-3.452235	0.602482	-2.849753	2832.921783
HLA A*2402	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.393802	1.543934	-2.849868	24762.953712
HLA B*3901	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.244768	1.394877	-2.849890	17569.830174
HLA A*3002	1:80-88	9	PEVRRQSRW	1.534965	0.193243	-4.578141	1.728208	-2.849933	37856.520101
HLA A*0203	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-3.921535	1.071321	-2.850214	8347.084597
HLA B*4601	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.095373	1.245153	-2.850221	12455.845434
HLA A*2501	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.462581	1.612334	-2.850247	29012.240559
HLA A*0216	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-3.920525	1.070235	-2.850290	8327.689739
HLA A*0301	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-3.979074	1.128647	-2.850427	9529.578738
HLA B*1501	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-3.921789	1.071321	-2.850467	8351.962957
HLA A*6802	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-2.661379	-0.189096	-2.850475	458.542016
HLA B*4002	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.599079	1.748514	-2.850565	39726.408127
HLA B*4501	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-3.951580	1.100579	-2.851002	8944.993499
HLA B*4501	1:43-51	9	AFNDEVRAV	1.149448	0.297268	-4.297894	1.446716	-2.851178	19856.107645
HLA B*4402	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.400374	1.548963	-2.851411	25140.502583
HLA B*1502	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.549538	1.697997	-2.851541	35443.618980
HLA B*1801	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.458853	1.606496	-2.852357	28764.222342
HLA A*3001	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.291426	1.437876	-2.853550	19562.573489
HLA A*0211	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.467024	1.612334	-2.854690	29310.562019
HLA B*4501	1:75-83	9	LDATKPEVR	1.264680	0.523618	-4.643003	1.788298	-2.854705	43954.457285
HLA A*2902	1:43-51	9	AFNDEVRAV	1.149448	0.297268	-4.301724	1.446716	-2.855008	20031.975443
HLA B*5801	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.137448	1.282277	-2.855171	13722.959695
HLA B*0803	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.399225	1.543934	-2.855291	25074.082891
HLA B*3501	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-3.741795	0.886414	-2.855381	5518.162854
HLA A*2603	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.597963	1.742555	-2.855408	39624.454333
HLA B*5101	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.342088	1.485661	-2.856427	21983.049179
HLA A*2602	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.554787	1.697997	-2.856789	35874.578632
HLA A*0219	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.102248	1.245153	-2.857095	12654.581975
HLA B*1502	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-3.980972	1.123686	-2.857286	9571.325517
HLA A*0206	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.463171	1.605818	-2.857353	29051.662522
HLA A*2602	1:91-99	9	AAFASAAAI	1.234627	0.369594	-4.461623	1.604221	-2.857401	28948.274353
HLA A*0202	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-3.887674	1.029850	-2.857824	7721.008618
HLA A*2902	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.463653	1.605818	-2.857834	29083.899481
HLA A*0211	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.112261	1.254367	-2.857895	12949.747743
HLA A*2601	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.253167	1.395101	-2.858066	17912.944182
HLA A*3301	1:147-155	9	SRDRNTGLL	1.371307	0.406957	-4.636356	1.778264	-2.858092	43286.874503
HLA A*6901	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-3.958732	1.100579	-2.858153	9093.516551
HLA B*4001	1:50-58	9	AVRETMAVV	1.181875	0.336648	-4.376914	1.518523	-2.858391	23818.496704
HLA B*4402	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.418336	1.559867	-2.858468	26202.079998
HLA B*0702	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.166229	1.307494	-2.858735	14663.207457
HLA B*7301	1:123-131	9	QVLTAPDVR	1.103297	0.644944	-4.607279	1.748241	-2.859038	40483.588581
HLA B*5401	1:165-173	9	RGTVYQMWL	1.283587	0.414410	-4.557200	1.697997	-2.859202	36074.450944
HLA A*2602	1:157-165	9	MNNVAPPSR	1.164592	0.577963	-4.601861	1.742555	-2.859306	39981.684726
HLA B*4403	1:146-154	9	FSRDRNTGL	1.328162	0.434196	-4.622210	1.762358	-2.859852	41899.609927
HLA B*4501	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-3.970874	1.110748	-2.860126	9351.343285
HLA B*1509	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.420316	1.559867	-2.860449	26321.848438
HLA A*3001	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.277945	1.417448	-2.860497	18964.641677
HLA B*1801	1:67-75	9	PAHLRTAIL	1.431896	0.180438	-4.472832	1.612334	-2.860498	29705.172102
HLA A*3001	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-3.625312	0.764021	-2.861291	4219.993150
HLA A*1101	1:50-58	9	AVRETMAVV	1.181875	0.336648	-4.379863	1.518523	-2.861340	23980.760479
HLA A*2403	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.347104	1.485661	-2.861443	22238.427875
HLA A*0206	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-2.672417	-0.189096	-2.861513	470.345525
HLA B*2705	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.467489	1.605818	-2.861671	29341.975085
HLA B*1503	1:63-71	9	TAEPPAHLR	1.007555	0.598941	-4.468178	1.606496	-2.861682	29388.521857
HLA B*1503	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-3.962688	1.100579	-2.862110	9176.739305
HLA A*2402	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.424449	1.562118	-2.862332	26573.522582
HLA A*2902	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.257579	1.395101	-2.862478	18095.863241
HLA A*3002	1:74-82	9	ILDATKPEV	0.983482	0.144529	-3.990708	1.128011	-2.862697	9788.324364
HLA B*2705	1:71-79	9	RTAILDATK	0.821937	0.327507	-4.012192	1.149444	-2.862748	10284.709835
HLA A*0202	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.258012	1.394877	-2.863134	18113.885187
HLA A*0250	1:142-150	9	ATVVFSRDR	0.986082	0.735154	-4.585170	1.721236	-2.863934	38474.266489
HLA A*6901	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-3.988744	1.124732	-2.864012	9744.154986
HLA A*2902	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.410916	1.546761	-2.864155	25758.234617
HLA B*7301	1:105-113	9	AFGLGVLTR	1.052600	0.695914	-4.613226	1.748514	-2.864711	41041.719625
HLA B*0702	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.414027	1.548963	-2.865064	25943.395282
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HLA A*3201      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.593363       1.728208        -2.865155       39206.944957
HLA B*1509      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.384040       1.518523        -2.865517       24212.539135
HLA A*0219      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.472181       1.606496        -2.865686       29660.691071
HLA A*3201      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -3.955814       1.090014        -2.865800       9032.621275
HLA A*0216      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.472313       1.606496        -2.865817       29669.678251
HLA A*2902      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.384494       1.518523        -2.865970       24237.832857
HLA B*3501      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.393342       1.526960        -2.866382       24736.710521
HLA A*6802      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.393551       1.526960        -2.866591       24748.623623
HLA B*4501      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.645230       1.778264        -2.866966       44180.460053
HLA B*5301      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.588977       1.721236        -2.867740       38812.937639
HLA B*0702      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.140215       1.271968        -2.868248       13810.693310
HLA B*5101      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.452328       1.584079        -2.868249       28335.319715
HLA A*6802      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.428413       1.559867        -2.868545       26817.155448
HLA B*3801      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.475459       1.606496        -2.868963       29885.381015
HLA A*0250      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.597233       1.728208        -2.869025       39557.843210
HLA B*5101      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.063928       1.194858        -2.869069       11585.844708
HLA B*3501      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.418138       1.548963        -2.869176       26190.175673
HLA B*5801      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.355069       1.485661        -2.869408       22650.032844
HLA A*0101      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.396544       1.526960        -2.869584       24919.785219
HLA B*0801      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.396758       1.526960        -2.869798       24932.056247
HLA B*3801      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.416769       1.546761        -2.870007       26107.702893
HLA B*4801      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.397261       1.526960        -2.870301       24960.937209
HLA B*0801      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.332812       1.462291        -2.870521       21518.508433
HLA A*0219      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.356535       1.485661        -2.870874       22726.623368
HLA B*5801      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.021026       1.149444        -2.871582       10496.055222
HLA A*2603      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.570251       1.697997        -2.872254       37175.012139
HLA A*2602      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.484704       1.612334        -2.872370       30528.398395
HLA B*3801      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.456560       1.584079        -2.872481       28612.746012
HLA A*8001      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.391011       1.518523        -2.872488       24604.313820
HLA A*0202      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.601222       1.728208        -2.873014       39922.895347
HLA B*1501      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -3.933780       1.060336        -2.873445       8585.791365
HLA A*0206      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.515865       1.641843        -2.874022       32799.350226
HLA B*5101      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.436589       1.562118        -2.874471       27326.808743
HLA A*2601      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.321441       1.446716        -2.874725       20962.383272
HLA B*3801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.504950       1.630187        -2.874762       31985.234040
HLA A*0203      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.830018       0.955042        -2.874976       6761.104917
HLA B*4001      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.402270       1.526960        -2.875310       25250.500439
HLA B*4402      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.422182       1.546761        -2.875420       26435.155853
HLA B*5401      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.511895       1.636392        -2.875502       32500.841859
HLA A*0212      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.361276       1.485661        -2.875615       22976.092737
HLA B*3501      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.435600       1.559867        -2.875732       27264.641028
HLA A*3002      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.158043       1.282277        -2.875766       14389.422793
HLA A*2601      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.270751       1.394877        -2.875873       18653.078518
HLA A*6801      1:147-155       9       SRDRNTGLL       1.371307        0.406957        -4.654170       1.778264        -2.875906       45099.323178
HLA B*5401      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.488632       1.612334        -2.876298       30805.790636
HLA B*7301      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.597583       1.721236        -2.876347       39589.742593
HLA A*2403      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.423333       1.546761        -2.876572       26505.324333
HLA A*8001      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.436518       1.559867        -2.876651       27322.374053
HLA B*1801      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.420939       1.543934        -2.877005       26359.611045
HLA A*0201      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.404467       1.526960        -2.877507       25378.547264
HLA A*1101      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.483426       1.605818        -2.877607       30438.686014
HLA A*0211      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.832757       0.955042        -2.877715       6803.888294
HLA B*5701      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.404721       1.526960        -2.877761       25393.379470
HLA A*0211      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.037971       1.160079        -2.877892       10913.664347
HLA B*0801      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.295542       1.417448        -2.878094       19748.871505
HLA A*0203      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.098005       1.219814        -2.878191       12531.545450
HLA A*2301      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.490801       1.612334        -2.878467       30959.998728
HLA B*0801      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -3.989895       1.111207        -2.878688       9770.019503
HLA B*4601      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.405747       1.526960        -2.878787       25453.483524
HLA A*2301      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.485099       1.605818        -2.879280       30556.157090
HLA B*7301      1:1-9   9       MTEHTDFEL       1.355528        0.362740        -4.597667       1.718268        -2.879399       39597.453684
HLA A*3201      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -3.950090       1.070235        -2.879856       8914.365891
HLA A*2301      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.516262       1.636392        -2.879870       32829.351442
HLA B*5101      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.426641       1.546761        -2.879880       26707.989556
HLA A*8001      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.423913       1.543934        -2.879979       26540.765551
HLA B*7301      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.578380       1.697997        -2.880383       37877.415422
HLA B*4501      1:146-154       9       FSRDRNTGL       1.328162        0.434196        -4.642850       1.762358        -2.880492       43939.003734
HLA B*4402      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.366485       1.485661        -2.880824       23253.320833
HLA B*0802      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.399697       1.518523        -2.881174       25101.362970
HLA B*1501      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -3.954136       1.072739        -2.881397       8997.798619
HLA A*0203      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.442265       1.559867        -2.882398       27686.322474
HLA A*0301      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.368468       1.485661        -2.882807       23359.737011
HLA A*0201      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.368522       1.485661        -2.882861       23362.643784
HLA A*0202      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.165717       1.282277        -2.883440       14645.924511
HLA A*6802      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.067668       1.184095        -2.883573       11686.059231
HLA B*4801      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.370122       1.485661        -2.884461       23448.873650
HLA B*5701      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.180363       1.295115        -2.885249       15148.285471
HLA B*5701      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.200085       1.314292        -2.885793       15852.036292
HLA A*0203      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -3.996554       1.110748        -2.885806       9920.963942
HLA A*2601      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.303354       1.417448        -2.885906       20107.326117
HLA B*3501      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.429851       1.543934        -2.885917       26906.090228
HLA B*3501      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -3.931821       1.045865        -2.885956       8547.140841
HLA A*0219      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.181299       1.295115        -2.886184       15180.936926
HLA B*0702      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.593194       0.706535        -2.886660       3919.171660
HLA A*1101      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.413879       1.526960        -2.886919       25934.554683
HLA B*0802      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.414128       1.526960        -2.887168       25949.431073
HLA A*2602      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -3.947577       1.060336        -2.887241       8862.913421
HLA A*2902      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.448026       1.559867        -2.888159       28056.029545
HLA A*0101      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.183451       1.295115        -2.888336       15256.352133
HLA A*2402      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.494194       1.605818        -2.888375       31202.801660
HLA B*1801      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.450597       1.562118        -2.888479       28222.569216
HLA A*0203      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.196885       1.307494        -2.889391       15735.663484
HLA A*2402      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.375570       1.485661        -2.889909       23744.905321
HLA A*2301      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.452084       1.562118        -2.889966       28319.381941
HLA B*4801      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.409034       1.518523        -2.890511       25646.857403
HLA B*1502      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.527401       1.636392        -2.891009       33682.259038
HLA A*6901      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.986446       1.094281        -2.892165       9692.736059
HLA A*2403      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.452053       1.559867        -2.892186       28317.390350
HLA B*4002      1:142-150       9       ATVVFSRDR       0.986082        0.735154        -4.613660       1.721236        -2.892424       41082.815950
HLA B*3801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.441438       1.548963        -2.892475       27633.650104
HLA B*1801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.442150       1.548963        -2.893187       27678.984230
HLA A*6801      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.477317       1.584079        -2.893238       30013.541221
HLA B*4001      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.355626       1.462291        -2.893334       22679.092067
HLA A*0301      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.018117       1.124732        -2.893386       10425.993373
HLA B*1801      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.453315       1.559867        -2.893447       28399.775108
HLA A*2301      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.500018       1.606496        -2.893522       31624.084650
HLA B*5801      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.201410       1.307749        -2.893661       15900.477532
HLA A*0101      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.379501       1.485661        -2.893840       23960.789877
HLA B*5101      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.356563       1.462291        -2.894272       22728.098798
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HLA B*5301      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.456738       1.562118        -2.894621       28624.512606
HLA A*3201      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.536569       1.641843        -2.894726       34400.828491
HLA A*2403      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.227499       1.332502        -2.894997       16884.913843
HLA A*0202      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -3.990079       1.094281        -2.895797       9774.143042
HLA B*5701      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.141155       1.245153        -2.896003       13840.611397
HLA A*0211      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.537948       1.641843        -2.896105       34510.245573
HLA A*0212      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.456179       1.559867        -2.896311       28587.680728
HLA B*1517      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -3.521981       0.625647        -2.896334       3326.453031
HLA A*2301      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.538268       1.641843        -2.896425       34535.645653
HLA B*5101      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.445663       1.548963        -2.896700       27903.753601
HLA A*0216      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.851915       0.955042        -2.896873       7110.741249
HLA B*4002      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.645141       1.748241        -2.896900       44171.378553
HLA B*1501      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.424080       1.526960        -2.897120       26550.961874
HLA B*4402      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.416271       1.518523        -2.897747       26077.777224
HLA A*3001      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.192008       1.294185        -2.897822       15559.926046
HLA B*1509      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.441892       1.543934        -2.897958       27662.517704
HLA A*0301      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.360353       1.462291        -2.898062       22927.295470
HLA B*4501      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.646553       1.748241        -2.898312       44315.228598
HLA A*3101      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.384097       1.485661        -2.898435       24215.683030
HLA A*3101      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.336837       1.437876        -2.898960       21718.850330
HLA B*4501      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.719606       0.820380        -2.899226       5243.315334
HLA A*3301      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.597418       1.697997        -2.899421       39574.753103
HLA B*5801      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.361774       1.462291        -2.899483       23002.459055
HLA B*3901      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.448538       1.548963        -2.899576       28089.137107
HLA B*4501      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.598440       1.697997        -2.900443       39667.994109
HLA A*3201      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.720828       0.820380        -2.900448       5258.086293
HLA B*4601      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.386512       1.485661        -2.900851       24350.730484
HLA A*3002      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.513732       1.612334        -2.901397       32638.629005
HLA A*2602      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.025119       1.123686        -2.901433       10595.437886
HLA A*3001      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.296555       1.394877        -2.901677       19794.972928
HLA B*1503      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.428852       1.526960        -2.901892       26844.298731
HLA A*0216      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.062542       1.160079        -2.902463       11548.923563
HLA B*4402      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.429602       1.526960        -2.902642       26890.665401
HLA A*3301      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.631096       1.728208        -2.902888       42765.714479
HLA A*0203      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.151235       1.248280        -2.902955       14165.586676
HLA A*2601      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.389296       1.485661        -2.903635       24507.337611
HLA B*4403      1:165-173       9       RGTVYQMWL       1.283587        0.414410        -4.602277       1.697997        -2.904279       40019.987539
HLA B*3801      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.464249       1.559867        -2.904382       29123.891482
HLA B*5101      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -3.935500       1.031086        -2.904414       8619.858842
HLA A*0216      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -3.508472       0.603848        -2.904623       3224.570354
HLA B*0801      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.061757       1.157030        -2.904727       11528.074620
HLA B*2705      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.153058       1.248280        -2.904778       14225.179857
HLA A*0212      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.249894       1.344429        -2.905466       17778.460043
HLA B*0801      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.391596       1.485661        -2.905935       24637.479699
HLA B*5801      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.100927       1.194858        -2.906069       12616.165949
HLA B*5401      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.368717       1.462291        -2.906426       23373.136453
HLA B*4403      1:123-131       9       QVLTAPDVR       1.103297        0.644944        -4.655051       1.748241        -2.906811       45190.909425
HLA B*2705      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.455782       1.548963        -2.906819       28561.555777
HLA A*0201      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.008099       1.100579        -2.907521       10188.241726
HLA A*3002      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.544101       1.636392        -2.907709       35002.684296
HLA B*1501      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.203459       1.295115        -2.908344       15975.664019
HLA B*2705      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.203497       1.295115        -2.908382       15977.046904
HLA A*1101      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.032308       1.123686        -2.908622       10772.297378
HLA A*0301      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.033041       1.123686        -2.909355       10790.495135
HLA B*5801      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.356168       1.446716        -2.909453       22707.451491
HLA B*1503      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.037604       1.128011        -2.909593       10904.457725
HLA B*0803      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.459438       1.548963        -2.910475       28802.995654
HLA A*3001      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.164956       1.254367        -2.910589       14620.275560
HLA B*2705      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.437564       1.526960        -2.910604       27388.229192
HLA A*2402      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.457372       1.546761        -2.910611       28666.354126
HLA B*1501      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.205555       1.294185        -2.911370       16052.942830
HLA B*0801      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -3.464381       0.553011        -2.911370       2913.274593
HLA B*3901      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.255991       1.344429        -2.911563       18029.805992
HLA B*4001      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.397449       1.485661        -2.911788       24971.742419
HLA A*6802      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.131833       1.219814        -2.912019       13546.668977
HLA A*0202      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -3.568877       0.656423        -2.912454       3705.758524
HLA B*7301      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.549169       1.636392        -2.912777       35413.527631
HLA A*3301      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.525482       1.612334        -2.913147       33533.716027
HLA A*0216      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.473121       1.559867        -2.913254       29724.944987
HLA B*1502      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.004594       1.090544        -2.914050       10106.337768
HLA A*2402      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.520665       1.606496        -2.914170       33163.872594
HLA A*0211      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.520757       1.605818        -2.914938       33170.870434
HLA A*0219      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.332387       1.417448        -2.914939       21497.448039
HLA A*0250      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.522004       1.606496        -2.915509       33266.295769
HLA B*1503      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.308995       1.393369        -2.915626       20370.206669
HLA B*1509      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.230229       1.314292        -2.915937       16991.391653
HLA B*0801      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.362716       1.446716        -2.916001       23052.413962
HLA A*0219      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.475994       1.559867        -2.916127       29922.266022
HLA B*0801      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.311246       1.394877        -2.916369       20476.052851
HLA B*1502      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.500455       1.584079        -2.916376       31655.922065
HLA A*2902      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.378975       1.462291        -2.916684       23931.771415
HLA A*0250      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.419234       0.502462        -2.916772       2625.631158
HLA B*5301      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.500951       1.584079        -2.916872       31692.077507
HLA A*0211      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.136748       1.219814        -2.916934       13700.854090
HLA A*0301      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.363825       1.446716        -2.917110       23111.352773
HLA A*3201      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -3.852657       0.934977        -2.917681       7122.907635
HLA B*1517      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.444643       1.526960        -2.917683       27838.315455
HLA B*1503      1:206-214       9       TALAFTVEP       0.912771        0.088698        -3.919467       1.001469        -2.917999       8307.441051
HLA B*0702      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.445261       1.526960        -2.918301       27877.952025
HLA A*0211      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.525390       1.606496        -2.918894       33526.641640
HLA B*5101      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.478964       1.559867        -2.919097       30127.578640
HLA A*0250      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.465889       1.546761        -2.919128       29234.074185
HLA A*0206      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.335916       0.416603        -2.919313       2167.286273
HLA A*0250      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.625974       0.706535        -2.919440       4226.436037
HLA A*0219      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.422091       0.502462        -2.919629       2642.960614
HLA A*1101      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.381926       1.462291        -2.919634       24094.937226
HLA B*5401      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.526245       1.606496        -2.919750       33592.727337
HLA A*3002      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.405606       1.485661        -2.919945       25445.222834
HLA A*0101      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.366767       1.446716        -2.920051       23268.421481
HLA B*3901      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.949921       1.029850        -2.920071       8910.894315
HLA A*2902      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.337521       1.417448        -2.920072       21753.068760
HLA B*0702      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.227969       1.307749        -2.920220       16903.192833
HLA B*1502      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.527260       1.606496        -2.920765       33671.327775
HLA A*0216      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.026872       1.105200        -2.921671       10638.285116
HLA B*0801      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.266122       1.344429        -2.921693       18455.339250
HLA A*0216      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -2.727733       -0.194071       -2.921805       534.236174
HLA B*4001      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.368545       1.446716        -2.921830       23363.907711
HLA A*6901      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.339353       1.417448        -2.921905       21845.054419
HLA A*2402      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.564103       1.641843        -2.922260       36652.408375
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HLA A*0212          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.449896           1.526960            -2.922936           28177.106942
HLA A*2403          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.450223           1.526960            -2.923263           28198.303379
HLA B*5801          1:34-42 9           AAAPSPVAA           1.462743            -0.118314           -4.267738           1.344429            -2.923310           18524.158084
HLA A*0301          1:24-32 9           DERADIDRR           1.029344            0.408532            -4.361537           1.437876            -2.923661           22989.893972
HLA B*3501          1:192-200           9         TPSTTATLT           0.881040            -0.429927           -3.374932           0.451113            -2.923819           2371.001498
HLA B*1501          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.409575           1.485661            -2.923913           25678.788996
HLA A*2402          1:44-52 9           FNDEVRAVR           1.108729            0.527663            -4.560550           1.636392            -2.924158           36353.823590
HLA A*0219          1:34-42 9           AAAPSPVAA           1.462743            -0.118314           -4.268815           1.344429            -2.924386           18570.112840
HLA A*3002          1:178-186           9         KGPRSAGTM           1.184612            0.123137            -4.232569           1.307749            -2.924820           17083.192613
HLA A*6801          1:165-173           9         RGTVYQMWL           1.283587            0.414410            -4.622861           1.697997            -2.924863           41962.445207
HLA A*3101          1:89-97 9           RTAAFASAA           1.280297            -0.151650           -4.053529           1.128647            -2.924882           11311.726148
HLA B*3901          1:81-89 9           EVRRQSRWR           0.986506            0.573361            -4.485672           1.559867            -2.925805           30596.518245
HLA A*3001          1:42-50 9           AAFNDEVRA           1.135376            -0.030176           -4.031181           1.105200            -2.925980           10744.360737
HLA A*0201          1:33-41 9           VAAAPSPVA           1.399199            -0.116922           -4.208454           1.282277            -2.926177           16160.467625
HLA B*1502          1:67-75 9           PAHLRTAIL           1.431896            0.180438            -4.538655           1.612334            -2.926321           34566.487029
HLA B*5101          1:125-133           9         LTAPDVRTV           1.116550            0.155418            -4.198553           1.271968            -2.926585           15796.220729
HLA B*5801          1:24-32 9           DERADIDRR           1.029344            0.408532            -4.364786           1.437876            -2.926910           23162.546601
HLA B*1502          1:117-125           9         PPTVAEQVL           1.608778            -0.002960           -4.532758           1.605818            -2.926940           34100.287248
HLA A*2902          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.412718           1.485661            -2.927057           25865.337500
HLA B*3501          1:43-51 9           AFNDEVRAV           1.149448            0.297268            -4.374734           1.446716            -2.928018           23699.218529
HLA A*2603          1:44-52 9           FNDEVRAVR           1.108729            0.527663            -4.564634           1.636392            -2.928241           36697.248296
HLA A*2902          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.455300           1.526960            -2.928340           28529.897791
HLA B*0802          1:79-87 9           KPEVRRQSR           0.893674            0.499695            -4.321878           1.393369            -2.928509           20983.487064
HLA A*6802          1:43-51 9           AFNDEVRAV           1.149448            0.297268            -4.375230           1.446716            -2.928514           23726.286315
HLA B*5701          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.414337           1.485661            -2.928676           25961.928216
HLA B*4403          1:46-54 9           DEVRAVRET           1.031728            -0.408046           -3.552647           0.623682            -2.928965           3569.824566
HLA A*0203          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.456212           1.526960            -2.929252           28589.845997
HLA B*5801          1:149-157           9         DRNTGLLVM           1.316454            0.100994            -4.346794           1.417448            -2.929346           22222.552963
HLA A*3002          1:129-137           9         DVRTVSRPL           1.249474            0.297287            -4.476244           1.546761            -2.929482           29939.429814
HLA A*2902          1:102-110           9         GLGAFGLGV           0.937231            0.015587            -3.882895           0.952818            -2.930078           7636.514570
HLA A*0250          1:44-52 9           FNDEVRAVR           1.108729            0.527663            -4.566661           1.636392            -2.930269           36868.978569
HLA A*2603          1:63-71 9           TAEPPAHLR           1.007555            0.598941            -4.537039           1.606496            -2.930543           34438.069568
HLA B*5301          1:44-52 9           FNDEVRAVR           1.108729            0.527663            -4.567220           1.636392            -2.930828           36916.479929
HLA B*4801          1:13-21 9           ATPYALNAV           1.259075            0.203216            -4.393380           1.462291            -2.931088           24738.851779
HLA A*1101          1:34-42 9           AAAPSPVAA           1.462743            -0.118314           -4.275574           1.344429            -2.931145           18861.403721
HLA B*4801          1:52-60 9           RETMAVVSA           1.427872            -0.179592           -4.179837           1.248280            -2.931557           15129.939667
HLA A*6802          1:188-196           9         TAAVTPSTT           1.185673            -0.299259           -3.817974           0.886414            -2.931561           6576.187922
HLA B*4601          1:160-168           9         VAPPSRGTV           1.092400            0.240102            -4.264118           1.332502            -2.931616           18370.370788
HLA B*4402          1:13-21 9           ATPYALNAV           1.259075            0.203216            -4.393950           1.462291            -2.931659           24771.394935
HLA A*0206          1:86-94 9           SRWRTAAFA           1.225790            -0.065711           -4.091764           1.160079            -2.931685           12352.771313
HLA B*1501          1:148-156           9         RDRNTGLLV           1.155258            0.152236            -4.239437           1.307494            -2.931942           17355.478114
HLA A*0219          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.458958           1.526960            -2.931998           28771.225701
HLA B*2705          1:134-142           9         SRPLGAGTA           1.158305            -0.105149           -3.985399           1.053156            -2.932243           9669.377514
HLA A*0206          1:25-33 9           ERADIDRRV           1.311800            0.083077            -4.327227           1.394877            -2.932350           21243.566906
HLA A*1101          1:221-229           9         PTGTILAEL           1.442456            0.106507            -4.481539           1.548963            -2.932576           30306.742868
HLA A*0211          1:84-92 9           RQSRWRTAA           1.066920            -0.037070           -3.963172           1.029850            -2.933322           9186.971905
HLA B*1501          1:122-130           9         EQVLTAPDV           1.040047            0.179767            -4.153561           1.219814            -2.933747           14241.658116
HLA A*2501          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.419492           1.485661            -2.933830           26271.914065
HLA A*3002          1:127-135           9         APDVRTVSR           1.139444            0.502399            -4.576158           1.641843            -2.934315           37684.063272
HLA B*3501          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.420180           1.485661            -2.934519           26313.590633
HLA A*2902          1:204-212           9         ASTALAFTV           1.108485            0.186630            -4.229945           1.295115            -2.934830           16980.272785
HLA B*4002          1:194-202           9         STTATLTDL           1.210982            0.351136            -4.497100           1.562118            -2.934982           31412.312078
HLA A*0206          1:148-156           9         RDRNTGLLV           1.155258            0.152236            -4.242634           1.307494            -2.935140           17483.735646
HLA A*0206          1:63-71 9           TAEPPAHLR           1.007555            0.598941            -4.541712           1.606496            -2.935216           34810.633327
HLA A*0101          1:149-157           9         DRNTGLLVM           1.316454            0.100994            -4.352726           1.417448            -2.935278           22528.195151
HLA B*1517          1:40-48 9           VAAAFNDEV           1.065598            0.129260            -4.130324           1.194858            -2.935466           13499.700990
HLA A*3301          1:91-99 9           AAFASAAAI           1.234627            0.369594            -4.539696           1.604221            -2.935475           34649.427758
HLA B*5401          1:50-58 9           AVRETMAVV           1.181875            0.336648            -4.454071           1.518523            -2.935548           28449.290185
HLA B*4403          1:64-72 9           AEPPAHLRT           1.338424            -0.305352           -3.968872           1.033072            -2.935801           9308.340017
HLA A*2403          1:93-101            9         FASAAAIAV           1.212843            0.182258            -4.330933           1.395101            -2.935832           21425.579476
HLA B*4801          1:89-97 9           RTAAFASAA           1.280297            -0.151650           -4.065276           1.128647            -2.936629           11621.877875
HLA A*0201          1:54-62 9           TMAVVSAAT           0.831597            -0.329135           -3.439435           0.502462            -2.936973           2750.645290
HLA B*5401          1:90-98 9           TAAFASAAA           0.917226            -0.153205           -3.701482           0.764021            -2.937461           5029.004796
HLA B*0702          1:83-91 9           RRQSRWRTA           1.364813            -0.029494           -4.272926           1.335319            -2.937607           18746.756632
HLA A*0250          1:25-33 9           ERADIDRRV           1.311800            0.083077            -4.332584           1.394877            -2.937707           21507.219359
HLA A*0211          1:25-33 9           ERADIDRRV           1.311800            0.083077            -4.332709           1.394877            -2.937831           21513.386882
HLA A*0301          1:79-87 9           KPEVRRQSR           0.893674            0.499695            -4.331323           1.393369            -2.937953           21444.829180
HLA B*5101          1:140-148           9         GTATVVFSR           0.913054            0.630880            -4.482110           1.543934            -2.938176           30346.610404
HLA B*1502          1:127-135           9         APDVRTVSR           1.139444            0.502399            -4.580246           1.641843            -2.938403           38040.465978
HLA B*2705          1:93-101            9         FASAAAIAV           1.212843            0.182258            -4.333653           1.395101            -2.938552           21560.224580
HLA B*1503          1:137-145           9         LGAGTATVV           1.105696            -0.034375           -4.010096           1.071321            -2.938775           10235.199278
HLA B*3801          1:50-58 9           AVRETMAVV           1.181875            0.336648            -4.458282           1.518523            -2.939758           28726.433652
HLA A*6801          1:129-137           9         DVRTVSRPL           1.249474            0.297287            -4.486558           1.546761            -2.939796           30658.984386
HLA A*0219          1:25-33 9           ERADIDRRV           1.311800            0.083077            -4.335805           1.394877            -2.940928           21667.330537
HLA A*3002          1:43-51 9           AFNDEVRAV           1.149448            0.297268            -4.387776           1.446716            -2.941060           24421.707020
HLA B*5301          1:63-71 9           TAEPPAHLR           1.007555            0.598941            -4.547750           1.606496            -2.941254           35298.000193
HLA A*0301          1:93-101            9         FASAAAIAV           1.212843            0.182258            -4.336891           1.395101            -2.941790           21721.552919
HLA A*6802          1:169-177           9         YQMWLLGGA           0.988610            -0.159143           -3.771544           0.829467            -2.942077           5909.404146
HLA A*0201          1:131-139           9         RTVSRPLGA           1.205386            -0.080654           -4.067062           1.124732            -2.942330           11669.759776
HLA A*0202          1:127-135           9         APDVRTVSR           1.139444            0.502399            -4.584409           1.641843            -2.942566           38406.887706
HLA A*3101          1:93-101            9         FASAAAIAV           1.212843            0.182258            -4.338249           1.395101            -2.943148           21789.580692
HLA B*1501          1:149-157           9         DRNTGLLVM           1.316454            0.100994            -4.360689           1.417448            -2.943241           22945.039213
HLA A*2601          1:24-32 9           DERADIDRR           1.029344            0.408532            -4.381374           1.437876            -2.943497           24064.324218
HLA A*2602          1:117-125           9         PPTVAEQVL           1.608778            -0.002960           -4.549381           1.605818            -2.943562           35430.774322
HLA B*4001          1:149-157           9         DRNTGLLVM           1.316454            0.100994            -4.362014           1.417448            -2.944566           23015.155514
HLA A*8001          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.430508           1.485661            -2.944847           26946.877623
HLA A*6801          1:89-97 9           RTAAFASAA           1.280297            -0.151650           -4.073678           1.128647            -2.945031           11848.900863
HLA B*3801          1:112-120           9         TRPSPPPTV           1.255605            0.230056            -4.430877           1.485661            -2.945216           26969.774746
HLA A*3001          1:26-34 9           RADIDRRVA           1.395400            -0.251450           -4.089227           1.143950            -2.945277           12280.808453
HLA B*4001          1:148-156           9         RDRNTGLLV           1.155258            0.152236            -4.253057           1.307494            -2.945562           17908.390130
HLA B*3501          1:13-21 9           ATPYALNAV           1.259075            0.203216            -4.407923           1.462291            -2.945632           25581.314130
HLA B*7301          1:103-111           9         LGAFGLGVL           1.333446            0.296741            -4.576134           1.630187            -2.945947           37682.024661
HLA A*0216          1:25-33 9           ERADIDRRV           1.311800            0.083077            -4.341118           1.394877            -2.946240           21933.987628
HLA B*3801          1:140-148           9         GTATVVFSR           0.913054            0.630880            -4.490437           1.543934            -2.946503           30934.048635
HLA A*0250          1:127-135           9         APDVRTVSR           1.139444            0.502399            -4.588561           1.641843            -2.946718           38775.790084
HLA B*1801          1:43-51 9           AFNDEVRAV           1.149448            0.297268            -4.393556           1.446716            -2.946840           24748.891399
HLA A*0250          1:117-125           9         PPTVAEQVL           1.608778            -0.002960           -4.552677           1.605818            -2.946859           35700.719695
HLA B*3501          1:56-64 9           AVVSAATTA           1.129368            -0.059133           -4.017131           1.070235            -2.946896           10402.330809
HLA A*0206          1:60-68 9           AATTAEPPA           0.798576            -0.138219           -3.607606           0.660357            -2.947249           4051.408426
HLA A*8001          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.474279           1.526960            -2.947319           29804.329470
HLA A*0201          1:160-168           9         VAPPSRGTV           1.092400            0.240102            -4.280130           1.332502            -2.947628           19060.296952
HLA B*0803          1:76-84 9           DATKPEVRR           0.992226            0.534734            -4.474773           1.526960            -2.947813           29838.208716
HLA A*6901          1:24-32 9           DERADIDRR           1.029344            0.408532            -4.386221           1.437876            -2.948344           24334.400852
HLA B*0702          1:183-191           9         AGTMGTAAV           0.865215            0.089827            -3.904031           0.955042            -2.948989           8017.355695
HLA A*3201          1:103-111           9         LGAFGLGVL           1.333446            0.296741            -4.579177           1.630187            -2.948989           37946.944537
HLA A*0301          1:149-157           9         DRNTGLLVM           1.316454            0.100994            -4.366602           1.417448            -2.949154           23259.611578
HLA B*3501          1:160-168           9         VAPPSRGTV           1.092400            0.240102            -4.281662           1.332502            -2.949160           19127.646049
HLA A*2402          1:13-21 9           ATPYALNAV           1.259075            0.203216            -4.411649           1.462291            -2.949358           25801.748278
HLA A*2403          1:49-57 9           RAVRETMAV           0.926962            0.318191            -4.194911           1.245153            -2.949759           15664.318031
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HLA A*6801      1:80-88 9       PEVRRQSRW       1.534965        0.193243        -4.677987       1.728208        -2.949779       47641.645562
HLA A*1101      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.244535       1.294185        -2.950350       17560.422661
HLA A*0201      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.021064       1.070235        -2.950829       10496.963781
HLA A*2501      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.477987       1.526960        -2.951027       30059.852344
HLA B*5301      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.500523       1.548963        -2.951560       31660.888850
HLA B*4801      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.197026       1.245153        -2.951873       15740.772005
HLA B*0702      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.398732       1.446716        -2.952016       25045.612985
HLA B*2705      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.414743       1.462291        -2.952452       25986.237640
HLA B*1501      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.285005       1.332502        -2.952503       19275.464118
HLA B*3901      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.414835       1.462291        -2.952544       25991.720942
HLA A*3002      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.225013       1.271968        -2.953045       16788.546342
HLA A*0101      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.390924       1.437876        -2.953048       24599.389369
HLA B*4601      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.225060       1.271968        -2.953092       16790.362924
HLA A*0203      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -3.699974       0.746698        -2.953275       5011.568610
HLA B*5701      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.416007       1.462291        -2.953716       26061.981287
HLA B*0801      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -3.983646       1.029850        -2.953795       9630.432699
HLA A*8001      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.416153       1.462291        -2.953862       26070.724284
HLA A*3301      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.472393       1.518523        -2.953869       29675.136082
HLA A*2402      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.472907       1.518523        -2.954384       29710.315001
HLA B*0801      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.287211       1.332502        -2.954709       19373.630402
HLA A*0216      1:201-209       9       DLGASTALA       1.029007        -0.426525       -3.557280       0.602482        -2.954798       3608.112400
HLA B*5701      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.350114       1.395101        -2.955013       22393.076938
HLA B*5701      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.401885       1.446716        -2.955169       25228.107579
HLA B*4601      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.372695       1.417448        -2.955247       23588.193003
HLA A*3301      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.539337       1.584079        -2.955258       34620.759841
HLA A*6801      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.585880       1.630187        -2.955693       38537.176604
HLA B*4402      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.350703       1.394877        -2.955826       22423.504752
HLA B*0802      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.351124       1.395101        -2.956023       22445.229522
HLA B*1502      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.515971       1.559867        -2.956104       32807.336036
HLA A*2602      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.598196       1.641843        -2.956353       39645.682043
HLA B*1509      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.403214       1.446716        -2.956499       25305.474363
HLA A*1101      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.442561       1.485661        -2.956900       27705.201180
HLA A*0216      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.483879       1.526960        -2.956919       30470.483905
HLA A*0202      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.564196       1.606496        -2.957701       36660.340652
HLA B*5701      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.052241       1.094281        -2.957960       11278.240847
HLA B*4501      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.395943       1.437876        -2.958066       24885.296908
HLA B*4403      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.178315       1.219814        -2.958501       15076.992886
HLA B*3501      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.253761       1.295115        -2.958647       17937.478449
HLA A*2603      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.600552       1.641843        -2.958709       39861.388921
HLA B*5101      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.485740       1.526960        -2.958780       30601.318811
HLA B*5401      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.543084       1.584079        -2.959005       34920.787097
HLA A*0201      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.397059       1.437876        -2.959182       24949.326822
HLA B*1517      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.029597       1.070235        -2.959362       10705.255285
HLA B*5801      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.354296       1.394877        -2.959418       22609.754959
HLA B*3901      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.486520       1.526960        -2.959560       30656.330714
HLA A*0203      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.354439       1.394877        -2.959562       22617.217482
HLA B*1501      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.084504       1.124732        -2.959773       12147.991874
HLA B*4501      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.295432       1.335319        -2.960113       19743.850700
HLA B*5701      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.109583       1.149444        -2.960139       12870.128873
HLA A*1101      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.507001       1.546761        -2.960239       32136.652246
HLA A*0212      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.088912       1.128647        -2.960265       12271.909012
HLA A*3002      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.050860       1.090544        -2.960316       11242.421596
HLA A*6802      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.085341       1.124732        -2.960609       12171.410485
HLA A*2602      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.597211       1.636392        -2.960819       39555.917225
HLA A*0201      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.215258       1.254367        -2.960891       16415.648042
HLA A*3002      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.145239       1.184095        -2.961144       13971.359897
HLA B*3501      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -3.894417       0.932973        -2.961444       7841.823427
HLA B*4402      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.379024       1.417448        -2.961576       23934.490402
HLA B*4801      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.379149       1.417448        -2.961701       23941.353982
HLA A*3101      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.379442       1.417448        -2.961994       23957.549466
HLA B*0802      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.399876       1.437876        -2.962000       25111.685557
HLA A*0101      1:21-29 9       VSDDERADI       0.727910        0.266210        -3.956364       0.994120        -2.962244       9044.063037
HLA B*4402      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.357757       1.395101        -2.962656       22790.646606
HLA B*0802      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.448675       1.485661        -2.963013       28097.952118
HLA B*5801      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.356446       1.393369        -2.963076       22721.951805
HLA B*5701      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.295629       1.332502        -2.963128       19752.824951
HLA B*4601      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.271124       1.307749        -2.963375       18669.130284
HLA A*0211      1:201-209       9       DLGASTALA       1.029007        -0.426525       -3.566415       0.602482        -2.963933       3684.807936
HLA B*4002      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.594141       1.630187        -2.963953       39277.214683
HLA B*1801      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.491184       1.526960        -2.964224       30987.311665
HLA B*4801      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.402136       1.437876        -2.964260       25242.715302
HLA B*0802      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.426817       1.462291        -2.964526       26718.828300
HLA B*0702      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.450613       1.485661        -2.964952       28223.638003
HLA A*2501      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.025551       1.060336        -2.965216       10605.990043
HLA A*3201      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.213721       1.248280        -2.965442       16357.670995
HLA B*5801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.090233       1.124732        -2.965501       12309.276782
HLA A*0212      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.298286       1.332502        -2.965785       19874.054781
HLA A*6801      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.578300       1.612334        -2.965966       37870.449034
HLA A*2603      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.273904       1.307749        -2.966154       18788.993978
HLA B*4601      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.405204       1.437876        -2.967328       25421.694570
HLA A*8001      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.384837       1.417448        -2.967389       24256.984522
HLA A*0202      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.573959       1.605818        -2.968140       37493.726436
HLA A*2603      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.453921       1.485661        -2.968260       28439.441809
HLA A*6801      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.361972       1.393369        -2.968602       23012.914453
HLA A*2301      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.515529       1.546761        -2.968768       32773.985997
HLA A*3201      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.606003       1.636392        -2.969611       40364.839715
HLA A*0202      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.302116       1.332502        -2.969615       20050.081539
HLA B*4402      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.189484       1.219814        -2.969670       15469.781571
HLA A*0101      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.364791       1.394877        -2.969914       23162.797216
HLA A*0250      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.513878       1.543934        -2.969944       32649.578265
HLA B*2705      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -3.553549       0.583145        -2.970404       3577.248219
HLA A*2603      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.600719       1.630187        -2.970532       39876.702706
HLA B*1502      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.456198       1.485661        -2.970536       28588.918004
HLA A*0201      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.388352       1.417448        -2.970904       24454.097569
HLA A*6802      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.848950       0.877544        -2.971405       7062.359572
HLA A*3301      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.533843       1.562118        -2.971726       34185.623040
HLA A*3101      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.217720       1.245153        -2.972568       16508.981938
HLA A*3301      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.521629       1.548963        -2.972666       33237.513512
HLA B*1501      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.410994       1.437876        -2.973117       25762.833551
HLA A*0203      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.390915       1.417448        -2.973467       24598.857054
HLA B*1509      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.245696       1.271968        -2.973728       17607.415397
HLA A*0301      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.368914       1.394877        -2.974037       23383.760337
HLA A*6901      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -3.721077       0.746698        -2.974378       5261.102398
HLA B*3501      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.103141       1.128647        -2.974494       12680.623490
HLA B*0702      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.392907       1.417448        -2.975459       24711.965676
HLA A*0301      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.320127       1.344429        -2.975699       20899.086099
HLA A*1101      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.422642       1.446716        -2.975927       26463.200926
HLA A*8001      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.422854       1.446716        -2.976138       26476.088732
HLA A*2301      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.461865       1.485661        -2.976203       28964.409364
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HLA A*3002      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.582659       1.605818        -2.976840       38252.405357
HLA A*2301      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.521039       1.543934        -2.977105       33192.411513
HLA B*5401      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.521093       1.543934        -2.977159       33196.541817
HLA B*1509      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.504433       1.526960        -2.977473       31947.188640
HLA B*4801      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.425022       1.446716        -2.978307       26608.623137
HLA B*4501      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.620474       1.641843        -2.978631       41732.433539
HLA B*0802      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.292970       1.314292        -2.978678       19632.228403
HLA A*2301      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.538698       1.559867        -2.978830       34569.853208
HLA A*0201      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.374501       1.394877        -2.979624       23686.529123
HLA A*0202      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.084918       1.105200        -2.979718       12159.563977
HLA A*2601      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.251750       1.271968        -2.979782       17854.604444
HLA B*1517      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.287519       1.307494        -2.980024       19387.365273
HLA A*0219      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -3.858263       0.877544        -2.980719       7215.446052
HLA B*2705      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.427454       1.446716        -2.980738       26758.028967
HLA A*1101      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.376116       1.395101        -2.981015       23774.726126
HLA B*4001      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.376036       1.394877        -2.981158       23770.353495
HLA A*3101      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.325940       1.344429        -2.981511       21180.681080
HLA B*5401      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.176440       1.194858        -2.981581       15012.044423
HLA A*2501      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.399361       1.417448        -2.981913       25081.951710
HLA A*0101      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.326464       1.344429        -2.982035       21206.248985
HLA B*7301      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.624205       1.641843        -2.982362       42092.497289
HLA B*4002      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.420253       1.437876        -2.982377       26318.003965
HLA B*1503      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -3.833368       0.850740        -2.982628       6813.465181
HLA B*5701      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.421303       1.437876        -2.983427       26381.723713
HLA A*0211      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.543333       1.559867        -2.983466       34940.818104
HLA A*6802      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.089095       1.105200        -2.983895       12277.088499
HLA B*4403      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.568458       1.584079        -2.984380       37021.879417
HLA B*3901      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.431204       1.446716        -2.984488       26990.062958
HLA B*2705      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.108201       1.123686        -2.984515       12829.253849
HLA B*4001      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.378049       1.393369        -2.984680       23880.815258
HLA B*4601      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.379558       1.394877        -2.984680       23963.901085
HLA A*3301      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.615110       1.630187        -2.984923       41220.175466
HLA B*1517      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.470699       1.485661        -2.985037       29559.612769
HLA A*0211      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.292993       1.307494        -2.985499       19633.290513
HLA B*5401      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.116415       1.130830        -2.985585       13074.202223
HLA A*8001      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.280891       1.295115        -2.985776       19093.735215
HLA A*3001      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.941172       0.955042        -2.986130       8733.167918
HLA A*2301      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.505809       1.518523        -2.987286       32048.628165
HLA B*4402      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.282416       1.295115        -2.987301       19160.891488
HLA B*4002      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.624881       1.636392        -2.988489       42158.130540
HLA A*0203      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.811649       0.822896        -2.988753       6481.110134
HLA B*4001      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.426721       1.437876        -2.988845       26712.902575
HLA A*2402      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.435976       1.446716        -2.989260       27288.251034
HLA A*2402      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.549313       1.559867        -2.989445       35425.216138
HLA B*5401      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.551693       1.562118        -2.989575       35619.886967
HLA A*6802      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.407596       1.417448        -2.990148       25562.084862
HLA B*4002      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.632198       1.641843        -2.990355       42874.359046
HLA A*3101      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.304689       1.314292        -2.990397       20169.207278
HLA A*2501      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.262499       1.271968        -2.990531       18302.024274
HLA A*3101      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.323097       1.332502        -2.990596       21042.485869
HLA A*2602      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.517613       1.526960        -2.990653       32931.632254
HLA B*5101      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.437479       1.446716        -2.990764       27382.895690
HLA A*3201      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.386312       1.395101        -2.991211       24339.535604
HLA A*2501      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.438060       1.446716        -2.991344       27419.510339
HLA A*2602      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.085867       1.094281        -2.991586       12186.168926
HLA B*3501      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.264097       1.271968        -2.992129       18369.476374
HLA A*6901      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.385741       1.393369        -2.992372       24307.559798
HLA A*0201      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.097746       1.105200        -2.992546       12524.090299
HLA A*2402      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.287890       1.295115        -2.992775       19403.943949
HLA B*5701      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.410277       1.417448        -2.992829       25720.359509
HLA B*1501      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.082921       1.090014        -2.992907       12103.777730
HLA B*1801      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.456003       1.462291        -2.993711       28576.083867
HLA B*1509      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.338399       1.344429        -2.993971       21797.126268
HLA B*1502      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.288541       1.294185        -2.994356       19433.043320
HLA B*4002      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.513149       1.518523        -2.994626       32594.868668
HLA A*2602      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.601478       1.606496        -2.994982       39946.443940
HLA A*6901      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.066404       1.071321        -2.995083       11652.096167
HLA B*0702      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.390107       1.394877        -2.995229       24553.121106
HLA B*0801      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.433361       1.437876        -2.995484       27124.436512
HLA A*3002      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.555485       1.559867        -2.995617       35932.265979
HLA A*0212      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.390527       1.394877        -2.995650       24576.909132
HLA B*1502      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.303427       1.307749        -2.995678       20110.698531
HLA B*1509      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.391016       1.395101        -2.995915       24604.580035
HLA A*3101      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.390830       1.394877        -2.995953       24594.066746
HLA B*1502      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.443581       1.446716        -2.996865       27770.326420
HLA B*3501      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.392160       1.394877        -2.997283       24669.489123
HLA B*5401      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.544151       1.546761        -2.997389       35006.661096
HLA A*0203      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.181571       1.184095        -2.997476       15190.466670
HLA B*7301      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.609831       1.612334        -2.997496       40722.135377
HLA B*5801      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.311803       1.314292        -2.997511       20502.322932
HLA A*3201      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.604370       1.606496        -2.997875       40213.358001
HLA B*5401      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.546893       1.548963        -2.997930       35228.369194
HLA B*1501      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.182102       1.184095        -2.998007       15209.050423
HLA A*0203      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -3.931243       0.932973        -2.998270       8535.773592
HLA B*7301      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.582374       1.584079        -2.998296       38227.373657
HLA A*6801      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.547713       1.548963        -2.998750       35294.944993
HLA B*3801      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.416231       1.417448        -2.998783       26075.379010
HLA A*0212      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.436866       1.437876        -2.998990       27344.258843
HLA B*3801      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.526323       1.526960        -2.999363       33598.725059
HLA B*0801      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.247714       1.248280        -2.999434       17689.429140
HLA B*3901      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.392865       1.393369        -2.999496       24709.559391
HLA B*3501      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -3.659863       0.660357        -2.999506       4569.443086
HLA A*6802      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.437468       1.437876        -2.999591       27382.155008
HLA B*5401      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.559878       1.559867        -3.000011       36297.619417
HLA B*7301      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.605947       1.605818        -3.000128       40359.599192
HLA B*1501      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.335592       1.335319        -3.000273       21656.666338
HLA A*0203      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.335782       1.335319        -3.000463       21666.158390
HLA B*7301      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.560938       1.559867        -3.001070       36386.288653
HLA A*2501      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.396190       1.395101        -3.001089       24899.436726
HLA A*0212      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.418843       1.417448        -3.001395       26232.715969
HLA A*2501      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.396319       1.394877        -3.001441       24906.846504
HLA A*6801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -3.765463       0.764021        -3.001442       5827.244295
HLA A*8001      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.396704       1.395101        -3.001603       24928.954208
HLA B*1501      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.396746       1.394877        -3.001869       24931.381858
HLA A*2403      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.273887       1.271968        -3.001919       18788.282467
HLA B*5401      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.530418       1.526960        -3.003458       33917.040522
HLA A*3201      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.609504       1.605818        -3.003686       40691.524877
HLA B*0802      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.421759       1.417448        -3.004311       26409.426355
HLA B*0803      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.489976       1.485661        -3.004315       30901.265463
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HLA A*0203      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.109625       1.105200        -3.004425       12871.382201
HLA B*7301      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.551190       1.546761        -3.004428       35578.673105
HLA B*1509      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.466745       1.462291        -3.004453       29291.698632
HLA B*1501      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -2.905932       -0.098967       -3.004899       805.252962
HLA A*0216      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.422847       1.417448        -3.005399       26475.659037
HLA A*2603      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.130164       1.124732        -3.005433       13494.735736
HLA B*1503      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.162742       1.157030        -3.005713       14545.958471
HLA A*2601      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.399133       1.393369        -3.005764       25068.793177
HLA A*2603      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.550151       1.543934        -3.006217       35493.700047
HLA B*3901      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.077606       1.071321        -3.006285       11956.564329
HLA B*3901      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.134464       1.128011        -3.006453       13628.998440
HLA B*0802      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.453306       1.446716        -3.006590       28399.160556
HLA B*0801      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.314390       1.307749        -3.006641       20624.805078
HLA A*0201      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.400172       1.393369        -3.006803       25128.808673
HLA A*0202      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.321138       1.314292        -3.006846       20947.759238
HLA A*0211      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.301035       1.294185        -3.006850       20000.247961
HLA B*1503      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.445266       1.437876        -3.007389       27878.253660
HLA B*4403      1:127-135       9       APDVRTVSR       1.139444        0.502399        -4.649377       1.641843        -3.007534       44604.335616
HLA B*4601      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.202740       1.194858        -3.007882       15949.239367
HLA B*1517      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.454901       1.446716        -3.008185       28503.671444
HLA A*0250      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.568080       1.559867        -3.008213       36989.647689
HLA A*0203      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.322517       1.314292        -3.008225       21014.386781
HLA A*0219      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.340742       1.332502        -3.008240       21915.010172
HLA B*4501      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.638515       1.630187        -3.008328       43502.619206
HLA A*0101      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.315992       1.307494        -3.008498       20701.041765
HLA B*4403      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.455249       1.446716        -3.008533       28526.502434
HLA B*1501      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.511634       0.502462        -3.009172       3248.136439
HLA A*0101      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.402947       1.393369        -3.009577       25289.872596
HLA A*0250      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.832621       0.822896        -3.009725       6801.753749
HLA A*0211      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.140803       1.130830        -3.009973       13829.384527
HLA B*3501      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.100848       1.090544        -3.010304       12613.845592
HLA B*1509      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.448226       1.437876        -3.010350       28068.933813
HLA B*2705      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.404002       1.393369        -3.010632       25351.377383
HLA A*0206      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.570517       1.559867        -3.010649       37197.744821
HLA A*2301      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.538108       1.526960        -3.011148       34522.943277
HLA B*4403      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.306301       1.295115        -3.011186       20244.197982
HLA A*0211      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.195875       1.184095        -3.011780       15699.100903
HLA B*5701      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.405254       1.393369        -3.011885       25424.582834
HLA B*2705      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.257081       1.245153        -3.011929       18075.121056
HLA B*1502      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -3.892880       0.880895        -3.011985       7814.127551
HLA B*0803      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.458709       1.446716        -3.011993       28754.731622
HLA B*4002      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.459170       1.446716        -3.012454       28785.237535
HLA B*1503      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.043750       1.031086        -3.012664       11059.877734
HLA B*3501      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.406212       1.393369        -3.012843       25480.762836
HLA B*4403      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.575093       1.562118        -3.012976       37591.824769
HLA B*4801      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.406377       1.393369        -3.013008       25490.414030
HLA B*0803      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.408278       1.395101        -3.013177       25602.219871
HLA B*5301      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.208163       1.194858        -3.013304       16149.630395
HLA B*4501      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.650016       1.636392        -3.013624       44670.018757
HLA B*5801      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.346239       1.332502        -3.013738       22194.198782
HLA B*3901      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.349127       1.335319        -3.013808       22342.254191
HLA A*0301      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.296348       1.282277        -3.014071       19785.551373
HLA B*5701      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.409856       1.394877        -3.014979       25695.464736
HLA B*0702      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.263465       1.248280        -3.015185       18342.763449
HLA A*0216      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.309451       1.294185        -3.015266       20391.596800
HLA B*5301      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.559246       1.543934        -3.015312       36244.835353
HLA A*0203      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.453327       1.437876        -3.015450       28400.543316
HLA A*3001      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.300023       1.284273        -3.015749       19953.668463
HLA B*0803      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.454180       1.437876        -3.016303       28456.370811
HLA B*5401      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.409906       1.393369        -3.016537       25698.384104
HLA A*6802      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -3.972068       0.955042        -3.017026       9377.078214
HLA A*2403      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.454971       1.437876        -3.017095       28508.297870
HLA B*4402      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.410550       1.393369        -3.017180       25736.505313
HLA B*0801      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.289210       1.271968        -3.017243       19463.028654
HLA B*5801      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.352618       1.335319        -3.017299       22522.589597
HLA A*2501      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.111904       1.094281        -3.017623       12939.103501
HLA A*0206      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.353098       1.335319        -3.017779       22547.459639
HLA A*0203      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -2.918920       -0.098967       -3.017887       829.698460
HLA B*4002      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.630431       1.612334        -3.018096       42700.290324
HLA A*8001      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.456087       1.437876        -3.018211       28581.649773
HLA B*1509      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.353955       1.335319        -3.018636       22592.026054
HLA B*4601      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.412041       1.393369        -3.018672       25825.069439
HLA B*3901      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -3.986465       0.967740        -3.018726       9693.155561
HLA B*4402      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.175796       1.157030        -3.018766       14989.808409
HLA B*4501      1:223-231       9       GTILAELPL       1.220795        0.363284        -4.603015       1.584079        -3.018936       40088.027473
HLA B*4403      1:44-52 9       FNDEVRAVR       1.108729        0.527663        -4.655483       1.636392        -3.019091       45235.915738
HLA B*5701      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.363652       1.344429        -3.019223       23102.102416
HLA B*4402      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.326718       1.307494        -3.019223       21218.642739
HLA A*2603      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.546308       1.526960        -3.019348       35180.946331
HLA B*4801      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.363778       1.344429        -3.019350       23108.852311
HLA A*3101      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.355355       1.335319        -3.020036       22664.986947
HLA B*1517      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.437653       1.417448        -3.020205       27393.860128
HLA A*8001      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.415281       1.394877        -3.020404       26018.451020
HLA A*6901      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.180598       1.160079        -3.020520       15156.482742
HLA B*4801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.328076       1.307494        -3.020581       21285.095493
HLA A*2403      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.329173       1.307749        -3.021424       21338.938532
HLA B*4402      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.356817       1.335319        -3.021498       22741.381979
HLA A*2403      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.366485       1.344429        -3.022056       23253.320833
HLA A*2403      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.439815       1.417448        -3.022367       27530.541912
HLA B*2705      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.330251       1.307749        -3.022502       21391.991928
HLA B*5101      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.417396       1.394877        -3.022519       26145.441162
HLA A*0212      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.524989       0.502462        -3.022527       3349.567518
HLA A*0211      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.549613       1.526960        -3.022653       35449.755385
HLA B*7301      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.541207       1.518523        -3.022683       34770.167706
HLA B*5101      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.367359       1.344429        -3.022930       23300.164768
HLA A*3001      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.217791       1.194858        -3.022932       16511.661508
HLA A*2902      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.418411       1.394877        -3.023533       26206.616401
HLA A*0202      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.317783       1.294185        -3.023597       20786.554540
HLA B*1503      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -3.977495       0.952818        -3.024677       9494.997371
HLA B*0702      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.462706       1.437876        -3.024829       29020.560261
HLA B*5701      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.153528       1.128647        -3.024881       14240.579516
HLA A*0202      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.510807       1.485661        -3.025145       32419.536313
HLA A*8001      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.149886       1.124732        -3.025154       14121.666841
HLA B*0802      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.420088       1.394877        -3.025211       26308.039428
HLA A*3301      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.631387       1.605818        -3.025569       42794.412468
HLA B*1501      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.220483       1.194858        -3.025625       16614.347384
HLA A*2402      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.209756       1.184095        -3.025660       16208.974470
HLA B*4402      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.370101       1.344429        -3.025672       23447.731975
HLA A*2301      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.472489       1.446716        -3.025773       29681.718919
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HLA B*7301      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.632447       1.606496        -3.025951       42898.952323
HLA A*3201      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.511686       1.485661        -3.026024       32485.197116
HLA A*0202      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -3.627055       0.600711        -3.026345       4236.966828
HLA B*0801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.334027       1.307494        -3.026532       21578.778068
HLA B*1501      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.419969       1.393369        -3.026600       26300.781927
HLA B*3801      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.421562       1.394877        -3.026684       26397.427828
HLA B*4801      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.421634       1.394877        -3.026757       26401.855221
HLA B*4403      1:103-111       9       LGAFGLGVL       1.333446        0.296741        -4.657004       1.630187        -3.026816       45394.527838
HLA B*4001      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.341183       1.314292        -3.026891       21937.310372
HLA A*2403      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.322021       1.295115        -3.026906       20990.412825
HLA A*0216      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.127505       1.100579        -3.026926       13412.346581
HLA B*5301      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.322247       1.295115        -3.027132       21001.317014
HLA A*0301      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.359975       1.332502        -3.027473       22907.334670
HLA B*4002      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.323064       1.295115        -3.027950       21040.892204
HLA A*3201      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.587853       1.559867        -3.027986       38712.699875
HLA B*3501      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.465943       1.437876        -3.028067       29237.711932
HLA B*4002      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.633913       1.605818        -3.028094       43044.014064
HLA A*2602      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.273676       1.245153        -3.028523       18779.136866
HLA A*2902      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.336062       1.307494        -3.028567       21680.111051
HLA B*1801      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.514592       1.485661        -3.028931       32703.318146
HLA A*3101      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.336677       1.307494        -3.029183       21710.862033
HLA A*0202      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.547408       0.518215        -3.029193       3527.016751
HLA A*0301      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.364958       1.335319        -3.029639       23171.695804
HLA A*3001      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.852676       0.822896        -3.029780       7123.215915
HLA B*4501      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.636300       1.606496        -3.029804       43281.254615
HLA A*0211      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.120348       1.090544        -3.029805       13193.141972
HLA B*5301      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.576837       1.546761        -3.030075       37743.026802
HLA B*1502      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.448003       1.417448        -3.030555       28054.511786
HLA A*2602      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.477407       1.446716        -3.030691       30019.711913
HLA A*3001      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.187755       1.157030        -3.030725       15408.308340
HLA A*8001      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.338230       1.307494        -3.030736       21788.637679
HLA B*0801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.155482       1.124732        -3.030751       14304.821228
HLA A*0219      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.468704       1.437876        -3.030828       29424.156901
HLA B*1502      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -3.966255       0.934977        -3.031278       9252.410922
HLA A*2501      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.469343       1.437876        -3.031467       29467.486121
HLA A*2902      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.470034       1.437876        -3.032157       29514.391668
HLA B*5101      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.449755       1.417448        -3.032307       28167.962325
HLA B*1503      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.855317       0.822896        -3.032421       7166.662121
HLA A*0101      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.304625       1.271968        -3.032657       20166.261437
HLA B*3801      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.479530       1.446716        -3.032815       30166.884091
HLA B*4501      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.645524       1.612334        -3.033189       44210.346580
HLA B*3501      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -3.782149       0.748881        -3.033268       6055.489673
HLA A*0202      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.593253       1.559867        -3.033385       39196.977279
HLA A*0250      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.253308       1.219814        -3.033494       17918.759548
HLA A*2603      1:117-125       9       PPTVAEQVL       1.608778        -0.002960       -4.639413       1.605818        -3.033594       43592.613705
HLA B*2705      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.327824       1.294185        -3.033639       21272.778007
HLA B*5301      1:81-89 9       EVRRQSRWR       0.986506        0.573361        -4.593553       1.559867        -3.033686       39224.129245
HLA B*4001      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.279500       1.245153        -3.034347       19032.682398
HLA A*3001      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.218453       1.184095        -3.034358       16536.870737
HLA A*0216      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.159401       1.124732        -3.034670       14434.487729
HLA A*0201      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.254715       1.219814        -3.034901       17976.919895
HLA B*5401      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.520602       1.485661        -3.034940       33159.028800
HLA B*4601      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.330357       1.295115        -3.035242       21397.200335
HLA B*5401      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -3.864752       0.829467        -3.035285       7324.069580
HLA A*0206      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.562354       1.526960        -3.035395       36505.180480
HLA A*0216      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.342969       1.307494        -3.035475       22027.691644
HLA A*2602      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.521302       1.485661        -3.035641       33212.529141
HLA B*5101      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.290061       1.254367        -3.035694       19501.182004
HLA B*0803      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.498639       1.462291        -3.036348       31523.818338
HLA B*0801      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.318706       1.282277        -3.036429       20830.795565
HLA A*3101      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.290864       1.254367        -3.036498       19537.296141
HLA A*0212      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.429907       1.393369        -3.036538       26909.583870
HLA B*0801      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.166065       1.128647        -3.037418       14657.655665
HLA B*4601      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.319890       1.282277        -3.037613       20887.669983
HLA B*0702      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.194658       1.157030        -3.037628       15655.168543
HLA A*2902      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.309949       1.271968        -3.037981       20414.997268
HLA B*2705      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.162855       1.124732        -3.038123       14549.736179
HLA A*0301      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.333639       1.295115        -3.038525       21559.524761
HLA A*3201      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.111303       1.072739        -3.038564       12921.196131
HLA A*2902      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.383004       1.344429        -3.038576       24154.842653
HLA A*0212      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.320999       1.282277        -3.038722       20941.074126
HLA B*4403      1:67-75 9       PAHLRTAIL       1.431896        0.180438        -4.651132       1.612334        -3.038798       44784.954797
HLA A*2402      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.565768       1.526960        -3.038808       36793.262729
HLA A*0101      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.371377       1.332502        -3.038875       23516.712593
HLA A*0301      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.353337       1.314292        -3.039045       22559.904957
HLA A*0101      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.167911       1.128647        -3.039264       14720.115251
HLA B*4801      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.374765       1.335319        -3.039445       23700.885319
HLA B*7301      1:194-202       9       STTATLTDL       1.210982        0.351136        -4.601591       1.562118        -3.039473       39956.818366
HLA B*4403      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.646607       1.606496        -3.040111       44320.742972
HLA A*2602      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.110429       1.070235        -3.040194       12895.218646
HLA B*5301      1:50-58 9       AVRETMAVV       1.181875        0.336648        -4.558717       1.518523        -3.040194       36200.744072
HLA A*0101      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.375519       1.335319        -3.040200       23742.079428
HLA B*5301      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.567540       1.526960        -3.040580       36943.651036
HLA A*0206      1:5-13  9       TDFELLELA       1.003059        -0.335657       -3.708465       0.667402        -3.041063       5110.515610
HLA B*7301      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.585116       1.543934        -3.041182       38469.479532
HLA A*3101      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.313290       1.271968        -3.041322       20572.652665
HLA A*6901      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.349616       1.307749        -3.041866       22367.409118
HLA B*0702      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -3.974873       0.932973        -3.041900       9437.844631
HLA B*4002      1:63-71 9       TAEPPAHLR       1.007555        0.598941        -4.648426       1.606496        -3.041930       44506.714272
HLA B*5801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.349768       1.307494        -3.042274       22375.275840
HLA B*0803      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.459804       1.417448        -3.042356       28827.313992
HLA B*2705      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.480426       1.437876        -3.042549       30229.127224
HLA B*1502      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.505262       1.462291        -3.042971       32008.256186
HLA B*1502      1:140-148       9       GTATVVFSR       0.913054        0.630880        -4.586979       1.543934        -3.043045       38634.869730
HLA B*3801      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.436429       1.393369        -3.043060       27316.757812
HLA A*2301      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.505403       1.462291        -3.043112       32018.647539
HLA B*5101      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.436998       1.393369        -3.043629       27352.544145
HLA A*0201      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.075450       1.029850        -3.045599       11897.331908
HLA B*5101      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.340777       1.295115        -3.045662       21916.788611
HLA B*4001      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.390151       1.344429        -3.045723       24555.644999
HLA A*3002      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.440907       1.395101        -3.045806       27599.884883
HLA A*1101      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.463265       1.417448        -3.045817       29057.949853
HLA B*3901      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.483764       1.437876        -3.045888       30462.407721
HLA B*2705      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.390534       1.344429        -3.046106       24577.308010
HLA B*1503      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -3.842287       0.795947        -3.046340       6954.832676
HLA A*2403      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.382095       1.335319        -3.046776       24104.324321
HLA A*0203      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.856741       0.809887        -3.046854       7190.195810
HLA A*0206      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.048341       1.001469        -3.046872       11177.410977
HLA A*0301      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.354691       1.307494        -3.047196       22630.313433
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HLA B*7301	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.596161	1.548963	-3.047198	39460.377861
HLA B*1517	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.485345	1.437876	-3.047469	30573.519090
HLA A*3002	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.574931	1.526960	-3.047971	37577.795023
HLA B*3801	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.383448	1.335319	-3.048129	24179.552862
HLA B*4403	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.592108	1.543934	-3.048174	39093.844212
HLA B*4501	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.654273	1.605818	-3.048455	45110.059679
HLA B*4501	1:194-202	9	STTATLTDL	1.210982	0.351136	-4.610625	1.562118	-3.048507	40796.665654
HLA A*1101	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.173339	1.124732	-3.048607	14905.224465
HLA B*1503	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-3.858672	0.809887	-3.048785	7222.241299
HLA A*2403	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.442199	1.393369	-3.048830	27682.128954
HLA A*0216	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-4.177887	1.128647	-3.049240	15062.155387
HLA A*6802	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.442829	1.393369	-3.049460	27722.293005
HLA A*0301	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.357263	1.307749	-3.049514	22764.769385
HLA A*0203	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.442989	1.393369	-3.049620	27732.493149
HLA A*0201	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.385199	1.335319	-3.049880	24277.201993
HLA A*0203	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.357761	1.307749	-3.050012	22790.893197
HLA B*0801	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-4.173710	1.123686	-3.050023	14917.970339
HLA A*0216	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-3.930928	0.880895	-3.050033	8529.588038
HLA B*4002	1:7-15	9	FELLELATP	0.903395	-0.108267	-3.845379	0.795128	-3.050251	7004.523686
HLA B*3901	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.364697	1.314292	-3.050405	23157.785431
HLA A*6901	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.358109	1.307494	-3.050615	22809.148342
HLA B*4501	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.446386	1.395101	-3.051285	27950.286872
HLA B*3801	1:13-21	9	ATPYALNAV	1.259075	0.203216	-4.513624	1.462291	-3.051333	32630.507732
HLA B*1503	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.145709	1.094281	-3.051427	13986.484779
HLA B*0801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.346756	1.295115	-3.051642	22220.629502
HLA B*1502	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.600856	1.548963	-3.051893	39889.216924
HLA A*0202	1:12-20	9	LATPYALNA	1.117892	-0.294996	-3.875067	0.822896	-3.052170	7500.093899
HLA A*2601	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.384675	1.332502	-3.052173	24247.931508
HLA A*6901	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.236453	1.184095	-3.052358	17236.644966
HLA B*2705	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.366924	1.314292	-3.052632	23276.856941
HLA A*8001	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.446208	1.393369	-3.052839	27938.797430
HLA A*3002	1:21-29	9	VSDDERADI	0.727910	0.266210	-4.047035	0.994120	-3.052915	11143.840974
HLA A*0202	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-3.985431	0.932462	-3.052969	9670.109885
HLA A*0206	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.360790	1.307749	-3.053041	22950.377429
HLA A*3002	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.470701	1.417448	-3.053253	29559.772683
HLA B*4001	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.385831	1.332502	-3.053329	24312.557358
HLA A*1101	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.446795	1.393369	-3.053426	27976.609443
HLA A*2402	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.325425	1.271968	-3.053457	21155.601795
HLA A*8001	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.361419	1.307749	-3.053670	22983.676174
HLA A*8001	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.298850	1.245153	-3.053698	19899.875484
HLA A*0212	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.308215	1.254367	-3.053849	20333.652920
HLA A*6802	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.055507	1.001469	-3.054038	11363.370026
HLA A*3301	1:23-31	9	DDERADIDR	0.950475	0.333798	-4.338430	1.284273	-3.054156	21798.659283
HLA B*4403	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.660102	1.605818	-3.054284	45719.605457
HLA A*2402	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.362150	1.307749	-3.054401	23022.378195
HLA A*6901	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.389987	1.335319	-3.054668	24546.347728
HLA A*0206	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-3.745624	0.690533	-3.055091	5567.037849
HLA B*5701	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.390659	1.335319	-3.055340	24584.355928
HLA A*2403	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.450230	1.394877	-3.055353	28198.761032
HLA B*4001	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.390711	1.335319	-3.055391	24587.282072
HLA A*0212	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-4.125667	1.070235	-3.055433	13355.725056
HLA B*7301	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-4.085816	1.029850	-3.055965	12184.718644
HLA A*3002	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.301569	1.245153	-3.056416	20024.824249
HLA A*0206	1:203-211	9	GASTALAFT	0.843184	-0.343048	-3.556824	0.500136	-3.056689	3604.327606
HLA A*2602	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-4.185495	1.128647	-3.056848	15328.326980
HLA B*4801	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.371214	1.314292	-3.056923	23507.935857
HLA B*4501	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.600858	1.543934	-3.056924	39889.432721
HLA B*5801	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.351192	1.294185	-3.057007	22448.751158
HLA B*4002	1:13-21	9	ATPYALNAV	1.259075	0.203216	-4.519326	1.462291	-3.057035	33061.764768
HLA B*4002	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.452138	1.395101	-3.057037	28322.905869
HLA A*0250	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.584325	1.526960	-3.057365	38399.408462
HLA A*0216	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.495298	1.437876	-3.057421	31282.240347
HLA B*4601	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.371938	1.314292	-3.057646	23547.138510
HLA B*3901	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-4.186712	1.128647	-3.058065	15371.342139
HLA A*3301	1:71-79	9	RTAILDATK	0.821937	0.327507	-4.207664	1.149444	-3.058220	16131.119057
HLA B*4801	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.367115	1.307749	-3.059365	23287.059119
HLA A*2402	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-4.183061	1.123686	-3.059374	15242.657444
HLA B*4601	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.395066	1.335319	-3.059747	24835.131780
HLA A*0101	1:40-48	9	VAAAFNDEV	1.065598	0.129260	-4.254783	1.194858	-3.059925	17979.740457
HLA A*0101	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.374236	1.314292	-3.059944	23672.053559
HLA A*2601	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.405042	1.344429	-3.060614	25412.206871
HLA A*3001	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.280555	1.219814	-3.060741	19078.969743
HLA B*0702	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.356004	1.294185	-3.061819	22698.853983
HLA B*4801	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.281941	1.219814	-3.062127	19139.963949
HLA A*2601	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.397738	1.335319	-3.062419	24988.364555
HLA A*2403	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.316913	1.254367	-3.062546	20744.988560
HLA A*0202	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-3.775308	0.712665	-3.062642	5960.841411
HLA B*5101	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.500772	1.437876	-3.062896	31679.049938
HLA A*0203	1:88-96	9	WRTAAFASA	1.223245	-0.112038	-4.174396	1.111207	-3.063188	14941.554695
HLA B*1517	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.457598	1.393369	-3.064229	28681.245845
HLA A*6901	1:12-20	9	LATPYALNA	1.117892	-0.294996	-3.887223	0.822896	-3.064327	7712.992980
HLA A*0219	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.136264	1.071321	-3.064942	13685.593854
HLA A*6801	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.337213	1.271968	-3.065245	21737.657920
HLA A*2403	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.372873	1.307494	-3.065379	23597.893320
HLA B*3501	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-3.756559	0.690533	-3.066026	5708.982046
HLA A*3101	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.373902	1.307749	-3.066153	23653.875570
HLA A*0219	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.401530	1.335319	-3.066211	25207.507323
HLA A*0206	1:19-27	9	NAVSDDERA	1.177173	-0.137631	-4.105767	1.039542	-3.066226	12757.551554
HLA A*0203	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.360435	1.294185	-3.066250	22931.637076
HLA A*6901	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-3.876279	0.809887	-3.066392	7521.059682
HLA B*0803	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.461719	1.394877	-3.066842	28954.695950
HLA B*4601	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.374541	1.307494	-3.067047	23688.707629
HLA B*4801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.362251	1.295115	-3.067137	23027.734404
HLA B*0801	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.361358	1.294185	-3.067173	22980.443583
HLA B*5301	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-3.877101	0.809887	-3.067215	7535.314007
HLA B*5801	1:23-31	9	DDERADIDR	0.950475	0.333798	-4.351507	1.284273	-3.067234	22465.030722
HLA A*2902	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.460744	1.393369	-3.067375	28889.762565
HLA B*1509	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.460899	1.393369	-3.067530	28900.079574
HLA A*3201	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.412121	1.344429	-3.067693	25829.820042
HLA B*1502	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.594853	1.526960	-3.067893	39341.650549
HLA A*6801	1:117-125	9	PPTVAEQVL	1.608778	-0.002960	-4.673800	1.605818	-3.067982	47184.566729
HLA A*6901	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.362679	1.294185	-3.068494	23050.418673
HLA A*0202	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.595532	1.526960	-3.068572	39403.207675
HLA A*0212	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.376172	1.307494	-3.068677	23777.813174
HLA B*1501	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-3.725268	0.656423	-3.068845	5312.124389
HLA A*6801	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-3.565837	0.496962	-3.068875	3679.907335
HLA A*0206	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.383493	1.314292	-3.069201	24182.038355
HLA A*2602	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.464273	1.394877	-3.069395	29125.467095
HLA B*1503	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.323797	1.254367	-3.069430	21076.436809
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HLA A*8001	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.402120	1.332502	-3.069618	25241.759398
HLA B*3501	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.071314	1.001469	-3.069846	11784.590175
HLA A*6801	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.130352	1.060336	-3.070017	13500.577401
HLA A*2601	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.130413	1.060336	-3.070078	13502.476487
HLA B*1517	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.464964	1.394877	-3.070086	29171.828225
HLA B*1801	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.463608	1.393369	-3.070239	29080.910162
HLA A*2402	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.402803	1.332502	-3.070302	25281.528233
HLA A*1101	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.508262	1.437876	-3.070386	32230.148514
HLA A*2902	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.384766	1.314292	-3.070474	24253.048014
HLA A*0250	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.201420	1.130830	-3.070589	15900.821615
HLA B*1503	1:71-79	9	RTAILDATK	0.821937	0.327507	-4.220605	1.149444	-3.071161	16619.021893
HLA A*2403	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.181924	1.110748	-3.071176	15202.798484
HLA B*4402	1:23-31	9	DDERADIDR	0.950475	0.333798	-4.355605	1.284273	-3.071331	22677.987872
HLA B*3901	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.378987	1.307494	-3.071492	23932.418765
HLA A*3101	1:23-31	9	DDERADIDR	0.950475	0.333798	-4.355976	1.284273	-3.071702	22697.380452
HLA B*1503	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-3.892420	0.820380	-3.072040	7805.846323
HLA A*0101	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.380067	1.307749	-3.072318	23992.049928
HLA B*7301	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.292258	1.219814	-3.072444	19600.073685
HLA B*4001	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.380768	1.307749	-3.073018	24030.759834
HLA A*3002	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.184823	1.110748	-3.074075	15304.628896
HLA A*2501	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.467482	1.393369	-3.074113	29341.498878
HLA A*3101	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.356460	1.282277	-3.074183	22722.689356
HLA A*2601	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.369321	1.295115	-3.074206	23405.655696
HLA A*0202	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.205155	1.130830	-3.074325	16038.186028
HLA B*4501	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.634232	1.559867	-3.074365	43075.695132
HLA B*0702	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.369485	1.295115	-3.074371	23414.520914
HLA A*0212	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.410176	1.335319	-3.074857	25714.377000
HLA B*1501	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.186082	1.110748	-3.075334	15349.072142
HLA B*0702	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-4.145582	1.070235	-3.075347	13982.399448
HLA B*4801	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.407850	1.332502	-3.075348	25577.024335
HLA B*7301	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.602326	1.526960	-3.075366	40024.534375
HLA B*0702	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-4.105927	1.029850	-3.076077	12762.245569
HLA A*2601	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.384414	1.307749	-3.076665	24233.375052
HLA A*2602	1:24-32	9	DERADIDRR	1.029344	0.408532	-4.514622	1.437876	-3.076746	32705.618204
HLA A*0301	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.321969	1.245153	-3.076817	20987.914746
HLA B*3801	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.391664	1.314292	-3.077373	24641.345298
HLA A*3002	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.032665	0.955042	-3.077624	10781.159115
HLA A*2601	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.385206	1.307494	-3.077711	24277.596007
HLA A*8001	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.422405	1.344429	-3.077977	26448.745414
HLA B*0802	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.410641	1.332502	-3.078140	25741.935920
HLA B*3501	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.149599	1.071321	-3.078278	14112.349525
HLA A*0250	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.386120	1.307494	-3.078625	24328.740715
HLA A*2902	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.203431	1.124732	-3.078699	15974.626934
HLA A*0201	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.386303	1.307494	-3.078808	24339.008913
HLA A*6801	1:50-58	9	AVRETMAVV	1.181875	0.336648	-4.597411	1.518523	-3.078888	39574.110823
HLA A*0202	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.203656	1.124732	-3.078925	15982.925501
HLA A*2902	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.373134	1.294185	-3.078949	23612.068056
HLA B*4002	1:140-148	9	GTATVVFSR	0.913054	0.630880	-4.622945	1.543934	-3.079011	41970.618442
HLA A*0201	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.386815	1.307749	-3.079066	24367.730198
HLA B*0802	1:34-42	9	AAAPSPVAA	1.462743	-0.118314	-4.423495	1.344429	-3.079067	26515.220150
HLA A*0219	1:79-87	9	KPEVRRQSR	0.893674	0.499695	-4.472437	1.393369	-3.079068	29678.186483
HLA B*0802	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.374424	1.295115	-3.079309	23682.300831
HLA B*4002	1:129-137	9	DVRTVSRPL	1.249474	0.297287	-4.626293	1.546761	-3.079532	42295.424172
HLA B*2705	1:89-97	9	RTAAFASAA	1.280297	-0.151650	-4.208412	1.128647	-3.079765	16158.894028
HLA B*4501	1:86-94	9	SRWRTAAFA	1.225790	-0.065711	-4.239848	1.160079	-3.079769	17371.916856
HLA A*2601	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.374647	1.294185	-3.080462	23694.475228
HLA B*4002	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.629522	1.548963	-3.080559	42610.985357
HLA B*3501	1:42-50	9	AAFNDEVRA	1.135376	-0.030176	-4.185838	1.105200	-3.080638	15340.438746
HLA B*0801	1:26-34	9	RADIDRRVA	1.395400	-0.251450	-4.224637	1.143950	-3.080687	16774.020762
HLA A*0203	1:27-35	9	ADIDRRVAA	1.371750	-0.214720	-4.237961	1.157030	-3.080931	17296.614481
HLA A*0301	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.352928	1.271968	-3.080961	22538.678843
HLA A*0201	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.395264	1.314292	-3.080972	24846.420191
HLA A*8001	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.395285	1.314292	-3.080993	24847.629968
HLA A*1101	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.363273	1.282277	-3.080996	23081.989426
HLA A*0301	1:23-31	9	DDERADIDR	0.950475	0.333798	-4.365672	1.284273	-3.081399	23209.835475
HLA B*5701	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.363769	1.282277	-3.081492	23108.352252
HLA A*3001	1:74-82	9	ILDATKPEV	0.983482	0.144529	-4.209737	1.128011	-3.081726	16208.272975
HLA B*4403	1:221-229	9	PTGTILAEL	1.442456	0.106507	-4.630804	1.548963	-3.081842	42737.035736
HLA A*0206	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.499292	1.417448	-3.081844	31571.264228
HLA B*1501	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.014870	0.932973	-3.081898	10348.334448
HLA A*0101	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.376184	1.294185	-3.081999	23778.456359
HLA A*1101	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.327310	1.245153	-3.082157	21247.589673
HLA A*2403	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.396582	1.314292	-3.082290	24921.942324
HLA B*0801	1:86-94	9	SRWRTAAFA	1.225790	-0.065711	-4.242493	1.160079	-3.082414	17478.061463
HLA B*1503	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.193276	1.110748	-3.082528	15605.448343
HLA A*0219	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.337283	1.254367	-3.082917	21741.186156
HLA B*4501	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.213750	1.130830	-3.082919	16358.732948
HLA A*3201	1:76-84	9	DATKPEVRR	0.992226	0.534734	-4.609910	1.526960	-3.082950	40729.626342
HLA B*5101	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.328144	1.245153	-3.082991	21288.435105
HLA B*1801	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.477970	1.394877	-3.083093	30058.714022
HLA B*1502	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.415772	1.332502	-3.083271	26047.885857
HLA B*5401	1:43-51	9	AFNDEVRAV	1.149448	0.297268	-4.530049	1.446716	-3.083333	33888.245226
HLA B*5701	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.391284	1.307494	-3.083789	24619.759033
HLA A*0202	1:88-96	9	WRTAAFASA	1.223245	-0.112038	-4.195090	1.111207	-3.083883	15670.759764
HLA A*6901	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-3.637167	0.553011	-3.084156	4336.778561
HLA B*4002	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.644081	1.559867	-3.084214	44063.737941
HLA A*0206	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-3.965169	0.880895	-3.084274	9229.314610
HLA A*2402	1:49-57	9	RAVRETMAV	0.926962	0.318191	-4.329490	1.245153	-3.084337	21354.528799
HLA A*0219	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.398835	1.314292	-3.084543	25051.575430
HLA A*0211	1:83-91	9	RRQSRWRTA	1.364813	-0.029494	-4.420074	1.335319	-3.084755	26307.185500
HLA B*0801	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.339186	1.254367	-3.084820	21836.665298
HLA B*4501	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-3.914402	0.829467	-3.084935	8211.108268
HLA A*6802	1:74-82	9	ILDATKPEV	0.983482	0.144529	-4.213082	1.128011	-3.085071	16333.618549
HLA A*2501	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.417786	1.332502	-3.085284	26168.931402
HLA A*1101	1:25-33	9	ERADIDRRV	1.311800	0.083077	-4.480289	1.394877	-3.085412	30219.643611
HLA A*0250	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.017948	0.932462	-3.085486	10421.933114
HLA A*0101	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.367834	1.282277	-3.085557	23325.641050
HLA A*1101	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.418075	1.332502	-3.085573	26186.350432
HLA A*6801	1:13-21	9	ATPYALNAV	1.259075	0.203216	-4.547933	1.462291	-3.085642	35312.898081
HLA B*4403	1:81-89	9	EVRRQSRWR	0.986506	0.573361	-4.645775	1.559867	-3.085908	44235.945508
HLA B*3801	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.481412	1.395101	-3.086311	30297.890531
HLA A*0216	1:52-60	9	RETMAVVSA	1.427872	-0.179592	-4.334807	1.248280	-3.086527	21617.570175
HLA A*3001	1:9-17	9	LLELATPYA	0.993939	-0.356018	-3.724841	0.637921	-3.086919	5306.896646
HLA B*4601	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.381491	1.294185	-3.087306	24070.834365
HLA B*4402	1:47-55	9	EVRAVRETM	1.250113	0.064179	-4.401894	1.314292	-3.087602	25228.653510
HLA B*3901	1:31-39	9	RRVAAAPSP	0.723092	0.213085	-4.024179	0.936177	-3.088002	10572.534618
HLA B*3901	1:33-41	9	VAAAPSPVA	1.399199	-0.116922	-4.370474	1.282277	-3.088197	23467.909744
HLA B*4801	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.382419	1.294185	-3.088234	24122.326478
HLA B*3501	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.188920	1.100579	-3.088342	15449.709051

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HLA B*5801      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.342800       1.254367        -3.088433       22019.113264
HLA A*0201      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.382739       1.294185        -3.088554       24140.080888
HLA B*1502      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.283682       1.194858        -3.088824       19216.844850
HLA B*1503      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.178907       1.090014        -3.088893       15097.561248
HLA A*0211      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.506514       1.417448        -3.089066       32100.684254
HLA A*2501      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.433986       1.344429        -3.089557       27163.497502
HLA B*4001      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.383930       1.294185        -3.089745       24206.383521
HLA A*3101      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.338148       1.248280        -3.089868       21784.512476
HLA B*5301      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.335183       1.245153        -3.090030       21636.290061
HLA B*5301      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.507569       1.417448        -3.090121       32178.752885
HLA B*0803      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.425481       1.335319        -3.090161       26636.708140
HLA A*2301      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.335925       1.245153        -3.090773       21673.309473
HLA A*0212      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.215526       1.124732        -3.090794       16425.775144
HLA A*0101      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.345264       1.254367        -3.090898       22144.426391
HLA B*1517      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -3.977363       0.886414        -3.090950       9492.121262
HLA A*6801      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.286109       1.194858        -3.091251       19324.537197
HLA B*0702      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.222100       1.130830        -3.091269       16676.301271
HLA B*1801      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.363995       1.271968        -3.092027       23120.356676
HLA B*1501      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.241516       1.149444        -3.092072       17438.771071
HLA B*3901      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.287314       1.194858        -3.092456       19378.242555
HLA A*2603      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.530580       1.437876        -3.092704       33929.703518
HLA A*0203      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.611252       0.518215        -3.093038       4085.567854
HLA B*3501      1:12-20 9       LATPYALNA       1.117892        -0.294996       -3.916460       0.822896        -3.093564       8250.113578
HLA B*4801      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.375949       1.282277        -3.093672       23765.595957
HLA B*0702      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.288531       1.194858        -3.093673       19432.622802
HLA A*1101      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.429019       1.335319        -3.093700       26854.611664
HLA A*8001      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.429052       1.335319        -3.093733       26856.645667
HLA B*3801      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.401746       1.307749        -3.093997       25220.056469
HLA A*2902      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.426965       1.332502        -3.094464       26727.936243
HLA B*1801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.402082       1.307494        -3.094588       25239.574611
HLA B*5701      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.289662       1.194858        -3.094803       19483.255379
HLA B*0702      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.195710       1.100579        -3.095132       15693.156901
HLA A*3101      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.220117       1.124732        -3.095385       16600.331741
HLA A*3002      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.440372       1.344429        -3.095943       27565.862662
HLA A*0203      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.513016       0.416603        -3.096413       3258.485260
HLA A*0211      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.190805       1.094281        -3.096523       15516.886812
HLA B*4601      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.350969       1.254367        -3.096602       22437.216823
HLA B*5301      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.582781       1.485661        -3.097120       38263.167817
HLA A*0216      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.490641       1.393369        -3.097272       30948.611492
HLA B*5101      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.404845       1.307494        -3.097351       25400.661408
HLA A*0206      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.208773       1.110748        -3.098025       16172.361982
HLA A*0101      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.343286       1.245153        -3.098134       22043.785115
HLA A*2902      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.226277       1.128011        -3.098266       16837.480926
HLA A*0219      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.258366       1.160079        -3.098287       18128.688343
HLA B*1509      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.406001       1.307494        -3.098507       25468.359526
HLA B*5101      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.066432       0.967740        -3.098693       11652.852630
HLA A*0211      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.412986       1.314292        -3.098694       25881.294282
HLA A*3002      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.353389       1.254367        -3.099022       22562.590142
HLA B*4501      1:221-229       9       PTGTILAEL       1.442456        0.106507        -4.648134       1.548963        -3.099171       44476.868012
HLA B*1801      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.383573       1.284273        -3.099299       24186.486717
HLA A*3001      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.145558       1.045865        -3.099693       13981.643036
HLA A*0206      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.283793       1.184095        -3.099697       19221.731638
HLA B*4002      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.585408       1.485661        -3.099746       38495.294527
HLA A*6901      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.384256       1.284273        -3.099983       24224.592952
HLA B*5301      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.546716       1.446716        -3.100000       35214.078476
HLA B*3801      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.538087       1.437876        -3.100210       34521.262430
HLA A*0206      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -3.813285       0.712665        -3.100619       6505.559347
HLA B*1501      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.257779       1.157030        -3.100749       18104.186367
HLA A*2301      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.539116       1.437876        -3.101239       34603.158637
HLA A*0219      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.409262       1.307494        -3.101768       25660.319361
HLA B*4402      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.434573       1.332502        -3.102072       27200.260234
HLA B*0702      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.173616       1.071321        -3.102294       14914.742505
HLA A*0216      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.437907       1.335319        -3.102588       27409.870161
HLA A*2601      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.387200       1.284273        -3.102927       24389.359373
HLA A*2403      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.385227       1.282277        -3.102950       24278.778088
HLA A*2601      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.385302       1.282277        -3.103025       24282.981507
HLA B*0802      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.348211       1.245153        -3.103058       22295.164929
HLA A*0212      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.351622       1.248280        -3.103342       22470.986644
HLA A*3001      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.035880       0.932462        -3.103417       10861.243521
HLA B*4501      1:13-21 9       ATPYALNAV       1.259075        0.203216        -4.565710       1.462291        -3.103418       36788.286879
HLA B*4402      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.375411       1.271968        -3.103443       23736.171831
HLA A*2902      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.176684       1.072739        -3.103945       15020.493003
HLA A*0212      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.418425       1.314292        -3.104133       26207.467065
HLA B*1509      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.411933       1.307749        -3.104184       25818.643543
HLA B*4403      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.651179       1.546761        -3.104418       44789.800692
HLA A*6802      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.439749       1.335319        -3.104430       27526.371987
HLA B*4402      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.137575       1.033072        -3.104503       13726.969224
HLA B*4501      1:129-137       9       DVRTVSRPL       1.249474        0.297287        -4.651393       1.546761        -3.104632       44811.856136
HLA A*2601      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.350064       1.245153        -3.104912       22390.533057
HLA B*5701      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.399103       1.294185        -3.104918       25067.030187
HLA B*4501      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.387978       1.282277        -3.105701       24433.071874
HLA B*3901      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.361027       1.254367        -3.106660       22962.920914
HLA A*0212      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.267135       1.160079        -3.107056       18498.421074
HLA B*5301      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.421585       1.314292        -3.107293       26398.855938
HLA A*0301      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.362049       1.254367        -3.107682       23017.023231
HLA A*2301      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.525204       1.417448        -3.107756       33512.316044
HLA B*2705      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.440423       1.332502        -3.107922       27569.143679
HLA B*5401      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.179447       1.071321        -3.108126       15116.358451
HLA A*3201      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.061132       0.952818        -3.108314       11511.497299
HLA A*0201      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.356857       1.248280        -3.108577       22743.473558
HLA B*5401      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.441476       1.332502        -3.108974       27636.042128
HLA A*6802      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.416966       1.307749        -3.109217       26119.569730
HLA A*0202      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.329032       1.219814        -3.109218       21332.013179
HLA A*8001      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.381634       1.271968        -3.109667       24078.779129
HLA A*2902      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.392029       1.282277        -3.109751       24662.016540
HLA A*0211      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.358252       1.248280        -3.109972       22816.676677
HLA A*3301      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.930515       0.820380        -3.110135       8521.470537
HLA B*1503      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.294405       1.184095        -3.110310       19697.228969
HLA A*3002      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.505600       1.394877        -3.110723       32033.201102
HLA A*1101      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.418582       1.307749        -3.110833       26216.968012
HLA A*0216      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.418998       1.307749        -3.111249       26242.084103
HLA A*0301      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.359641       1.248280        -3.111361       22889.743915
HLA A*0219      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.240083       1.128647        -3.111436       17381.317413
HLA A*0212      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.419395       1.307749        -3.111646       26266.087457
HLA B*4001      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.383728       1.271968        -3.111760       24195.124109
HLA B*0802      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.406137       1.294185        -3.111952       25476.352078
HLA B*5401      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.212547       1.100579        -3.111968       16313.484190
HLA A*0201      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.396316       1.284273        -3.112043       24906.711761
HLA A*0219      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.406614       1.294185        -3.112429       25504.345768
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HLA A*2402	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.447848	1.335319	-3.112529	28044.496636
HLA A*8001	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.406722	1.294185	-3.112537	25510.693439
HLA A*2402	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.530336	1.417448	-3.112888	33910.619070
HLA B*1517	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.218092	1.105200	-3.112891	16523.099229
HLA A*0101	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.397233	1.284273	-3.112959	24959.316831
HLA B*5301	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.506331	1.393369	-3.112962	32087.141542
HLA A*3002	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.273208	1.160079	-3.113129	18758.930728
HLA B*1501	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.045804	0.932462	-3.113342	11112.295349
HLA A*2402	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.508697	1.395101	-3.113596	32262.421544
HLA B*5801	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.185001	1.071321	-3.113680	15310.922712
HLA B*1501	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.204596	1.090544	-3.114052	16017.549292
HLA A*2902	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.449450	1.335319	-3.114131	28148.159167
HLA B*0802	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.421928	1.307749	-3.114179	26419.715147
HLA A*0211	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.552113	1.437876	-3.114237	35654.396909
HLA A*0206	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.552247	1.437876	-3.114371	35665.393125
HLA A*1101	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.174734	1.060336	-3.114398	14953.199060
HLA A*2602	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.334649	1.219814	-3.114836	21609.736035
HLA B*4402	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.422703	1.307749	-3.114954	26466.923425
HLA B*4801	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.299083	1.184095	-3.114988	19910.536294
HLA A*6802	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.363334	1.248280	-3.115054	23085.236301
HLA A*0212	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-4.144966	1.029850	-3.115116	13962.594960
HLA B*4403	1:50-58 9	AVRETMAVV	1.181875	0.336648	-4.633894	1.518523	-3.115371	43042.151198
HLA B*7301	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.577730	1.462291	-3.115438	37820.697135
HLA A*3201	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.310311	1.194858	-3.115453	20432.012557
HLA A*2301	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.510804	1.395101	-3.115704	32419.360927
HLA B*5801	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.364187	1.248280	-3.115907	23130.615394
HLA A*2403	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-3.519731	0.403811	-3.115919	3309.257707
HLA B*5401	1:12-20 9	LATPYALNA	1.117892	-0.294996	-3.938832	0.822896	-3.115935	8686.237979
HLA B*5101	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.430562	1.314292	-3.116271	26950.230762
HLA A*0211	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.424214	1.307749	-3.116465	26559.150488
HLA A*6802	1:201-209	9	DLGASTALA	1.029007	-0.426525	-3.719094	0.602482	-3.116612	5237.135245
HLA B*4001	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.399213	1.282277	-3.116936	25073.404660
HLA B*3501	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.452572	1.335319	-3.117253	28351.266458
HLA A*0216	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.432484	1.314292	-3.118192	27069.757606
HLA A*0211	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-3.864983	0.746698	-3.118284	7327.953605
HLA A*6801	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.462720	1.344429	-3.118291	29021.502264
HLA B*2705	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.390342	1.271968	-3.118374	24566.407666
HLA B*1502	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.401605	1.282277	-3.119328	25211.871535
HLA A*6802	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.279422	1.160079	-3.119344	19029.284866
HLA B*1801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.414760	1.295115	-3.119645	25987.221737
HLA B*0802	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.404114	1.284273	-3.119841	25357.961348
HLA A*2601	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.339908	1.219814	-3.120094	21872.962551
HLA B*3501	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.414396	1.294185	-3.120211	25965.439733
HLA B*4402	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.402655	1.282277	-3.120378	25272.913175
HLA A*0203	1:203-211	9	GASTALAFT	0.843184	-0.343048	-3.620575	0.500136	-3.120440	4174.218555
HLA B*4001	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-3.950401	0.829467	-3.120934	8920.733961
HLA B*1517	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.192351	1.071321	-3.121029	15572.220812
HLA A*1101	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.428772	1.307494	-3.121278	26839.361546
HLA B*5401	1:49-57 9	RAVRETMAV	0.926962	0.318191	-4.366438	1.245153	-3.121285	23250.805011
HLA A*2403	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.369840	1.248280	-3.121560	23433.655893
HLA B*0803	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.429087	1.307494	-3.121593	26858.825128
HLA A*1101	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.222697	1.100579	-3.122118	16699.232125
HLA A*3001	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.123685	1.001469	-3.122216	13294.882538
HLA B*3901	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.430135	1.307749	-3.122386	26923.708629
HLA A*2403	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.416783	1.294185	-3.122598	26108.550345
HLA B*4501	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.430170	1.307494	-3.122676	26925.893532
HLA B*0702	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.247484	1.124732	-3.122752	17680.053236
HLA B*0802	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.458077	1.335319	-3.122758	28712.916439
HLA A*3301	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-4.569504	1.446716	-3.122788	37111.113282
HLA B*0802	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.394921	1.271968	-3.122953	24826.803148
HLA B*4601	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.307367	1.184095	-3.123272	20293.980658
HLA B*5401	1:25-33 9	ERADIDRRV	1.311800	0.083077	-4.518318	1.394877	-3.123441	32985.122593
HLA B*1501	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.377847	1.254367	-3.123480	23869.707282
HLA B*5101	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.195372	1.071321	-3.124051	15680.936315
HLA A*0202	1:149-157	9	DRNTGLLVM	1.316454	0.100994	-4.541505	1.417448	-3.124057	34794.064964
HLA A*6802	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.431561	1.307494	-3.124067	27012.266099
HLA B*4002	1:76-84 9	DATKPEVRR	0.992226	0.534734	-4.651174	1.526960	-3.124214	44789.316079
HLA B*5801	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.308385	1.184095	-3.124289	20341.574665
HLA A*3301	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.586585	1.462291	-3.124293	38599.771941
HLA A*1101	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.379050	1.254367	-3.124683	23935.914757
HLA A*2501	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.419071	1.294185	-3.124886	26246.485442
HLA B*0803	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.420072	1.295115	-3.124957	26307.043182
HLA B*1509	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.344957	1.219814	-3.125143	22128.738296
HLA A*2902	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.432898	1.307749	-3.125149	27095.544093
HLA A*2601	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.379579	1.254367	-3.125212	23965.067891
HLA A*3002	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-4.155078	1.029850	-3.125228	14291.516770
HLA B*5701	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-4.249142	1.123686	-3.125456	17747.709228
HLA B*3801	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.397470	1.271968	-3.125502	24972.958298
HLA B*1501	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.230772	1.105200	-3.125572	17012.638803
HLA B*7301	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.563480	1.437876	-3.125604	36599.900374
HLA A*3002	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.433140	1.307494	-3.125645	27110.646441
HLA A*6901	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.058139	0.932462	-3.125676	11432.430557
HLA B*4001	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.380420	1.254367	-3.126053	24011.526980
HLA A*0219	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-4.196378	1.070235	-3.126143	15717.286533
HLA B*2705	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.346002	1.219814	-3.126188	22182.075211
HLA B*1517	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.173019	1.045865	-3.127154	14894.262055
HLA B*1509	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.422351	1.295115	-3.127236	26445.454669
HLA B*1517	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.462572	1.335319	-3.127253	29011.612753
HLA B*5401	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.565376	1.437876	-3.127500	36760.036812
HLA A*8001	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.410629	1.282277	-3.128352	25741.239624
HLA A*2301	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.522049	1.393369	-3.128680	33269.715317
HLA A*2403	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.278314	1.149444	-3.128869	18980.756187
HLA B*4501	1:76-84 9	DATKPEVRR	0.992226	0.534734	-4.656301	1.526960	-3.129341	45321.158963
HLA B*3901	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.462450	1.332502	-3.129948	29003.452522
HLA B*3501	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.437700	1.307494	-3.130206	27396.824243
HLA A*0101	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.378575	1.248280	-3.130295	23909.771933
HLA A*3101	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.325270	1.194858	-3.130412	21148.049479
HLA B*3501	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.241196	1.110748	-3.130448	17425.945303
HLA B*5301	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.592790	1.462291	-3.130498	39155.225425
HLA A*0219	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.438344	1.307749	-3.130595	27437.464933
HLA B*4801	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.414884	1.284273	-3.130611	25994.673969
HLA B*5401	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.385657	1.254367	-3.131290	24302.826216
HLA B*1517	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.191711	1.060336	-3.131376	15549.323298
HLA B*5301	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.463953	1.332502	-3.131452	29104.046061
HLA B*5401	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.403466	1.271968	-3.131498	25320.126883
HLA A*6802	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.425903	1.294185	-3.131718	26662.659068
HLA B*5801	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.351902	1.219814	-3.132088	22485.457602
HLA A*0250	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.233022	1.100579	-3.132444	17101.038636
HLA A*0206	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-3.845632	0.712622	-3.133011	7008.617401
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HLA A*2501      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.282622       1.149444        -3.133178       19170.015590
HLA A*2501      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.440733       1.307494        -3.133239       27588.837983
HLA A*2902      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.378503       1.245153        -3.133350       23905.762444
HLA B*0801      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.954033       0.820380        -3.133653       8995.657082
HLA A*2301      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.528585       1.394877        -3.133708       33774.221866
HLA A*6901      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.382043       1.248280        -3.133763       24101.455654
HLA A*0202      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.382147       1.248280        -3.133867       24107.193330
HLA A*0212      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.428070       1.294185        -3.133885       26795.982446
HLA A*2501      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.388446       1.254367        -3.134079       24459.389900
HLA A*2301      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.467473       1.332502        -3.134971       29340.863948
HLA A*0250      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.263803       1.128647        -3.135156       18357.058470
HLA B*4601      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.419633       1.284273        -3.135359       26280.443138
HLA B*4402      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.380760       1.245153        -3.135608       24030.369825
HLA B*1801      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.430224       1.294185        -3.136039       26929.244061
HLA B*5301      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.480557       1.344429        -3.136129       30238.286640
HLA B*4801      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.408273       1.271968        -3.136305       25601.942862
HLA A*3002      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.451008       1.314292        -3.136716       28249.301037
HLA B*3501      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.421118       1.284273        -3.136844       26370.451068
HLA B*5701      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.946829       0.809887        -3.136943       8847.679262
HLA B*5801      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.237679       1.100579        -3.137101       17285.389393
HLA B*3501      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.391476       1.254367        -3.137110       24630.683049
HLA B*5301      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.054628       0.917388        -3.137241       11340.401779
HLA A*2902      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.248621       1.110748        -3.137873       17726.407106
HLA B*1509      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.470494       1.332502        -3.137993       29545.703504
HLA B*4501      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.243215       1.105200        -3.138014       17507.113775
HLA B*5101      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.446046       1.307749        -3.138296       27928.370316
HLA A*3001      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.250077       1.111207        -3.138870       17785.963627
HLA B*4001      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.423335       1.284273        -3.139062       26505.467724
HLA B*0702      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.323280       1.184095        -3.139185       21051.367069
HLA A*0250      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.393593       1.254367        -3.139227       24751.033712
HLA A*6802      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.296296       1.157030        -3.139267       19783.196685
HLA A*0203      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.299400       1.160079        -3.139321       19925.082968
HLA B*5401      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.056893       0.917388        -3.139506       11399.697969
HLA A*2403      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.268359       1.128647        -3.139712       18550.633387
HLA B*1503      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.433920       1.294185        -3.139735       27159.383172
HLA B*3901      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.642228       0.502462        -3.139766       4387.610206
HLA B*2705      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.234096       1.094281        -3.139815       17143.370172
HLA B*5401      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.435480       1.295115        -3.140365       27257.119633
HLA B*5701      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.394777       1.254367        -3.140411       24818.611574
HLA B*5701      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.388702       1.248280        -3.140422       24473.817315
HLA B*4002      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.557989       1.417448        -3.140541       36140.083928
HLA B*3901      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.388822       1.248280        -3.140542       24480.570679
HLA A*2603      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.535711       1.394877        -3.140834       34332.967309
HLA A*2602      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.536177       1.395101        -3.141076       34369.763047
HLA B*3501      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -3.961556       0.820380        -3.141176       9152.841518
HLA B*0802      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.449011       1.307494        -3.141516       28119.697502
HLA B*4403      1:76-84 9       DATKPEVRR       0.992226        0.534734        -4.668523       1.526960        -3.141563       46614.714451
HLA A*6802      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.426007       1.284273        -3.141733       26669.006473
HLA B*5101      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.361997       1.219814        -3.142184       23014.283964
HLA B*0801      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.075501       0.932973        -3.142529       11898.747983
HLA A*8001      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.397430       1.254367        -3.143063       24970.661688
HLA B*5701      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.427536       1.284273        -3.143263       26763.095975
HLA A*0250      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.560863       1.417448        -3.143414       36379.990133
HLA B*1517      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.391794       1.248280        -3.143514       24648.678271
HLA A*2603      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.590231       1.446716        -3.143515       38925.225704
HLA A*3001      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.080022       0.936177        -3.143845       12023.244404
HLA B*1502      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.582233       1.437876        -3.144357       38214.967319
HLA B*5401      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.561847       1.417448        -3.144399       36462.547774
HLA A*2603      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.539590       1.395101        -3.144489       34640.993555
HLA B*3901      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.416806       1.271968        -3.144838       26109.962827
HLA B*0801      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.205226       1.060336        -3.144890       16040.789183
HLA A*3201      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.146545       1.001469        -3.145076       14013.447593
HLA A*0202      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.452619       1.307494        -3.145125       28354.334168
HLA B*1801      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.489685       1.344429        -3.145256       30880.543034
HLA B*4403      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.540474       1.394877        -3.145596       34711.529149
HLA A*2902      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.295176       1.149444        -3.145732       19732.211620
HLA A*0301      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.206090       1.060336        -3.145755       16072.755625
HLA A*8001      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.269489       1.123686        -3.145803       18598.967901
HLA A*0206      1:7-15  9       FELLELATP       0.903395        -0.108267       -3.940979       0.795128        -3.145851       8729.294649
HLA A*2603      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.417880       1.271968        -3.145912       26174.594856
HLA B*0803      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.478417       1.332502        -3.145915       30089.626626
HLA A*3002      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.583848       1.437876        -3.145971       38357.261092
HLA B*3501      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.852507       0.706535        -3.145972       7120.441877
HLA B*3801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.453848       1.307494        -3.146354       28434.672728
HLA A*0301      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.366173       1.219814        -3.146359       23236.595732
HLA A*3201      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.563917       1.417448        -3.146469       36636.747170
HLA B*4403      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.454295       1.307494        -3.146800       28463.915156
HLA A*2902      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.207162       1.060336        -3.146826       16112.454604
HLA B*5801      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.141024       0.994120        -3.146904       13836.418966
HLA A*6901      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -3.895888       0.748881        -3.147007       7868.425493
HLA A*0202      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.563863       0.416603        -3.147260       3663.222645
HLA A*6801      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.542600       1.394877        -3.147723       34881.891752
HLA B*4801      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.238278       1.090544        -3.147735       17309.251419
HLA B*1517      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.291919       1.143950        -3.147969       19584.810703
HLA B*0803      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.455770       1.307749        -3.148021       28560.783214
HLA A*0212      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.432416       1.284273        -3.148143       27065.511052
HLA B*4501      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.543241       1.394877        -3.148364       34933.446870
HLA B*4501      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -3.772634       0.623682        -3.148952       5924.256498
HLA B*3801      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.481471       1.332502        -3.148970       30301.988513
HLA B*3501      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.368790       1.219814        -3.148976       23377.056610
HLA A*6901      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.180077       1.031086        -3.148991       15138.290803
HLA A*0201      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.309106       1.160079        -3.149027       20375.386754
HLA B*4002      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.484511       1.335319        -3.149192       30514.858668
HLA B*1502      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.493651       1.344429        -3.149222       31163.832360
HLA B*0702      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.433659       1.284273        -3.149386       27143.078920
HLA A*3301      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.635066       1.485661        -3.149405       43158.501954
HLA B*1501      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.433770       1.284273        -3.149496       27149.981327
HLA B*4001      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.344428       1.194858        -3.149570       22101.819028
HLA A*2501      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.444720       1.295115        -3.149606       27843.285772
HLA B*3501      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.105001       0.955042        -3.149960       12735.071860
HLA B*4402      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.404432       1.254367        -3.150065       25376.487920
HLA A*1101      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.422053       1.271968        -3.150085       26427.291403
HLA A*0219      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.398367       1.248280        -3.150088       25024.620219
HLA A*0203      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.196326       1.045865        -3.150461       15715.416011
HLA B*4601      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.398891       1.248280        -3.150611       25054.828271
HLA A*0216      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.240672       1.090014        -3.150658       17404.935226
HLA B*4001      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.180772       1.029850        -3.150922       15162.551579
HLA A*1101      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.465426       1.314292        -3.151135       29202.934620
HLA B*3501      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.262450       1.111207        -3.151242       18299.945142
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HLA A*0212	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.282359	1.130830	-3.151529	19158.403851
HLA A*2602	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.335801	1.184095	-3.151706	21667.096103
HLA A*3002	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.487152	1.335319	-3.151833	30700.976129
HLA A*6801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.447042	1.295115	-3.151927	27992.505745
HLA A*0206	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.545318	1.393369	-3.151949	35100.910676
HLA A*0206	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.446269	1.294185	-3.152084	27942.727497
HLA B*5101	1:12-20 9	LATPYALNA	1.117892	-0.294996	-3.975169	0.822896	-3.152273	9444.280094
HLA B*1502	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.424339	1.271968	-3.152371	26566.766729
HLA B*4001	1:7-15  9	FELLELATP	0.903395	-0.108267	-3.947525	0.795128	-3.152397	8861.858641
HLA B*3501	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.301872	1.149444	-3.152428	20038.803965
HLA B*5301	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.424433	1.271968	-3.152465	26572.516282
HLA A*0202	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.312578	1.160079	-3.152499	20538.957670
HLA A*3201	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.460434	1.307749	-3.152685	28869.139595
HLA A*6901	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.192534	1.039542	-3.152992	15578.793229
HLA A*2301	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.467339	1.314292	-3.153047	29331.817686
HLA A*2501	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.488404	1.335319	-3.153085	30789.629253
HLA A*2601	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.401377	1.248280	-3.153097	25198.644843
HLA B*0803	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.497647	1.344429	-3.153219	31451.932393
HLA B*3801	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.497871	1.344429	-3.153442	31468.100937
HLA B*5801	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.226305	1.072739	-3.153566	16838.574028
HLA A*0101	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.281612	1.128011	-3.153601	19125.473125
HLA A*0301	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.248109	1.094281	-3.153827	17705.513687
HLA A*0201	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.284702	1.130830	-3.153871	19262.012933
HLA B*4501	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.639653	1.485661	-3.153991	43616.675126
HLA A*0216	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.265025	1.110748	-3.154277	18408.772193
HLA A*6802	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.303758	1.149444	-3.154314	20126.044711
HLA B*1503	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.109846	0.955042	-3.154804	12877.929345
HLA A*2402	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.304369	1.149444	-3.154925	20154.373343
HLA A*2402	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.592820	1.437876	-3.154944	39157.979252
HLA B*1801	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.490580	1.335319	-3.155261	30944.258656
HLA B*1502	1:25-33 9	ERADIDRRV	1.311800	0.083077	-4.550532	1.394877	-3.155654	35524.820433
HLA B*4001	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.339750	1.184095	-3.155655	21865.035857
HLA A*2902	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.350706	1.194858	-3.155847	22423.626061
HLA B*7301	1:43-51 9	AFNDEVRAV	1.149448	0.297268	-4.602808	1.446716	-3.156092	40068.947298
HLA A*0202	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.594230	1.437876	-3.156354	39285.289957
HLA A*6901	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.111721	0.955042	-3.156679	12933.644722
HLA B*3501	1:54-62 9	TMAVVSAAT	0.831597	-0.329135	-3.659360	0.502462	-3.156898	4564.156029
HLA B*4403	1:13-21 9	ATPYALNAV	1.259075	0.203216	-4.619510	1.462291	-3.157219	41639.971306
HLA B*0801	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.441774	1.284273	-3.157501	27655.036158
HLA B*4402	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.452525	1.294185	-3.158340	28348.199080
HLA A*3301	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.553760	1.395101	-3.158659	35789.866941
HLA B*0801	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.353626	1.194858	-3.158768	22574.921682
HLA B*3801	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.453886	1.295115	-3.158771	28437.134090
HLA A*0250	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.473107	1.314292	-3.158815	29723.980151
HLA A*0212	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.248999	1.090014	-3.158985	17741.853393
HLA B*3501	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.407286	1.248280	-3.159006	25543.837356
HLA A*0250	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.597120	1.437876	-3.159243	39547.572373
HLA A*2902	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.413665	1.254367	-3.159298	25921.790246
HLA A*0101	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.379236	1.219814	-3.159422	23946.146704
HLA A*0212	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.260528	1.100579	-3.159949	18219.141512
HLA B*5701	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.284721	1.124732	-3.159989	19262.850594
HLA A*2301	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.495554	1.335319	-3.160235	31300.692233
HLA A*8001	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.355139	1.194858	-3.160281	22653.709168
HLA A*2501	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.344548	1.184095	-3.160453	22107.917857
HLA A*2501	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.468749	1.307749	-3.160999	29427.181504
HLA B*3501	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.234084	1.072739	-3.161345	17142.906460
HLA A*1101	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-3.787403	0.625647	-3.161755	6129.184806
HLA B*7301	1:93-101	9	FASAAAIAV	1.212843	0.182258	-4.557141	1.395101	-3.162040	36069.572304
HLA B*1502	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.290155	1.128011	-3.162144	19505.402430
HLA B*1502	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.469768	1.307494	-3.162274	29496.354518
HLA B*1502	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.382093	1.219814	-3.162279	24104.193920
HLA A*0202	1:203-211	9	GASTALAFT	0.843184	-0.343048	-3.662875	0.500136	-3.162740	4601.244509
HLA A*0101	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.287596	1.124732	-3.162865	19390.826737
HLA B*3901	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.194178	1.031086	-3.163092	15637.900758
HLA B*1801	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.382964	1.219814	-3.163150	24152.621279
HLA B*2705	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.417563	1.254367	-3.163196	26155.485611
HLA B*1502	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.347612	1.184095	-3.163516	22264.429469
HLA A*0211	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.557066	1.393369	-3.163697	36063.328609
HLA B*5101	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.499137	1.335319	-3.163818	31559.993636
HLA A*6901	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.210507	1.045865	-3.164642	16237.059174
HLA A*0301	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-4.194850	1.029850	-3.165000	15662.114888
HLA B*0801	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.384844	1.219814	-3.165030	24257.378208
HLA B*3801	1:49-57 9	RAVRETMAV	0.926962	0.318191	-4.410437	1.245153	-3.165284	25729.823062
HLA B*1517	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.419795	1.254367	-3.165428	26290.254995
HLA B*5101	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.296426	1.130830	-3.165595	19789.083930
HLA A*3001	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.255848	1.090014	-3.165834	18023.857080
HLA B*0702	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.315318	1.149444	-3.165874	20668.925476
HLA B*4403	1:112-120	9	TRPSPPPTV	1.255605	0.230056	-4.651550	1.485661	-3.165889	44828.101701
HLA B*0702	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.238647	1.072739	-3.165908	17323.959321
HLA B*5301	1:24-32 9	DERADIDRR	1.029344	0.408532	-4.604063	1.437876	-3.166186	40184.869072
HLA A*2402	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.559570	1.393369	-3.166201	36271.904571
HLA B*4601	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-4.290037	1.123686	-3.166351	19500.127041
HLA B*1501	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.101364	0.934977	-3.166388	12628.867221
HLA A*0212	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.271918	1.105200	-3.166718	18703.298812
HLA A*0219	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.291520	1.124732	-3.166788	19566.807201
HLA A*2501	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.386693	1.219814	-3.166879	24360.876173
HLA B*0702	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-3.915779	0.748881	-3.166898	8237.180388
HLA A*0211	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-3.857746	0.690533	-3.167213	7206.863513
HLA A*6901	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.272529	1.105200	-3.167329	18729.624844
HLA B*0801	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.295354	1.128011	-3.167343	19740.326217
HLA B*3901	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.327862	1.160079	-3.167783	21274.619421
HLA A*3201	1:25-33 9	ERADIDRRV	1.311800	0.083077	-4.562770	1.394877	-3.167893	36540.152771
HLA B*1503	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-3.997437	0.829467	-3.167970	9941.164895
HLA A*2902	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.268739	1.100579	-3.168161	18566.898326
HLA A*3002	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.561614	1.393369	-3.168245	36443.024427
HLA A*0301	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.363339	1.194858	-3.168481	23085.486079
HLA B*2705	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.450796	1.282277	-3.168519	28235.550082
HLA A*2402	1:25-33 9	ERADIDRRV	1.311800	0.083077	-4.563837	1.394877	-3.168960	36630.008965
HLA A*2501	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.451273	1.282277	-3.168996	28266.575608
HLA B*1801	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.501590	1.332502	-3.169088	31738.746406
HLA B*1501	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.297102	1.128011	-3.169091	19819.940306
HLA A*3001	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.240623	1.071321	-3.169302	17402.958004
HLA A*2902	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-4.293010	1.123686	-3.169323	19634.034025
HLA A*6801	1:205-213	9	STALAFTVE	0.973168	-0.590501	-3.552717	0.382667	-3.170051	3570.403984
HLA A*3101	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.390311	1.219814	-3.170497	24564.680007
HLA A*2601	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.354613	1.184095	-3.170518	22626.273686
HLA B*4801	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.425039	1.254367	-3.170672	26609.630804
HLA A*0212	1:201-209	9	DLGASTALA	1.029007	-0.426525	-3.773282	0.602482	-3.170800	5933.108787
HLA B*1509	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.453301	1.282277	-3.171024	28398.853285
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HLA B*7301      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.419304       1.248280        -3.171024       26260.546274
HLA A*2902      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.455335       1.284273        -3.171062       28532.213039
HLA A*6801      1:112-120       9       TRPSPPPTV       1.255605        0.230056        -4.656881       1.485661        -3.171220       45381.759507
HLA A*0219      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.282265       1.110748        -3.171517       19154.258505
HLA A*6901      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.282775       1.111207        -3.171568       19176.757773
HLA B*4601      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.391500       1.219814        -3.171686       24632.015578
HLA A*2902      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.300455       1.128647        -3.171808       19973.540625
HLA B*1517      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.466336       1.294185        -3.172151       29264.138722
HLA A*0203      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.456466       1.284273        -3.172192       28606.555010
HLA A*2402      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.486739       1.314292        -3.172447       30671.758398
HLA A*1101      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.421068       1.248280        -3.172788       26367.455353
HLA A*2301      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.427177       1.254367        -3.172810       26740.952977
HLA B*5301      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.568092       1.394877        -3.173214       36990.648252
HLA A*6901      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.051499       0.877544        -3.173954       11258.976883
HLA B*5301      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -3.625218       0.451113        -3.174105       4219.080061
HLA A*6802      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.107191       0.932973        -3.174219       12799.444453
HLA B*5101      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.358823       1.184095        -3.174728       22846.691275
HLA A*6801      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.457182       1.282277        -3.174905       28653.795252
HLA A*0216      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.359246       1.184095        -3.175151       22868.949762
HLA A*2602      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.299978       1.124732        -3.175246       19951.617573
HLA A*1101      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.371010       1.194858        -3.176152       23496.874207
HLA A*2301      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.483910       1.307494        -3.176415       30472.626926
HLA A*8001      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.396380       1.219814        -3.176566       24910.350076
HLA A*2402      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.484462       1.307494        -3.176968       30511.392143
HLA A*6901      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.326462       1.149444        -3.177017       21206.134262
HLA A*0219      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.461437       1.284273        -3.177164       28935.905047
HLA B*5801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.308199       1.130830        -3.177369       20332.882915
HLA A*0301      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.361474       1.184095        -3.177378       22986.536152
HLA B*5701      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.361643       1.184095        -3.177548       22995.491428
HLA B*4601      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.248910       1.071321        -3.177588       17738.206473
HLA A*0201      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.249018       1.071321        -3.177696       17742.621262
HLA A*3201      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.485235       1.307494        -3.177741       30565.746308
HLA B*1509      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.422953       1.245153        -3.177800       26482.105189
HLA B*4801      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.372812       1.194858        -3.177954       23594.574342
HLA A*2403      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.373024       1.194858        -3.178165       23606.065102
HLA A*3101      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.273262       1.094281        -3.178981       18761.264999
HLA A*0202      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.269942       1.090544        -3.179399       18618.397385
HLA A*2501      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.427809       1.248280        -3.179529       26779.896351
HLA A*2403      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.463895       1.284273        -3.179621       29100.110086
HLA B*0801      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.252370       1.072739        -3.179631       17880.122800
HLA B*1501      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.134746       0.955042        -3.179704       13637.849077
HLA A*0206      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.173949       0.994120        -3.179830       14926.204476
HLA B*3901      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.474575       1.294185        -3.180390       29824.652399
HLA A*8001      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.309721       1.128647        -3.181074       20404.287119
HLA B*1509      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.341195       1.160079        -3.181116       21937.903772
HLA A*2601      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.304842       1.123686        -3.181155       20176.300881
HLA B*0702      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.309172       1.128011        -3.181161       20378.473388
HLA B*1509      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.435757       1.254367        -3.181390       27274.525231
HLA A*2301      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.526085       1.344429        -3.181657       33580.371771
HLA B*5701      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.326039       1.143950        -3.182089       21185.494203
HLA A*0219      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.287357       1.105200        -3.182157       19380.129662
HLA A*0211      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.272484       1.090014        -3.182470       18727.699764
HLA B*0803      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.454459       1.271968        -3.182491       28474.696261
HLA A*3301      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.600155       1.417448        -3.182707       39824.961453
HLA B*0802      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.431265       1.248280        -3.182985       26993.859569
HLA A*0201      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.367869       1.184095        -3.183774       23327.533963
HLA A*8001      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.468622       1.284273        -3.184348       29418.586079
HLA B*0803      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.432654       1.248280        -3.184374       27080.303656
HLA A*3201      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.519702       1.335319        -3.184383       33090.394834
HLA A*3201      1:24-32 9       DERADIDRR       1.029344        0.408532        -4.622320       1.437876        -3.184444       41910.264877
HLA A*3201      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.577979       1.393369        -3.184609       37842.391567
HLA B*1801      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.439037       1.254367        -3.184670       27481.287818
HLA A*3002      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.478882       1.294185        -3.184697       30121.874640
HLA A*2601      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.379567       1.194858        -3.184708       23964.419658
HLA A*2602      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.529426       1.344429        -3.184998       33839.697147
HLA A*2602      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.480278       1.295115        -3.185163       30218.826198
HLA B*4403      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.602648       1.417448        -3.185200       40054.209747
HLA B*0702      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.439824       1.254367        -3.185457       27531.137667
HLA B*5801      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -3.995826       0.809887        -3.185939       9904.339778
HLA B*4601      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.317221       1.130830        -3.186391       20759.695651
HLA B*1801      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.469251       1.282277        -3.186974       29461.269559
HLA A*3001      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -3.998950       0.811766        -3.187184       9975.860005
HLA B*0803      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.481448       1.294185        -3.187263       30300.349254
HLA B*4402      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -3.810968       0.623682        -3.187286       6470.950101
HLA A*0206      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.120513       0.932973        -3.187540       13198.139059
HLA A*0216      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.318588       1.130830        -3.187758       20825.161712
HLA B*1501      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.332006       1.143950        -3.188056       21478.615885
HLA A*6802      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.894751       0.706535        -3.188216       7847.849864
HLA A*3001      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.121438       0.932973        -3.188466       13226.300847
HLA B*1501      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.300544       1.111207        -3.189337       19977.647123
HLA A*8001      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.437658       1.248280        -3.189378       27394.156525
HLA B*5701      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.409260       1.219814        -3.189446       25660.180542
HLA A*2601      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.318158       1.128647        -3.189511       20804.554802
HLA A*0212      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.373876       1.184095        -3.189781       23652.467998
HLA A*0202      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.896452       0.706535        -3.189917       7878.648282
HLA A*2603      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.497473       1.307494        -3.189979       31439.343705
HLA A*6901      1:9-17  9       LLELATPYA       0.993939        -0.356018       -3.828058       0.637921        -3.190137       6730.668556
HLA A*0206      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.280980       1.090544        -3.190437       19097.660828
HLA B*4001      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.347492       1.157030        -3.190462       22258.287464
HLA A*2301      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.498256       1.307749        -3.190507       31496.032512
HLA A*3101      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.335354       1.143950        -3.191404       21644.836393
HLA B*0801      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.262894       1.071321        -3.191573       18318.665839
HLA A*2902      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.375758       1.184095        -3.191663       23755.184130
HLA B*3501      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.376433       1.184095        -3.192338       23792.095984
HLA B*4402      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.376520       1.184095        -3.192424       23796.858826
HLA A*2501      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.437583       1.245153        -3.192430       27389.414556
HLA A*6802      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.015495       0.822896        -3.192599       10363.236737
HLA A*6901      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.283222       1.090544        -3.192678       19196.479293
HLA A*0203      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.079096       0.886414        -3.192682       11997.644196
HLA A*3101      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.321189       1.128011        -3.193178       20950.252537
HLA B*1502      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.528794       1.335319        -3.193475       33790.487399
HLA B*1509      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.388377       1.194858        -3.193519       24455.552846
HLA B*4001      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.317355       1.123686        -3.193669       20766.098174
HLA A*3201      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.299417       1.105200        -3.194216       19925.837530
HLA A*3001      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.004523       0.809887        -3.194637       10104.697676
HLA B*0803      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.479646       1.284273        -3.195372       30174.881926
HLA B*5401      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.443816       1.248280        -3.195536       27785.353923
HLA B*5801      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.356098       1.160079        -3.196019       22703.766446
HLA B*0802      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.478743       1.282277        -3.196466       30112.261770
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HLA B*3801      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.346167       1.149444        -3.196722       22190.476982
HLA B*5801      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.324873       1.128011        -3.196862       21128.723261
HLA A*6901      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.354200       1.157030        -3.197170       22604.740548
HLA B*1801      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.504942       1.307749        -3.197193       31984.714935
HLA B*5801      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.354785       1.157030        -3.197755       22635.211062
HLA B*2705      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.482183       1.284273        -3.197910       30351.700157
HLA B*1509      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.492114       1.294185        -3.197929       31053.767441
HLA B*1503      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -3.799225       0.600711        -3.198515       6298.328740
HLA A*0250      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.309609       1.110748        -3.198861       20398.989331
HLA A*2501      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.322684       1.123686        -3.198997       21022.460002
HLA B*4402      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.394364       1.194858        -3.199506       24794.992015
HLA A*3101      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.359592       1.160079        -3.199513       22887.143613
HLA B*1502      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.593083       1.393369        -3.199714       39181.712558
HLA A*2402      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.544174       1.344429        -3.199746       35008.554969
HLA A*1101      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.294339       1.094281        -3.200058       19694.245520
HLA A*0216      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.484427       1.284273        -3.200153       30508.916294
HLA A*2403      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.344329       1.143950        -3.200379       22096.797726
HLA A*2301      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.495535       1.295115        -3.200421       31299.337597
HLA A*0219      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.081568       0.880895        -3.200672       12066.119899
HLA A*3101      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.357970       1.157030        -3.200941       22801.869201
HLA B*3501      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -3.177072       -0.023878       -3.200950       1503.392219
HLA A*0202      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.509545       1.307749        -3.201796       32325.490651
HLA A*6802      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.232940       1.031086        -3.201854       17097.800928
HLA A*8001      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.262210       1.060336        -3.201874       18289.849859
HLA B*5401      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -3.912814       0.710864        -3.201949       8181.134389
HLA A*0101      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.362275       1.160079        -3.202196       23028.980212
HLA A*2501      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.486826       1.284273        -3.202552       30677.898453
HLA B*5401      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.538164       1.335319        -3.202845       34527.425935
HLA A*0201      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.313835       1.110748        -3.203087       20598.489494
HLA B*0801      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.308518       1.105200        -3.203318       20347.848235
HLA A*0101      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.263751       1.060336        -3.203416       18354.873787
HLA B*4001      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.331452       1.128011        -3.203441       21451.210908
HLA B*0803      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.485893       1.282277        -3.203616       30612.081437
HLA B*5301      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.243161       1.039542        -3.203619       17504.935545
HLA A*0250      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.597012       1.393369        -3.203643       39537.731990
HLA A*0301      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.363729       1.160079        -3.203650       23106.227118
HLA A*2902      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.423700       1.219814        -3.203886       26527.702750
HLA A*0101      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.327702       1.123686        -3.204016       21266.794514
HLA B*5401      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -3.864442       0.660357        -3.204085       7318.841290
HLA A*0203      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.353791       1.149444        -3.204346       22583.472249
HLA A*3002      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.329081       1.124732        -3.204349       21334.436797
HLA A*2602      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.077334       0.872785        -3.204549       11949.063375
HLA A*2403      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.328294       1.123686        -3.204608       21295.807138
HLA B*7301      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.487089       1.282277        -3.204812       30696.492057
HLA A*2403      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.299294       1.094281        -3.205013       19920.232896
HLA B*0802      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.459475       1.254367        -3.205109       28805.488898
HLA A*0301      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.306009       1.100579        -3.205431       20230.622197
HLA A*6901      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.349484       1.143950        -3.205534       22360.633853
HLA B*5401      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.513297       1.307494        -3.205803       32605.979643
HLA A*0201      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.349926       1.143950        -3.205976       22383.387510
HLA A*0301      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.336957       1.130830        -3.206126       21724.843482
HLA A*6801      1:43-51 9       AFNDEVRAV       1.149448        0.297268        -4.653345       1.446716        -3.206630       45013.766634
HLA B*4402      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.366943       1.160079        -3.206864       23277.864365
HLA A*8001      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.367467       1.160079        -3.207388       23305.963849
HLA A*6801      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.209093       1.001469        -3.207624       16184.265094
HLA A*0301      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.364713       1.157030        -3.207684       23158.662415
HLA A*6802      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.318610       1.110748        -3.207861       20826.175693
HLA A*3301      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.602763       1.394877        -3.207886       40064.828907
HLA B*1501      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.367979       1.160079        -3.207900       23333.466088
HLA A*0301      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.336134       1.128011        -3.208123       21683.747253
HLA B*5801      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.352113       1.143950        -3.208163       22496.408213
HLA A*2902      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.456444       1.248280        -3.208164       28605.162220
HLA B*1801      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.319411       1.111207        -3.208203       20864.630702
HLA A*0203      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.352289       1.143950        -3.208339       22505.537795
HLA A*0250      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.320040       1.111207        -3.208833       20894.903233
HLA B*5101      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.503502       1.294185        -3.209317       31878.820922
HLA A*3201      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.299985       1.090544        -3.209442       19951.941384
HLA B*0702      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.141912       0.932462        -3.209450       13864.742537
HLA B*4801      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.359110       1.149444        -3.209666       22861.775216
HLA A*2603      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.464094       1.254367        -3.209728       29113.494575
HLA A*8001      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.162865       0.952818        -3.210047       14550.051032
HLA A*0202      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.603630       1.393369        -3.210261       40144.888168
HLA A*6901      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.321011       1.110748        -3.210263       20941.640579
HLA B*0802      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.359829       1.149444        -3.210385       22899.652538
HLA B*2705      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.394801       1.184095        -3.210706       24819.954270
HLA A*2602      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.604117       1.393369        -3.210747       40189.869484
HLA A*0212      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.282124       1.071321        -3.210803       19148.042169
HLA A*0101      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.368207       1.157030        -3.211178       23345.713753
HLA A*3001      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.164020       0.952818        -3.211203       14588.829986
HLA B*1501      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.023127       0.811766        -3.211360       10546.941728
HLA B*1801      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.302330       1.090544        -3.211786       20059.954622
HLA B*0801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.342743       1.130830        -3.211913       22016.254547
HLA B*4403      1:93-101        9       FASAAAIAV       1.212843        0.182258        -4.607058       1.395101        -3.211957       40463.006712
HLA B*0803      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.431836       1.219814        -3.212022       27029.369115
HLA A*2403      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.245127       1.033072        -3.212056       17584.378972
HLA B*1517      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.431998       1.219814        -3.212184       27039.460585
HLA A*0101      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.361673       1.149444        -3.212229       22997.108724
HLA B*0702      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.432487       1.219814        -3.212673       27069.904051
HLA B*3901      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.496966       1.284273        -3.212692       31402.627155
HLA B*1517      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.497720       1.284273        -3.213447       31457.207531
HLA A*0101      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.397759       1.184095        -3.213664       24989.581243
HLA A*0201      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.308284       1.094281        -3.214002       20336.843251
HLA A*3002      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -3.839669       0.625647        -3.214022       6913.044614
HLA B*4601      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.342727       1.128647        -3.214080       22015.420824
HLA B*1517      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.169147       0.955042        -3.214105       14762.062490
HLA B*4002      1:25-33 9       ERADIDRRV       1.311800        0.083077        -4.609328       1.394877        -3.214450       40675.017978
HLA B*1801      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.287279       1.072739        -3.214540       19376.670107
HLA A*6901      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.101092       0.886414        -3.214678       12620.944497
HLA A*0301      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.285010       1.070235        -3.214775       19275.672675
HLA B*4501      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.632322       1.417448        -3.214874       42886.653921
HLA A*2403      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.434792       1.219814        -3.214978       27213.948664
HLA B*7301      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.559458       1.344429        -3.215029       36262.486899
HLA B*0702      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.326321       1.111207        -3.215113       21199.252009
HLA A*3001      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.268408       1.053156        -3.215252       18552.741001
HLA A*0101      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.309923       1.094281        -3.215642       20413.782432
HLA B*2705      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.410519       1.194858        -3.215661       25734.695365
HLA A*2603      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.548561       1.332502        -3.216059       35363.942314
HLA A*0250      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.551599       1.335319        -3.216279       35612.179815
HLA B*0803      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.470856       1.254367        -3.216489       29570.328964
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HLA A*2902      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.376823       1.160079        -3.216744       23813.471872
HLA A*3101      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.327695       1.110748        -3.216947       21266.449364
HLA A*0301      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.360905       1.143950        -3.216955       22956.462026
HLA A*0203      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.307024       1.090014        -3.217010       20277.957911
HLA B*4001      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.361427       1.143950        -3.217476       22984.049194
HLA A*3101      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.401795       1.184095        -3.217700       25222.921824
HLA A*0301      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.307781       1.090014        -3.217767       20313.312580
HLA A*6901      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.290594       1.072739        -3.217855       19525.145041
HLA B*5301      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.500222       1.282277        -3.217945       31638.972356
HLA B*4601      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.323616       1.105200        -3.218416       21067.659006
HLA A*0203      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.309331       1.090544        -3.218788       20385.971446
HLA B*1502      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.514117       1.295115        -3.219003       32667.599558
HLA B*1801      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.049013       0.829467        -3.219546       11194.718369
HLA B*4001      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.348321       1.128647        -3.219674       22300.834525
HLA A*1101      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.504113       1.284273        -3.219840       31923.692303
HLA A*0202      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.259832       1.039542        -3.220291       18189.990052
HLA A*8001      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.369819       1.149444        -3.220375       23432.514960
HLA A*6802      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.738590       0.518215        -3.220375       5477.593707
HLA B*4402      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.321389       1.100579        -3.220810       20959.888529
HLA A*6901      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.153955       0.932973        -3.220983       14254.607693
HLA A*2602      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.528863       1.307749        -3.221113       33795.789095
HLA B*0702      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.381510       1.160079        -3.221431       24071.876152
HLA B*4601      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.378923       1.157030        -3.221894       23928.923283
HLA B*4801      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.333642       1.111207        -3.222434       21559.641395
HLA B*1801      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.467738       1.245153        -3.222586       29358.806014
HLA B*4501      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.317216       1.094281        -3.222935       20759.471037
HLA A*0101      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.323741       1.100579        -3.223162       21073.700478
HLA A*2601      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.323825       1.100579        -3.223247       21077.805107
HLA B*4001      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.372810       1.149444        -3.223366       23594.446698
HLA B*5401      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.155966       0.932462        -3.223504       14320.771939
HLA B*4402      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.354434       1.130830        -3.223604       22616.972770
HLA B*3501      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.367702       1.143950        -3.223752       23318.575529
HLA B*0801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.334506       1.110748        -3.223758       21602.605928
HLA A*3101      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.329424       1.105200        -3.224224       21351.294326
HLA A*3002      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.444070       1.219814        -3.224256       27801.592761
HLA A*0201      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.381966       1.157030        -3.224936       24097.153293
HLA B*7301      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.330528       1.105200        -3.225328       21405.652227
HLA A*6901      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.219990       0.994120        -3.225870       16595.482928
HLA A*0101      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.369824       1.143950        -3.225874       23432.768496
HLA A*0250      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.351051       1.124732        -3.226319       22441.465625
HLA B*4001      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.259466       1.033072        -3.226394       18174.645219
HLA B*4001      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.386566       1.160079        -3.226487       24353.760571
HLA B*1503      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -3.578247       0.351592        -3.226655       3786.577609
HLA B*5401      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.383770       1.157030        -3.226741       24197.480297
HLA A*0202      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.299644       1.072739        -3.226905       19936.296541
HLA A*6801      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.266559       1.039542        -3.227018       18473.919086
HLA A*2601      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.384078       1.157030        -3.227048       24214.635020
HLA A*0202      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.317078       1.090014        -3.227064       20752.846014
HLA A*0201      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.376590       1.149444        -3.227146       23800.721291
HLA B*5101      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.511458       1.284273        -3.227184       32468.154681
HLA A*3201      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.448167       1.219814        -3.228353       28065.137824
HLA B*7301      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.622053       1.393369        -3.228683       41884.425638
HLA B*5101      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.038877       0.809887        -3.228991       10936.478261
HLA A*3002      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.058519       0.829467        -3.229052       11442.454354
HLA A*3101      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.360148       1.130830        -3.229318       22916.507040
HLA A*0212      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.340641       1.111207        -3.229433       21909.912781
HLA B*3801      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.514037       1.284273        -3.229764       32661.591356
HLA A*0219      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.330376       1.100579        -3.229797       21398.126407
HLA A*2501      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.358544       1.128647        -3.229897       22831.987838
HLA A*6801      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.562526       1.332502        -3.230024       36519.600023
HLA A*0206      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.379663       1.149444        -3.230219       23969.735687
HLA A*6802      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.165299       0.934977        -3.230322       14631.827856
HLA B*0801      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.414478       1.184095        -3.230383       25970.356653
HLA B*1502      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.359098       1.128647        -3.230451       22861.156826
HLA A*0203      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.303237       1.072739        -3.230498       20101.887933
HLA B*2705      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.331682       1.100579        -3.231104       21462.586693
HLA A*0203      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.270769       1.039542        -3.231228       18653.885825
HLA A*2301      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.503251       1.271968        -3.231283       31860.372947
HLA B*5401      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.164284       0.932973        -3.231311       14597.672147
HLA A*0301      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.342168       1.110748        -3.231420       21987.093030
HLA B*4501      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -3.891880       0.660357        -3.231523       7796.139748
HLA A*0250      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.391639       1.160079        -3.231560       24639.878965
HLA A*0216      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.343025       1.111207        -3.231818       22030.551846
HLA B*5801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.302057       1.070235        -3.231823       20047.370004
HLA B*1503      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.066883       0.834848        -3.232035       11664.962722
HLA A*2601      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.392327       1.160079        -3.232248       24678.966547
HLA B*4001      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.332866       1.100579        -3.232288       21521.186093
HLA B*0803      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.477524       1.245153        -3.232371       30027.833177
HLA B*5401      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.526680       1.294185        -3.232495       33626.364759
HLA A*0206      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.322655       1.090014        -3.232641       21021.095296
HLA B*5701      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.393147       1.160079        -3.233068       24725.605716
HLA A*2403      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.344292       1.111207        -3.233084       22094.885149
HLA B*0802      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.427999       1.194858        -3.233141       26791.633900
HLA A*2603      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.453080       1.219814        -3.233266       28384.415299
HLA A*8001      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.417431       1.184095        -3.233336       26147.562908
HLA B*1509      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.382828       1.149444        -3.233384       24145.044014
HLA A*6801      1:149-157       9       DRNTGLLVM       1.316454        0.100994        -4.650914       1.417448        -3.233466       44762.428272
HLA A*0216      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.324150       1.090544        -3.233606       21093.546928
HLA A*0212      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.390638       1.157030        -3.233608       24583.158969
HLA B*2705      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.377856       1.143950        -3.233906       23870.223817
HLA B*3901      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.324020       1.090014        -3.234006       21087.271605
HLA A*0216      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.263911       1.029850        -3.234061       18361.627282
HLA A*2603      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.529210       1.295115        -3.234096       33822.858989
HLA A*0219      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.365017       1.130830        -3.234186       23174.829924
HLA A*3201      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.567068       1.332502        -3.234566       36903.500797
HLA A*2403      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.394954       1.160079        -3.234875       24828.683563
HLA A*0101      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.346315       1.111207        -3.235107       22198.041296
HLA B*7301      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.549653       1.314292        -3.235361       35453.015782
HLA A*2301      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.529572       1.294185        -3.235387       33851.049330
HLA A*2601      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.366281       1.130830        -3.235450       23242.378992
HLA B*5801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.346216       1.110748        -3.235468       22192.998133
HLA B*1517      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.363995       1.128011        -3.235984       23120.356676
HLA B*5101      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.484389       1.248280        -3.236109       30506.275611
HLA B*5801      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.297149       1.060336        -3.236814       19822.084896
HLA A*2403      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.337398       1.100579        -3.236820       21746.950173
HLA A*0216      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -3.983594       0.746698        -3.236896       9629.286577
HLA B*1509      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.485334       1.248280        -3.237054       30572.692104
HLA B*5101      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.360776       1.123686        -3.237089       22949.632487
HLA B*4002      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.457351       1.219814        -3.237537       28664.958424
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HLA A*2603	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.630999	1.393369	-3.237630	42756.229863
HLA B*1801	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.298042	1.060336	-3.237706	19862.876217
HLA B*4001	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.332072	1.094281	-3.237791	21481.869646
HLA B*5401	1:47-55 9	EVRAVRETM	1.250113	0.064179	-4.552421	1.314292	-3.238129	35679.673974
HLA A*6901	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.328517	1.090014	-3.238503	21306.754707
HLA A*0212	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.119676	0.880895	-3.238781	13172.744953
HLA B*3801	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.458669	1.219814	-3.238855	28752.087225
HLA A*3101	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.311794	1.072739	-3.239055	20501.879275
HLA A*0202	1:83-91 9	RRQSRWRTA	1.364813	-0.029494	-4.575152	1.335319	-3.239833	37596.909303
HLA B*0802	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.424036	1.184095	-3.239940	26548.232896
HLA A*8001	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.368466	1.128011	-3.240455	23359.610637
HLA B*4002	1:46-54 9	DEVRAVRET	1.031728	-0.408046	-3.864320	0.623682	-3.240638	7316.782685
HLA A*2603	1:49-57 9	RAVRETMAV	0.926962	0.318191	-4.485940	1.245153	-3.240787	30615.393775
HLA B*0803	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.331482	1.090544	-3.240939	21452.719594
HLA A*0212	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.351714	1.110748	-3.240966	22475.728201
HLA A*0219	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.352971	1.111207	-3.241763	22540.873721
HLA A*6901	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-3.760172	0.518215	-3.241957	5756.681277
HLA A*0250	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.490512	1.248280	-3.242232	30939.404291
HLA A*2601	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.366990	1.124732	-3.242258	23280.383114
HLA B*4601	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.402345	1.160079	-3.242266	25254.872094
HLA B*7301	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.574807	1.332502	-3.242305	37567.022107
HLA A*2402	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.524737	1.282277	-3.242460	33476.257172
HLA B*4002	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.586911	1.344429	-3.242483	38628.808905
HLA A*0301	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.347684	1.105200	-3.242484	22268.163673
HLA B*0803	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.392005	1.149444	-3.242561	24660.682388
HLA B*4001	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.353810	1.110748	-3.243061	22584.449663
HLA A*3101	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.343744	1.100579	-3.243166	22067.052000
HLA B*1503	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.527725	1.284273	-3.243452	33707.414413
HLA B*3801	1:52-60 9	RETMAVVSA	1.427872	-0.179592	-4.492039	1.248280	-3.243759	31048.391988
HLA A*3301	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.576266	1.332502	-3.243764	37693.442302
HLA B*0803	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.404053	1.160079	-3.243974	25354.394821
HLA A*2601	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.393659	1.149444	-3.244215	24754.783206
HLA B*4801	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.074261	0.829467	-3.244794	11864.808640
HLA A*1101	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.350283	1.105200	-3.245083	22401.801009
HLA A*2501	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.440071	1.194858	-3.245212	27546.780852
HLA B*5701	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.345866	1.100579	-3.245287	22175.116154
HLA B*4801	1:86-94 9	SRWRTAAFA	1.225790	-0.065711	-4.405376	1.160079	-3.245297	25431.736137
HLA B*4001	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.370101	1.124732	-3.245369	23447.731975
HLA A*0212	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.395367	1.149444	-3.245923	24852.335216
HLA B*4002	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.639375	1.393369	-3.246006	43588.840569
HLA A*2501	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.336571	1.090544	-3.246028	21705.577275
HLA B*3901	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.340481	1.094281	-3.246200	21901.854209
HLA A*0101	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.377084	1.130830	-3.246253	23827.776102
HLA A*2402	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.500699	1.254367	-3.246333	31673.737599
HLA B*4801	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.182577	0.936177	-3.246400	15225.679922
HLA A*2601	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.375075	1.128011	-3.247064	23717.816293
HLA B*3901	1:27-35 9	ADIDRRVAA	1.371750	-0.214720	-4.404096	1.157030	-3.247066	25356.863902
HLA B*4402	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.357834	1.110748	-3.247086	22794.715700
HLA A*3001	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.280179	1.033072	-3.247107	19062.462471
HLA B*1509	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.531402	1.284273	-3.247129	33994.008956
HLA B*4601	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.396575	1.149444	-3.247131	24921.537853
HLA A*2402	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.541376	1.294185	-3.247191	34783.713742
HLA A*8001	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.348164	1.100579	-3.247585	22292.752772
HLA A*3301	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.592130	1.344429	-3.247701	39095.747699
HLA B*4601	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.375754	1.128011	-3.247743	23754.927105
HLA B*5301	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.555619	1.307749	-3.247869	35943.347893
HLA B*7301	1:148-156	9	RDRNTGLLV	1.155258	0.152236	-4.555804	1.307494	-3.248310	35958.712689
HLA A*0203	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.301484	1.053156	-3.248328	20020.924674
HLA B*5701	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.379661	1.130830	-3.248831	23969.606014
HLA A*0202	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.432940	1.184095	-3.248845	27098.182731
HLA B*1503	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.392813	1.143950	-3.248863	24706.618695
HLA B*0702	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.309294	1.060336	-3.248958	20384.206949
HLA B*0802	1:122-130	9	EQVLTAPDV	1.040047	0.179767	-4.468779	1.219814	-3.248965	29429.251148
HLA A*1101	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.433182	1.184095	-3.249087	27113.286550
HLA B*1503	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.243339	0.994120	-3.249219	17512.134206
HLA B*4601	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.343805	1.094281	-3.249524	22070.156106
HLA A*0250	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.557404	1.307749	-3.249655	36091.433754
HLA A*0201	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.360912	1.111207	-3.249705	22956.834605
HLA A*0212	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.393791	1.143950	-3.249841	24762.283897
HLA A*2602	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.532204	1.282277	-3.249926	34056.778038
HLA A*0219	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.434162	1.184095	-3.250067	27174.521102
HLA A*0101	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.340638	1.090544	-3.250095	21909.794251
HLA A*0202	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.060070	0.809887	-3.250183	11483.382969
HLA B*0801	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.350805	1.100579	-3.250226	22428.721632
HLA B*0702	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.340923	1.090544	-3.250379	21924.141022
HLA B*4002	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.361824	1.111207	-3.250616	23005.072459
HLA A*0203	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-3.947887	0.697019	-3.250868	8869.244735
HLA A*0216	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.400376	1.149444	-3.250932	25140.638591
HLA A*2402	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.362000	1.110748	-3.251252	23014.408470
HLA B*5801	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.356481	1.105200	-3.251281	22723.795728
HLA B*4001	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.362552	1.111207	-3.251345	23043.685845
HLA A*2403	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.376219	1.124732	-3.251487	23780.386019
HLA B*5701	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.356775	1.105200	-3.251574	22739.167577
HLA A*0206	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.395562	1.143950	-3.251612	24863.496937
HLA A*3201	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.382633	1.130830	-3.251803	24134.204821
HLA B*4501	1:79-87 9	KPEVRRQSR	0.893674	0.499695	-4.646024	1.393369	-3.252655	44261.319808
HLA B*5801	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.363931	1.111207	-3.252724	23116.979802
HLA A*0216	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-3.853456	0.600711	-3.252746	7136.021299
HLA B*1501	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-3.853884	0.600711	-3.253173	7143.050885
HLA B*0801	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.403261	1.149444	-3.253817	25308.212508
HLA A*2301	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.538331	1.284273	-3.254058	34540.690540
HLA B*1502	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.325541	1.071321	-3.254219	21161.210562
HLA B*5401	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.562089	1.307749	-3.254340	36482.871045
HLA B*1509	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-4.378256	1.123686	-3.254570	23892.186910
HLA B*4801	1:27-35 9	ADIDRRVAA	1.371750	-0.214720	-4.411800	1.157030	-3.254770	25810.683239
HLA A*0250	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.344846	1.090014	-3.254832	22123.112452
HLA A*2301	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.537114	1.282277	-3.254837	34444.031881
HLA B*1801	1:32-40 9	RVAAAPSPV	0.757389	0.366297	-4.378646	1.123686	-3.254960	23913.652725
HLA A*0202	1:27-35 9	ADIDRRVAA	1.371750	-0.214720	-4.412013	1.157030	-3.254984	25823.392964
HLA B*3801	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.537311	1.282277	-3.255034	34459.687863
HLA B*3501	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-3.904872	0.649819	-3.255054	8032.898277
HLA A*2602	1:160-168	9	VAPPSRGTV	1.092400	0.240102	-4.587642	1.332502	-3.255140	38693.855635
HLA B*7301	1:204-212	9	ASTALAFTV	1.108485	0.186630	-4.550295	1.295115	-3.255180	35505.415016
HLA B*4403	1:34-42 9	AAAPSPVAA	1.462743	-0.118314	-4.600097	1.344429	-3.255668	39819.575602
HLA A*2403	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.346247	1.090544	-3.255703	22194.558990
HLA B*1801	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-4.384412	1.128647	-3.255765	24233.243952
HLA A*2601	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.399798	1.143950	-3.255848	25107.202860
HLA A*0212	1:53-61 9	ETMAVVSAA	1.064440	-0.244060	-4.076352	0.820380	-3.255972	11922.073084
HLA B*0801	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.346108	1.090014	-3.256094	22187.475984
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HLA B*5401      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.379797       1.123686        -3.256111       23977.128223
HLA A*2403      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.346554       1.090014        -3.256540       22210.293748
HLA B*2705      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.384583       1.128011        -3.256572       24242.816081
HLA A*0301      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.367904       1.111207        -3.256697       23329.427031
HLA B*0801      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -3.857469       0.600711        -3.256759       7202.264358
HLA B*1801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -3.705199       0.448362        -3.256837       5072.229961
HLA B*3501      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.346890       1.090014        -3.256876       22227.482594
HLA A*0201      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.347421       1.090544        -3.256878       22254.675311
HLA B*4002      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.502262       1.245153        -3.257109       31787.891502
HLA B*0702      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.367899       1.110748        -3.257151       23329.174613
HLA B*0801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.327622       1.070235        -3.257388       21262.883140
HLA B*4402      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.407173       1.149444        -3.257729       25537.205130
HLA B*0702      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.021933       0.764021        -3.257912       10517.996166
HLA A*3001      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.289051       1.031086        -3.257965       19455.870058
HLA A*2403      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.415176       1.157030        -3.258146       26012.117729
HLA B*3901      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.318494       1.060336        -3.258159       20820.655727
HLA A*0206      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.542518       1.284273        -3.258244       34875.287626
HLA A*2301      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.382137       1.123686        -3.258451       24106.671667
HLA B*0801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.352736       1.094281        -3.258455       22528.682657
HLA A*0201      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.191223       0.932462        -3.258761       15531.836154
HLA B*4801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.389592       1.130830        -3.258762       24524.048635
HLA A*2601      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.329246       1.070235        -3.259011       21342.517513
HLA B*4801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.384268       1.124732        -3.259536       24225.248223
HLA A*0211      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.403713       1.143950        -3.259763       25334.513773
HLA B*1801      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.409337       1.149444        -3.259893       25664.761969
HLA B*4402      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.388676       1.128647        -3.260029       24472.360951
HLA A*0101      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.306117       1.045865        -3.260252       20235.657312
HLA A*6801      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.146785       0.886414        -3.260371       14021.182470
HLA A*0101      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.331755       1.071321        -3.260434       21466.186412
HLA A*2601      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.354949       1.094281        -3.260668       22643.784464
HLA A*0211      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.418066       1.157030        -3.261036       26185.783777
HLA A*0206      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -3.864987       0.603848        -3.261139       7328.032892
HLA B*3501      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.418183       1.157030        -3.261153       26192.867845
HLA A*0216      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.779555       0.518215        -3.261341       6019.430942
HLA B*1517      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.025495       0.764021        -3.261474       10604.613079
HLA B*5801      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.352047       1.090544        -3.261504       22493.000785
HLA A*0212      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.216569       0.955042        -3.261527       16465.277127
HLA B*1502      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.515931       1.254367        -3.261564       32804.318946
HLA B*3801      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.556009       1.294185        -3.261823       35975.641013
HLA B*4601      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.405853       1.143950        -3.261903       25459.680802
HLA B*4001      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.392917       1.130830        -3.262086       24712.500438
HLA B*1801      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.457159       1.194858        -3.262300       28652.245155
HLA A*0203      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.068554       -0.194071       -3.262626       1170.992962
HLA A*3002      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.407110       1.143950        -3.263160       25533.475259
HLA B*5801      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.353236       1.090014        -3.263222       22554.657564
HLA B*1517      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.083969       0.820380        -3.263589       12133.017114
HLA A*2902      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.353636       1.090014        -3.263622       22575.410199
HLA B*1509      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.317099       1.053156        -3.263943       20753.856474
HLA B*4501      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.197073       0.932973        -3.264100       15742.475213
HLA B*4002      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.093729       0.829467        -3.264262       12408.765314
HLA B*1503      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.197313       0.932973        -3.264340       15751.164445
HLA A*0101      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.375343       1.110748        -3.264595       23732.448231
HLA B*1503      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.076361       0.811766        -3.264595       11922.331075
HLA A*2603      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.558840       1.294185        -3.264655       36210.929289
HLA B*5701      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.421945       1.157030        -3.264915       26420.715661
HLA B*4601      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.389679       1.124732        -3.264947       24528.958005
HLA B*4601      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.365580       1.100579        -3.265002       23204.939049
HLA A*3001      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -3.971588       0.706535        -3.265054       9366.735216
HLA A*0202      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.414560       1.149444        -3.265116       25975.274505
HLA A*2601      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.375909       1.110748        -3.265161       23763.410380
HLA B*5401      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.370481       1.105200        -3.265281       23468.290623
HLA B*5301      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.600604       1.335319        -3.265285       39866.133408
HLA B*2705      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.338047       1.072739        -3.265308       21779.445438
HLA A*3001      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.259468       0.994120        -3.265348       18174.743542
HLA B*5801      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.311225       1.045865        -3.265360       20475.055917
HLA B*5401      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.394127       1.128647        -3.265480       24781.447762
HLA A*3001      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.305060       1.039542        -3.265519       20186.454529
HLA A*0216      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.359803       1.094281        -3.265522       22898.289848
HLA A*0212      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.360012       1.094281        -3.265731       22909.317574
HLA B*2705      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -3.862859       0.596633        -3.266226       7292.203447
HLA A*3101      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.267727       1.001469        -3.266258       18523.657023
HLA B*4601      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.356904       1.090544        -3.266360       22745.934484
HLA A*3001      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.086741       0.820380        -3.266361       12210.718026
HLA B*3501      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.360849       1.094281        -3.266567       22953.481614
HLA A*0211      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.377842       1.111207        -3.266635       23869.449018
HLA A*2601      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.379116       1.111207        -3.267908       23939.540770
HLA B*4402      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.393053       1.124732        -3.268321       24720.255784
HLA B*1517      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.428627       1.160079        -3.268548       26830.360781
HLA A*2602      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.603992       1.335319        -3.268673       40178.347731
HLA B*5101      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.396721       1.128011        -3.268709       24929.898266
HLA A*1101      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.412901       1.143950        -3.268951       25876.254235
HLA A*0219      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.341945       1.072739        -3.269205       21975.795898
HLA A*2902      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.400501       1.130830        -3.269671       25147.848052
HLA A*0216      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.426763       1.157030        -3.269734       26715.503951
HLA A*2402      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.464764       1.194858        -3.269905       29158.416918
HLA B*1509      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.360459       1.090544        -3.269915       22932.877685
HLA A*3201      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.264254       0.994120        -3.270134       18376.135829
HLA A*3002      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.518445       1.248280        -3.270165       32994.760076
HLA A*2301      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.454539       1.184095        -3.270444       28479.934271
HLA A*0202      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.271937       1.001469        -3.270468       18704.108292
HLA A*0219      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.427736       1.157030        -3.270706       26775.405563
HLA B*3901      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.091266       0.820380        -3.270886       12338.612084
HLA B*1501      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.311075       1.039542        -3.271533       20467.968006
HLA A*2501      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.428605       1.157030        -3.271576       26829.054470
HLA A*2501      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.396316       1.124732        -3.271585       24906.711761
HLA A*1101      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.491475       1.219814        -3.271661       31008.105741
HLA A*3001      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.206654       0.934977        -3.271677       16093.637617
HLA A*0206      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -3.928165       0.656423        -3.271742       8475.494800
HLA A*2403      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.399765       1.128011        -3.271754       25105.301351
HLA A*1101      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.429240       1.157030        -3.272210       26868.271501
HLA B*4601      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.383514       1.111207        -3.272307       24183.215783
HLA B*4001      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.363074       1.090544        -3.272530       23071.377831
HLA B*0801      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.363104       1.090544        -3.272560       23073.000465
HLA A*0201      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.312141       1.039542        -3.272600       20518.300957
HLA B*3501      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.432830       1.160079        -3.272751       27091.293493
HLA B*4601      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.345565       1.072739        -3.272826       22159.765960
HLA B*0802      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.396551       1.123686        -3.272865       24920.189662
HLA B*5301      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.580485       1.307494        -3.272991       38061.462831
HLA A*3301      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.545039       1.271968        -3.273071       35078.320795
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HLA B*5401      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.433192       1.160079        -3.273113       27113.873276
HLA A*2301      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.493045       1.219814        -3.273231       31120.365739
HLA A*2902      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.367718       1.094281        -3.273437       23319.458602
HLA A*2603      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.557768       1.284273        -3.273495       36121.710298
HLA B*0802      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.364305       1.090544        -3.273761       23136.872944
HLA A*0219      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.364079       1.090014        -3.274065       23124.859943
HLA A*2902      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.344748       1.070235        -3.274513       22118.086313
HLA B*3801      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.402535       1.128011        -3.274524       25265.941230
HLA A*2603      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.424151       1.149444        -3.274707       26555.271356
HLA A*0211      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.385603       1.110748        -3.274855       24299.802465
HLA B*5701      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.402925       1.128011        -3.274914       25288.641288
HLA A*2402      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.494917       1.219814        -3.275103       31254.836538
HLA A*2301      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.470198       1.194858        -3.275340       29525.570655
HLA A*2601      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.348650       1.072739        -3.275911       22317.731229
HLA B*2705      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.433065       1.157030        -3.276035       27105.953548
HLA B*1503      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.337039       1.060336        -3.276703       21728.957386
HLA A*3301      1:204-212       9       ASTALAFTV       1.108485        0.186630        -4.572105       1.295115        -3.276990       37334.029188
HLA A*2902      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.434033       1.157030        -3.277003       27166.436691
HLA B*4402      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.421038       1.143950        -3.277088       26365.601033
HLA B*3501      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.405103       1.128011        -3.277092       25415.781531
HLA A*2403      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.407967       1.130830        -3.277137       25583.943714
HLA A*2603      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.401034       1.123686        -3.277348       25178.749708
HLA A*0212      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.024052       0.746698        -3.277354       10569.446472
HLA A*0101      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.382800       1.105200        -3.277600       24143.476601
HLA B*2705      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.408473       1.130830        -3.277642       25613.718381
HLA B*4403      1:79-87 9       KPEVRRQSR       0.893674        0.499695        -4.671122       1.393369        -3.277752       46894.462092
HLA A*0211      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.562115       1.284273        -3.277841       36485.042161
HLA B*1501      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.323894       1.045865        -3.278028       21081.112196
HLA A*2301      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.427492       1.149444        -3.278047       26760.345195
HLA B*4001      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.383411       1.105200        -3.278211       24177.460014
HLA A*6802      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.422309       1.143950        -3.278359       26442.879589
HLA B*4001      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.350046       1.071321        -3.278724       22389.564036
HLA B*4501      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.523926       1.245153        -3.278774       33413.834963
HLA B*4402      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.390017       1.111207        -3.278810       24548.074098
HLA B*3901      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.463227       1.184095        -3.279132       29055.434758
HLA A*3201      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -3.844274       0.565014        -3.279260       6986.736272
HLA B*3501      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.211724       0.932462        -3.279262       16282.624466
HLA B*0803      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.474312       1.194858        -3.279454       29806.586890
HLA B*4601      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.390548       1.110748        -3.279800       24578.105786
HLA A*2301      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.528367       1.248280        -3.280087       33757.233664
HLA B*1509      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.351824       1.071321        -3.280503       22481.443714
HLA B*0802      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.408571       1.128011        -3.280560       25619.538872
HLA A*0101      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.370695       1.090014        -3.280681       23479.846905
HLA B*4402      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.386035       1.105200        -3.280835       24324.003008
HLA A*8001      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.375176       1.094281        -3.280894       23723.334298
HLA A*2403      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.386178       1.105200        -3.280978       24332.031332
HLA A*0201      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.101496       0.820380        -3.281116       12632.693764
HLA B*5701      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.352440       1.071321        -3.281118       22513.331302
HLA B*0803      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.404838       1.123686        -3.281152       25400.249167
HLA A*0301      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.234009       0.952818        -3.281192       17139.938997
HLA A*3201      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.409283       1.128011        -3.281272       25661.568767
HLA A*3201      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.535937       1.254367        -3.281570       34350.802745
HLA A*1101      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.311535       1.029850        -3.281685       20489.682486
HLA B*4501      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.477179       1.194858        -3.282320       30003.962924
HLA B*1509      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.168931       0.886414        -3.282517       14754.717095
HLA A*3002      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.217979       0.934977        -3.283002       16518.809155
HLA B*1509      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.411259       1.128011        -3.283248       25778.587636
HLA B*4801      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.411482       1.128011        -3.283471       25791.839674
HLA B*5401      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -3.974041       0.690533        -3.283508       9419.787504
HLA A*3101      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.394733       1.111207        -3.283525       24816.060652
HLA A*2603      1:34-42 9       AAAPSPVAA       1.462743        -0.118314       -4.628081       1.344429        -3.283653       42469.910214
HLA A*0216      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.427696       1.143950        -3.283746       26772.943193
HLA B*5401      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.568588       1.284273        -3.284314       37032.896690
HLA B*4403      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.441436       1.157030        -3.284406       27633.500610
HLA B*1502      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.529676       1.245153        -3.284523       33859.108027
HLA B*4403      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.568867       1.284273        -3.284594       37056.745286
HLA B*5701      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.395858       1.111207        -3.284651       24880.450818
HLA B*4801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.379243       1.094281        -3.284961       23946.535345
HLA A*1101      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.415890       1.130830        -3.285060       26054.932619
HLA A*2603      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.620422       1.335319        -3.285103       41727.466942
HLA A*0212      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.375780       1.090544        -3.285236       23756.340774
HLA A*6901      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.787746       0.502462        -3.285284       6134.027817
HLA B*4001      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.375361       1.090014        -3.285347       23733.475373
HLA B*1503      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.338510       1.053156        -3.285354       21802.669215
HLA A*0301      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.358917       1.072739        -3.286178       22851.635732
HLA B*4801      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.430292       1.143950        -3.286342       26933.469235
HLA A*2501      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.359371       1.072739        -3.286632       22875.507782
HLA B*1509      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.359425       1.072739        -3.286686       22878.354300
HLA A*6901      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.316594       1.029850        -3.286743       20729.731154
HLA A*6801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.357078       1.070235        -3.286843       22755.042228
HLA A*0219      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.381153       1.094281        -3.286872       24052.089909
HLA B*4403      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.622407       1.335319        -3.287088       41918.654722
HLA A*2601      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.392564       1.105200        -3.287364       24692.454789
HLA A*1101      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.447592       1.160079        -3.287513       28027.964290
HLA A*0219      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.437367       1.149444        -3.287922       27375.785968
HLA A*6802      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.377988       1.090014        -3.287974       23877.456487
HLA A*3201      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.582302       1.294185        -3.288117       38220.963213
HLA B*3801      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.432104       1.143950        -3.288154       27046.044008
HLA B*5401      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.508328       1.219814        -3.288514       32235.031006
HLA B*1801      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.445768       1.157030        -3.288739       27910.547458
HLA B*1509      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.473013       1.184095        -3.288918       29717.548709
HLA B*2705      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.241805       0.952818        -3.288987       17450.378976
HLA B*0803      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.473257       1.184095        -3.289162       29734.273353
HLA A*0301      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.360496       1.071321        -3.289175       22934.862801
HLA A*2501      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.417311       1.128011        -3.289300       26140.349676
HLA B*7301      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.597197       1.307749        -3.289448       39554.633287
HLA A*2403      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.319425       1.029850        -3.289574       20865.307965
HLA B*3901      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.439077       1.149444        -3.289633       27483.815336
HLA B*1509      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.400842       1.111207        -3.289634       25167.582617
HLA B*0802      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.446739       1.157030        -3.289709       27972.977270
HLA B*5301      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.473910       1.184095        -3.289815       29779.025833
HLA A*0250      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.446856       1.157030        -3.289827       27980.544829
HLA A*3301      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.625293       1.335319        -3.289973       42198.061831
HLA B*5801      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.113135       0.822896        -3.290239       12975.835076
HLA A*0211      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.439702       1.149444        -3.290258       27523.393855
HLA B*4601      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.360881       1.070235        -3.290647       22955.220141
HLA A*6802      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.363405       1.072739        -3.290666       23088.983262
HLA A*2602      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.598161       1.307494        -3.290666       39642.464993
HLA A*0219      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.330341       1.039542        -3.290799       21396.390055
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HLA A*3201      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.573134       1.282277        -3.290857       37422.598236
HLA B*3901      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.415707       1.124732        -3.290975       26043.940503
HLA B*0802      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.451099       1.160079        -3.291020       28255.261864
HLA A*8001      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.448571       1.157030        -3.291542       28091.264615
HLA A*2902      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.402789       1.111207        -3.291582       25280.707625
HLA B*3901      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.422419       1.130830        -3.291589       26449.603937
HLA A*0219      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.321474       1.029850        -3.291623       20963.970991
HLA A*0211      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.285832       0.994120        -3.291712       19312.204989
HLA A*0219      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.436126       1.143950        -3.292176       27297.700761
HLA B*5701      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.403452       1.110748        -3.292704       25319.305022
HLA A*2601      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.364034       1.071321        -3.292713       23122.483110
HLA A*0203      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.123248       0.830057        -3.293190       13281.511432
HLA B*3801      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.453320       1.160079        -3.293241       28400.082388
HLA A*0201      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.116472       0.822896        -3.293575       13075.899853
HLA A*2902      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.228584       0.934977        -3.293608       16927.168252
HLA A*2601      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.383991       1.090014        -3.293977       24209.788561
HLA A*2602      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.588189       1.294185        -3.294004       38742.660154
HLA A*2602      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.549157       1.254367        -3.294791       35412.569728
HLA B*7301      1:125-133       9       LTAPDVRTV       1.116550        0.155418        -4.567211       1.271968        -3.295243       36915.681081
HLA A*3001      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -3.921323       0.625647        -3.295676       8343.021474
HLA B*4801      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.368553       1.072739        -3.295813       23364.286903
HLA B*4501      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.610105       1.314292        -3.295814       40747.918898
HLA B*2705      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.401264       1.105200        -3.296064       25192.102243
HLA A*2601      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.386890       1.090544        -3.296347       24371.949018
HLA A*2603      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.407606       1.111207        -3.296398       25562.638021
HLA A*8001      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.427325       1.130830        -3.296495       26750.068463
HLA A*6901      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.214365       0.917388        -3.296977       16381.936108
HLA A*0201      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.252312       0.955042        -3.297270       17877.704726
HLA A*3001      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.265069       0.967740        -3.297330       18410.664489
HLA B*0802      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.370185       1.072739        -3.297446       23452.299007
HLA A*0216      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.343319       1.045865        -3.297454       22045.454740
HLA A*0219      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.252537       0.955042        -3.297496       17886.991912
HLA A*0211      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.010359       0.712665        -3.297694       10241.402742
HLA B*0702      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.403137       1.105200        -3.297937       25300.957073
HLA B*4402      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.426000       1.128011        -3.297989       26668.573647
HLA A*2501      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.458416       1.160079        -3.298337       28735.293206
HLA A*0201      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.388615       1.090014        -3.298601       24468.918982
HLA A*0203      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.011346       0.712622        -3.298724       10264.699237
HLA A*8001      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.389414       1.090544        -3.298870       24513.967607
HLA B*4601      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.359289       1.060336        -3.298953       22871.176803
HLA B*4402      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.423117       1.123686        -3.299431       26492.135656
HLA A*3101      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.359773       1.060336        -3.299437       22896.679501
HLA A*0250      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.329293       1.029850        -3.299442       21344.826851
HLA A*0203      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.330705       1.031086        -3.299619       21414.339155
HLA A*6901      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -3.110953       -0.189096       -3.300049       1291.079815
HLA B*1501      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.135305       0.834848        -3.300457       13655.419848
HLA A*1101      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.301992       1.001469        -3.300523       20044.333521
HLA A*0101      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.373416       1.072739        -3.300677       23627.401673
HLA A*1101      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.371017       1.070235        -3.300783       23497.255557
HLA B*5801      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.341026       1.039542        -3.301484       21929.360359
HLA B*5701      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.362338       1.060336        -3.302002       23032.344232
HLA B*5301      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.556370       1.254367        -3.302004       36005.625633
HLA B*1517      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.234672       0.932462        -3.302210       17166.107451
HLA B*4002      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.616646       1.314292        -3.302355       41366.273529
HLA A*2403      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.355541       1.053156        -3.302385       22674.675608
HLA A*2902      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.348326       1.045865        -3.302461       22301.075816
HLA A*2402      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.550755       1.248280        -3.302475       35543.082733
HLA B*5701      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.392618       1.090014        -3.302604       24695.527399
HLA A*8001      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.446781       1.143950        -3.302831       27975.701356
HLA A*3101      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.392945       1.090014        -3.302931       24714.104792
HLA B*5101      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.403539       1.100579        -3.302960       25324.373591
HLA A*6802      1:11-19 9       ELATPYALN       0.932404        -0.621088       -3.614467       0.311316        -3.303151       4115.916193
HLA B*2705      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.373545       1.070235        -3.303311       23634.432908
HLA B*1801      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.463505       1.160079        -3.303426       29073.988707
HLA B*1517      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.460800       1.157030        -3.303771       28893.513778
HLA B*4002      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.586101       1.282277        -3.303824       38556.778882
HLA B*2705      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.415086       1.110748        -3.304338       26006.770817
HLA B*3801      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.558807       1.254367        -3.304440       36208.186833
HLA A*3101      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.374687       1.070235        -3.304452       23696.654465
HLA A*0211      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.127368       0.822896        -3.304472       13408.138801
HLA B*1502      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.259536       0.955042        -3.304495       18177.595142
HLA A*3201      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.822828       0.518215        -3.304613       6650.101151
HLA B*0802      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.448764       1.143950        -3.304814       28103.728971
HLA B*4402      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.334859       1.029850        -3.305008       21620.143198
HLA B*4501      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.375585       1.070235        -3.305350       23745.676077
HLA B*4601      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.395574       1.090014        -3.305560       24864.169490
HLA B*1801      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.335460       1.029850        -3.305610       21650.106362
HLA A*1101      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.433835       1.128011        -3.305824       27154.094234
HLA A*3301      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.560360       1.254367        -3.305993       36337.896797
HLA A*0101      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.376308       1.070235        -3.306074       23785.275194
HLA B*3901      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.192515       0.886414        -3.306101       15578.119008
HLA A*6802      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.258998       0.952818        -3.306181       18155.089507
HLA A*6901      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.359514       1.053156        -3.306358       22883.058019
HLA B*3501      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.431422       1.124732        -3.306691       27003.645607
HLA B*5401      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.401504       1.094281        -3.307223       25206.007300
HLA B*4801      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.412737       1.105200        -3.307537       25866.456953
HLA B*0801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.360724       1.053156        -3.307568       22946.901240
HLA B*5701      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.377873       1.070235        -3.307638       23871.127781
HLA A*2402      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.592167       1.284273        -3.307894       39099.131904
HLA A*0301      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.353887       1.045865        -3.308022       22588.481942
HLA B*3901      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.452032       1.143950        -3.308082       28316.011638
HLA B*4002      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.640585       1.332502        -3.308084       43710.452461
HLA A*2902      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.413329       1.105200        -3.308129       25901.744537
HLA A*6802      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.302459       0.994120        -3.308339       20065.924228
HLA B*5801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.361596       1.053156        -3.308440       22993.003501
HLA A*0201      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.354378       1.045865        -3.308513       22614.036433
HLA A*0101      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.261376       0.952818        -3.308558       18254.757716
HLA A*2902      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.452920       1.143950        -3.308970       28373.975375
HLA B*5301      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.369450       1.060336        -3.309114       23412.620942
HLA A*3101      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.380488       1.071321        -3.309167       24015.294366
HLA A*2501      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.420471       1.111207        -3.309264       26331.248402
HLA B*2705      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.380897       1.071321        -3.309575       24037.911103
HLA A*2403      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.379976       1.070235        -3.309741       23986.988484
HLA A*8001      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.420977       1.111207        -3.309769       26361.892784
HLA A*3002      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.415063       1.105200        -3.309863       26005.363917
HLA A*2602      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.558276       1.248280        -3.309996       36163.944490
HLA B*4801      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.410590       1.100579        -3.310011       25738.872360
HLA A*0212      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.304184       0.994120        -3.310064       20145.761583
HLA B*0803      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.438304       1.128011        -3.310293       27434.941677
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HLA A*1101      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.421122       1.110748        -3.310374       26370.736392
HLA B*4402      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.380810       1.070235        -3.310575       24033.100015
HLA B*5301      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.383493       1.072739        -3.310754       24182.038355
HLA A*0211      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.211840       -0.098967       -3.310807       1628.695803
HLA A*2403      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.371278       1.060336        -3.310942       23511.369842
HLA B*7301      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.468018       1.157030        -3.310988       29377.712618
HLA B*5301      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.605200       1.294185        -3.311015       40290.226457
HLA B*0801      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.279063       0.967740        -3.311323       19013.540596
HLA B*5801      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.341277       1.029850        -3.311427       21942.058023
HLA B*0801      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.357348       1.045865        -3.311483       22769.203392
HLA A*0219      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -3.876848       0.565014        -3.311833       7530.912650
HLA A*2603      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.440484       1.128647        -3.311837       27573.021748
HLA B*1801      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.383359       1.071321        -3.312038       24174.582642
HLA B*5801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.343303       1.031086        -3.312217       22044.619912
HLA B*4001      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.382454       1.070235        -3.312220       24124.284044
HLA B*3901      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.423119       1.110748        -3.312371       26492.278976
HLA A*6802      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.342353       1.029850        -3.312503       21996.491909
HLA A*6802      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.230222       0.917388        -3.312834       16991.115890
HLA B*5101      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.473102       1.160079        -3.313023       29723.658546
HLA B*0801      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.352729       1.039542        -3.313187       22528.317026
HLA A*0201      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.385953       1.072739        -3.313214       24319.397788
HLA A*3002      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.414398       1.100579        -3.313820       25965.580203
HLA B*3501      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.191571       0.877544        -3.314026       15544.276910
HLA B*4002      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.598875       1.284273        -3.314601       39707.714881
HLA B*5401      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.360567       1.045865        -3.314702       22938.585355
HLA B*1509      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.425457       1.110748        -3.314709       26635.267163
HLA B*2705      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.404763       1.090014        -3.314749       25395.852347
HLA B*7301      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.569170       1.254367        -3.314804       37082.615314
HLA A*2602      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.464268       1.149444        -3.314824       29125.151965
HLA B*4402      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.110156       0.795128        -3.315028       12887.128827
HLA A*0211      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.833265       0.518215        -3.315050       6811.843530
HLA B*7301      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.560386       1.245153        -3.315233       36340.059285
HLA B*0801      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.270321       0.955042        -3.315279       18634.620928
HLA A*0101      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.368480       1.053156        -3.315324       23360.368887
HLA B*4002      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.569800       1.254367        -3.315433       37136.418549
HLA B*4801      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.405524       1.090014        -3.315510       25440.405336
HLA A*0301      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.368710       1.053156        -3.315554       23372.757117
HLA B*4801      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.388201       1.071321        -3.316880       24445.632221
HLA A*0250      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.601206       1.284273        -3.316932       39921.383527
HLA A*3001      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.147081       0.830057        -3.317023       14030.743211
HLA B*7301      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.611377       1.294185        -3.317191       40867.352562
HLA B*0803      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.390189       1.072739        -3.317450       24557.770585
HLA B*4601      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.272581       0.955042        -3.317539       18731.854131
HLA A*3002      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.388225       1.070235        -3.317990       24446.954738
HLA A*2602      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.602296       1.284273        -3.318022       40021.719606
HLA A*6802      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.408614       1.090544        -3.318070       25622.033773
HLA B*0803      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.446783       1.128647        -3.318136       27975.852701
HLA A*0250      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.502370       1.184095        -3.318275       31795.803059
HLA A*2602      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.250815       0.932462        -3.318353       17816.202411
HLA B*5701      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.153387       0.834848        -3.318538       14235.957869
HLA B*4402      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.391502       1.072739        -3.318763       24632.148835
HLA B*5801      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.352233       1.033072        -3.319162       22502.615926
HLA B*5701      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.409856       1.090544        -3.319313       25695.464736
HLA B*1801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.389832       1.070235        -3.319597       24537.584953
HLA A*0202      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.603978       1.284273        -3.319704       40177.043589
HLA A*0212      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.365618       1.045865        -3.319753       23206.947714
HLA A*0203      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.313882       0.994120        -3.319763       20600.718325
HLA B*3801      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.504061       1.184095        -3.319966       31919.893049
HLA B*0802      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.444742       1.124732        -3.320010       27844.641466
HLA A*8001      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.431465       1.110748        -3.320717       27006.275296
HLA A*0101      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.350579       1.029850        -3.320728       22417.076314
HLA A*0212      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.360350       1.039542        -3.320809       22927.171437
HLA A*0219      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.411478       1.090544        -3.320934       25791.560614
HLA B*4801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.431704       1.110748        -3.320956       27021.181706
HLA B*4501      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.653627       1.332502        -3.321126       45042.998460
HLA B*5301      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.569457       1.248280        -3.321177       37107.098159
HLA B*5301      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.605503       1.284273        -3.321229       40318.353841
HLA B*5101      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.426646       1.105200        -3.321446       26708.278532
HLA B*5101      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.479030       1.157030        -3.322000       30132.142618
HLA A*3301      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.629841       1.307494        -3.322347       42642.347710
HLA B*5301      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.316561       0.994120        -3.322441       20728.161176
HLA B*1503      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.086281       0.763535        -3.322746       12197.777396
HLA A*6802      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.013282       0.690533        -3.322749       10310.558825
HLA A*0211      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.395729       1.072739        -3.322990       24873.048893
HLA A*2403      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.394559       1.071321        -3.323238       24806.127983
HLA A*2902      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.394719       1.071321        -3.323397       24815.255153
HLA A*0206      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -3.888642       0.565014        -3.323628       7738.236969
HLA B*3801      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.447444       1.123686        -3.323757       28018.413343
HLA B*0803      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.480957       1.157030        -3.323927       30266.109015
HLA B*1503      1:58-66 9       VSAATTAEP       0.530485        0.115863        -3.970601       0.646348        -3.324253       9345.476717
HLA A*0216      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.318419       0.994120        -3.324299       20817.051641
HLA A*3101      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.370174       1.045865        -3.324309       23451.664644
HLA B*4002      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.453477       1.128647        -3.324830       28410.378221
HLA B*7301      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -3.908213       0.583145        -3.325068       8094.932563
HLA B*1501      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.326654       1.001469        -3.325185       21215.543622
HLA A*2603      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.385532       1.060336        -3.325197       24295.859008
HLA B*3901      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.280423       0.955042        -3.325382       19073.190572
HLA B*0803      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.436641       1.111207        -3.325433       27330.061307
HLA B*3501      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.242907       0.917388        -3.325519       17494.710958
HLA B*4001      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.379036       1.053156        -3.325880       23935.137826
HLA B*4001      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.398856       1.072739        -3.326117       25052.795196
HLA B*1501      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.359272       1.033072        -3.326201       22870.310706
HLA A*3101      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.281380       0.955042        -3.326338       19115.232666
HLA A*6901      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.294079       0.967740        -3.326339       19682.422721
HLA B*1509      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.420666       1.094281        -3.326385       26343.074335
HLA A*6801      1:49-57 9       RAVRETMAV       0.926962        0.318191        -4.571962       1.245153        -3.326809       37321.710870
HLA B*4402      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.421101       1.094281        -3.326820       26369.452459
HLA A*0203      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.294664       0.967740        -3.326924       19708.954038
HLA B*4002      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.634735       1.307749        -3.326986       43125.593444
HLA B*3801      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.399742       1.072739        -3.327003       25103.943219
HLA B*3801      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.521950       1.194858        -3.327092       33262.156786
HLA B*1801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.438076       1.110748        -3.327328       27420.548715
HLA B*5301      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.458279       1.130830        -3.327449       28726.278245
HLA B*0803      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.358668       1.031086        -3.327582       22838.535258
HLA A*2301      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.455723       1.128011        -3.327712       28557.693167
HLA B*3901      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.428314       1.100579        -3.327736       26811.062871
HLA B*3901      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.157761       0.829467        -3.328294       14380.084403
HLA A*3002      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.163189       0.834848        -3.328340       14560.917642
HLA A*6901      1:5-13  9       TDFELLELA       1.003059        -0.335657       -3.995793       0.667402        -3.328391       9903.589667
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HLA A*1101      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.439655       1.111207        -3.328448       27520.416046
HLA A*0211      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.261479       0.932973        -3.328507       18259.103506
HLA B*0702      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.374483       1.045865        -3.328618       23685.504013
HLA B*5101      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.388967       1.060336        -3.328631       24488.783161
HLA A*0201      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.322792       0.994120        -3.328672       21027.692195
HLA B*5701      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.374574       1.045865        -3.328709       23690.501843
HLA B*1503      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.035457       0.706535        -3.328922       10850.672206
HLA A*2402      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.401748       1.072739        -3.329009       25220.192907
HLA A*0301      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.368668       1.039542        -3.329126       23370.481236
HLA B*3901      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.330658       1.001469        -3.329189       21412.022296
HLA A*3001      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.216184       0.886414        -3.329770       16450.675252
HLA A*2601      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.375700       1.045865        -3.329835       23751.971524
HLA A*2501      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.474362       1.143950        -3.330412       29809.973339
HLA A*0203      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -3.895700       0.565014        -3.330686       7865.020845
HLA B*4403      1:47-55 9       EVRAVRETM       1.250113        0.064179        -4.645209       1.314292        -3.330917       44178.309002
HLA B*1502      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.615317       1.284273        -3.331043       41239.803837
HLA A*3301      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.613451       1.282277        -3.331174       41063.040152
HLA A*0101      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.371118       1.039542        -3.331577       23502.722247
HLA B*1801      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.459879       1.128011        -3.331868       28832.304906
HLA B*3901      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.402115       1.070235        -3.331880       25241.486289
HLA B*0802      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.462725       1.130830        -3.331894       29021.816272
HLA B*5701      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.333395       1.001469        -3.331926       21547.398170
HLA A*3002      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.616306       1.284273        -3.332032       41333.837145
HLA B*0702      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.422288       1.090014        -3.332274       26441.592143
HLA A*8001      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.403651       1.071321        -3.332330       25330.950543
HLA A*2601      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.385666       1.053156        -3.332510       24303.352124
HLA B*4402      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.378453       1.045865        -3.332588       23903.046720
HLA B*0802      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.461383       1.128647        -3.332736       28932.304850
HLA A*1101      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.422920       1.090014        -3.332906       26480.099551
HLA B*4403      1:160-168       9       VAPPSRGTV       1.092400        0.240102        -4.665408       1.332502        -3.332906       46281.519708
HLA B*3901      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.405811       1.072739        -3.333072       25457.201710
HLA A*2403      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.334783       1.001469        -3.333315       21616.400720
HLA A*2602      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.528219       1.194858        -3.333360       33745.730382
HLA A*0301      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.366501       1.033072        -3.333430       23254.201435
HLA B*1502      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.444467       1.110748        -3.333719       27827.022581
HLA B*3901      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.386923       1.053156        -3.333767       24373.794982
HLA A*6802      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.387001       1.053156        -3.333845       24378.146734
HLA B*4402      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.424611       1.090544        -3.334068       26583.443860
HLA B*1503      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.220502       0.886414        -3.334088       16615.066453
HLA A*2501      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.404361       1.070235        -3.334126       25372.369735
HLA B*5801      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.335627       1.001469        -3.334158       21658.423811
HLA B*5101      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.445627       1.111207        -3.334420       27901.489350
HLA B*1801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.465575       1.130830        -3.334744       29212.889349
HLA B*4402      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.424867       1.090014        -3.334853       26599.124153
HLA B*1517      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.445759       1.110748        -3.335011       27909.943492
HLA B*1501      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.207946       0.872785        -3.335161       16141.594565
HLA B*7301      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.619618       1.284273        -3.335345       41650.334906
HLA A*2403      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.408181       1.072739        -3.335442       25596.541788
HLA B*3801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.460394       1.124732        -3.335662       28866.484677
HLA A*0301      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.366992       1.031086        -3.335906       23280.509059
HLA B*1502      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.585036       1.248280        -3.336756       38462.404252
HLA A*0201      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.390086       1.053156        -3.336930       24551.925668
HLA A*8001      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.427123       1.090014        -3.337109       26737.625876
HLA B*3901      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.428023       1.090544        -3.337479       26793.083337
HLA A*2902      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.331720       0.994120        -3.337600       21464.444537
HLA A*6801      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.442813       1.105200        -3.337613       27721.243203
HLA A*3301      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.645468       1.307749        -3.337718       44204.606799
HLA B*4501      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.449018       1.111207        -3.337810       28120.153879
HLA A*0219      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.383756       1.045865        -3.337891       24196.694875
HLA A*2501      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.468904       1.130830        -3.338073       29437.690434
HLA B*4801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.369448       1.031086        -3.338362       23412.494283
HLA B*1801      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.428460       1.090014        -3.338446       26820.057161
HLA A*2601      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.378465       1.039542        -3.338923       23903.693293
HLA B*0801      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.189667       0.850740        -3.338927       15476.310753
HLA B*3501      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.368792       1.029850        -3.338942       23377.183077
HLA A*0202      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.086018       0.746698        -3.339319       12190.388909
HLA A*8001      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.385403       1.045865        -3.339538       24288.630999
HLA A*0250      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -3.700735       0.360868        -3.339867       5020.360611
HLA B*7301      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.169636       0.829467        -3.340169       14778.682953
HLA A*3201      1:23-31 9       DDERADIDR       0.950475        0.333798        -4.624576       1.284273        -3.340302       42128.491758
HLA A*8001      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.446069       1.105200        -3.340869       27929.881251
HLA B*0801      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.152884       0.811766        -3.341118       14219.486205
HLA A*0206      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.038323       0.697019        -3.341304       10922.524198
HLA B*0802      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.441981       1.100579        -3.341402       27668.205032
HLA A*0301      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.343763       1.001469        -3.342294       22068.007063
HLA B*1509      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.499607       1.157030        -3.342577       31594.159329
HLA B*5401      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.453331       1.110748        -3.342583       28400.850605
HLA B*4403      1:178-186       9       KGPRSAGTM       1.184612        0.123137        -4.650352       1.307749        -3.342603       44704.589486
HLA A*1101      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.414013       1.071321        -3.342691       25942.553190
HLA B*4601      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.344240       1.001469        -3.342771       22092.255626
HLA A*6802      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.106317       0.763535        -3.342782       12773.711744
HLA B*3801      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.472085       1.128647        -3.343438       29654.112897
HLA A*0216      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.396880       1.053156        -3.343724       24939.070976
HLA B*1502      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.173202       0.829467        -3.343735       14900.548334
HLA B*5301      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.563553       1.219814        -3.343739       36606.038932
HLA B*4801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.414017       1.070235        -3.343783       25942.833885
HLA B*0802      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.449603       1.105200        -3.344403       28158.059005
HLA B*1501      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.375632       1.031086        -3.344546       23748.245446
HLA A*3101      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.397938       1.053156        -3.344782       24999.857861
HLA B*1509      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.488900       1.143950        -3.344950       30824.795270
HLA B*2705      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.405313       1.060336        -3.344977       25428.021671
HLA B*1501      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.155074       0.809887        -3.345187       14291.362139
HLA A*6801      1:83-91 9       RRQSRWRTA       1.364813        -0.029494       -4.680585       1.335319        -3.345266       47927.556098
HLA B*0802      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.456907       1.111207        -3.345700       28635.664369
HLA A*6801      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.469446       1.123686        -3.345760       29474.501252
HLA A*0206      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.398927       1.053156        -3.345771       25056.861511
HLA B*5701      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.385908       1.039542        -3.346367       24316.898177
HLA B*0802      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.377563       1.031086        -3.346477       23854.087366
HLA B*1517      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.457847       1.111207        -3.346640       28697.697772
HLA B*1501      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.399928       1.053156        -3.346772       25114.674467
HLA A*8001      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.417046       1.070235        -3.346811       26124.374507
HLA B*1501      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.314620       0.967740        -3.346880       20635.742612
HLA A*0216      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.279387       0.932462        -3.346925       19027.740734
HLA B*1509      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.471949       1.124732        -3.347217       29644.809680
HLA A*0212      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.420316       1.072739        -3.347577       26321.848438
HLA B*4001      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.407960       1.060336        -3.347625       25583.528499
HLA A*2603      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.595922       1.248280        -3.347642       39438.609288
HLA B*4001      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.393539       1.045865        -3.347674       24747.954196
HLA A*0203      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.381136       1.033072        -3.348065       24051.179092
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HLA A*2402	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.473079	1.124732	-3.348347	29722.050572
HLA B*1501	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.225906	0.877544	-3.348361	16823.095028
HLA B*1502	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.479366	1.130830	-3.348536	30155.462289
HLA B*4601	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.401716	1.053156	-3.348560	25218.282841
HLA B*5401	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.492854	1.143950	-3.348904	31106.731750
HLA A*0101	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.382039	1.033072	-3.348967	24101.194883
HLA B*1509	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-4.477799	1.128647	-3.349152	30046.845521
HLA B*4501	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.656924	1.307749	-3.349174	45386.178907
HLA A*2501	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.450456	1.100579	-3.349877	28213.409844
HLA B*1503	1:70-78 9	LRTAILDAT	0.824289	-0.241144	-3.933296	0.583145	-3.350151	8576.228369
HLA B*4601	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.389792	1.039542	-3.350250	24535.328381
HLA B*5301	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.455502	1.105200	-3.350302	28543.174428
HLA B*0801	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.351845	1.001469	-3.350377	22482.538340
HLA B*0801	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.285435	0.934977	-3.350458	19294.556464
HLA A*8001	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.423204	1.072739	-3.350465	26497.439009
HLA B*1801	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.534631	1.184095	-3.350535	34247.634259
HLA B*4001	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.381858	1.031086	-3.350772	24091.157345
HLA A*0202	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.396744	1.045865	-3.350879	24931.246982
HLA B*4403	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.623169	1.271968	-3.351201	41992.194343
HLA B*0803	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.495326	1.143950	-3.351376	31284.271215
HLA B*0803	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.476829	1.124732	-3.352097	29979.787270
HLA B*4002	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.646389	1.294185	-3.352203	44298.449942
HLA B*4501	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.624252	1.271968	-3.352284	42097.051850
HLA B*5401	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.480400	1.128011	-3.352389	30227.328379
HLA B*1501	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.346627	0.994120	-3.352507	22214.018873
HLA A*2601	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.383721	1.031086	-3.352635	24194.731434
HLA B*4402	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.405930	1.053156	-3.352775	25464.226432
HLA B*5701	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.346954	0.994120	-3.352834	22230.729533
HLA B*3901	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.458049	1.105200	-3.352849	28711.052496
HLA A*0202	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-3.917940	0.565014	-3.352926	8278.279835
HLA B*0803	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.483868	1.130830	-3.353037	30469.659707
HLA A*3101	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.288743	0.934977	-3.353766	19442.086656
HLA B*4402	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.425095	1.071321	-3.353774	26613.085952
HLA A*2301	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.464592	1.110748	-3.353844	29146.903894
HLA B*5101	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.503338	1.149444	-3.353894	31866.750945
HLA B*0702	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.407086	1.053156	-3.353931	25532.093964
HLA B*0802	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.448273	1.094281	-3.353992	28071.970974
HLA B*4403	1:49-57 9	RAVRETMAV	0.926962	0.318191	-4.599178	1.245153	-3.354025	39735.435602
HLA B*5101	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-4.424315	1.070235	-3.354081	26565.329536
HLA B*4601	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.399953	1.045865	-3.354088	25116.169055
HLA A*0101	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.385222	1.031086	-3.354136	24278.515398
HLA B*4501	1:23-31 9	DDERADIDR	0.950475	0.333798	-4.638807	1.284273	-3.354533	43531.811695
HLA A*6901	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.387651	1.033072	-3.354580	24414.705731
HLA B*5401	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-4.425060	1.070235	-3.354825	26610.926432
HLA A*0216	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.287798	0.932973	-3.354826	19399.850427
HLA B*1517	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.061489	0.706535	-3.354954	11520.967133
HLA B*1517	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.356822	1.001469	-3.355353	22741.628037
HLA A*6801	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.610075	1.254367	-3.355708	40745.053257
HLA A*2603	1:33-41 9	VAAAPSPVA	1.399199	-0.116922	-4.638043	1.282277	-3.355766	43455.340702
HLA B*5101	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.499969	1.143950	-3.356019	31620.492115
HLA B*4501	1:152-160	9	TGLLVMNNV	1.174900	0.079467	-4.610441	1.254367	-3.356075	40779.454261
HLA B*4402	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.416562	1.060336	-3.356226	26095.276750
HLA B*5101	1:89-97 9	RTAAFASAA	1.280297	-0.151650	-4.484974	1.128647	-3.356327	30547.397158
HLA B*5301	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.067278	0.710864	-3.356414	11675.569375
HLA A*0212	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.409626	1.053156	-3.356470	25681.845405
HLA A*3101	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.387957	1.031086	-3.356871	24431.882281
HLA A*0206	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.390083	1.033072	-3.357012	24551.792845
HLA A*0202	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.290376	0.932973	-3.357403	19515.324027
HLA A*2402	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.447420	1.090014	-3.357406	28016.897619
HLA B*5701	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-4.387395	1.029850	-3.357545	24400.313162
HLA A*3002	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.488435	1.130830	-3.357605	30791.794720
HLA B*5101	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.468363	1.110748	-3.357615	29401.084645
HLA A*2403	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.397158	1.039542	-3.357616	24954.996336
HLA B*1801	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.458258	1.100579	-3.357680	28724.879625
HLA B*4002	1:125-133	9	LTAPDVRTV	1.116550	0.155418	-4.629724	1.271968	-3.357756	42630.814751
HLA A*0216	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.430499	1.072739	-3.357760	26946.294510
HLA B*5401	1:217-225	9	GSPQPTGTI	1.015707	0.168388	-4.542081	1.184095	-3.357986	34840.212388
HLA A*3001	1:82-90 9	VRRQSRWRT	1.037980	-0.242033	-4.153936	0.795947	-3.357990	14253.990780
HLA B*4501	1:173-181	9	LLGGAKGPR	0.734546	0.559639	-4.652239	1.294185	-3.358054	44899.214959
HLA B*1509	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.489058	1.130830	-3.358227	30835.970129
HLA A*0206	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.016858	0.658536	-3.358322	10395.804904
HLA A*3002	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.429933	1.071321	-3.358612	26911.185274
HLA A*2501	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.464174	1.105200	-3.358974	29118.850094
HLA A*0201	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.390088	1.031086	-3.359002	24552.058492
HLA B*2705	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.404883	1.045865	-3.359017	25402.860140
HLA B*1801	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.502988	1.143950	-3.359038	31841.074352
HLA A*3301	1:49-57 9	RAVRETMAV	0.926962	0.318191	-4.604401	1.245153	-3.359248	40216.186248
HLA B*0802	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.449370	1.090014	-3.359356	28142.982177
HLA A*3101	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.392581	1.033072	-3.359509	24693.389891
HLA A*2602	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.490404	1.130830	-3.359574	30931.705827
HLA A*1101	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.405472	1.045865	-3.359607	25437.377661
HLA A*0201	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.361100	1.001469	-3.359631	22966.772270
HLA A*0211	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-3.960724	0.600711	-3.360014	9135.329678
HLA A*0201	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.393368	1.033072	-3.360296	24738.182616
HLA A*2501	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.431775	1.071321	-3.360454	27025.567509
HLA B*5101	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.485254	1.124732	-3.360522	30567.069195
HLA B*4001	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.315640	0.955042	-3.360598	20684.250028
HLA B*1509	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.421458	1.060336	-3.361123	26391.145060
HLA A*8001	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.414323	1.053156	-3.361167	25961.085523
HLA B*1509	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.392261	1.031086	-3.361175	24675.228536
HLA B*1502	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.239458	0.877544	-3.361913	17356.323155
HLA A*0216	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.401516	1.039542	-3.361974	25206.689118
HLA B*1517	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.452013	1.090014	-3.361999	28314.786173
HLA A*2301	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.434761	1.072739	-3.362022	27212.034814
HLA B*4402	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.401603	1.039542	-3.362061	25211.735142
HLA B*3801	1:27-35 9	ADIDRRVAA	1.371750	-0.214720	-4.519347	1.157030	-3.362318	33063.374551
HLA A*6801	1:178-186	9	KGPRSAGTM	1.184612	0.123137	-4.670191	1.307749	-3.362442	46794.106866
HLA B*4601	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.356725	0.994120	-3.362605	22736.584380
HLA B*5801	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.330519	0.967740	-3.362779	21405.189024
HLA A*2601	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.396072	1.033072	-3.363001	24892.702478
HLA B*0802	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.474441	1.110748	-3.363693	29815.456977
HLA B*5701	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.416881	1.053156	-3.363726	26114.483282
HLA A*6802	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-3.780683	0.416603	-3.364080	6035.082192
HLA B*1509	1:84-92 9	RQSRWRTAA	1.066920	-0.037070	-4.394157	1.029850	-3.364307	24783.190667
HLA B*0803	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.475370	1.110748	-3.364621	29879.237935
HLA B*4002	1:40-48 9	VAAAFNDEV	1.065598	0.129260	-4.559495	1.194858	-3.364637	36265.625851
HLA B*4001	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.359909	0.994120	-3.365789	22903.865001
HLA A*2403	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.411680	1.045865	-3.365815	25803.562941
HLA A*2403	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.333851	0.967740	-3.366111	21570.024434
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HLA A*2602      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.526642       1.160079        -3.366563       33623.454247
HLA A*0101      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.187121       0.820380        -3.366741       15385.818314
HLA B*4403      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.467994       1.100579        -3.367416       29376.123359
HLA B*4801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.420742       1.053156        -3.367586       26347.635150
HLA A*3101      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.240398       0.872785        -3.367612       17393.922136
HLA B*5401      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.369147       1.001469        -3.367678       23396.287543
HLA A*8001      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.400891       1.033072        -3.367819       25170.442009
HLA B*4801      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.428596       1.060336        -3.368260       26828.473907
HLA B*1517      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.458984       1.090544        -3.368441       28772.937893
HLA A*3101      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.321295       0.952818        -3.368477       20955.353393
HLA B*1801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.399573       1.031086        -3.368487       25094.166836
HLA A*2301      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.528585       1.160079        -3.368506       33774.221866
HLA A*0211      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.025377       0.656423        -3.368954       10601.744978
HLA A*2403      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.301449       0.932462        -3.368987       20019.300076
HLA A*3002      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.441760       1.072739        -3.369021       27654.138509
HLA A*0301      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.363459       0.994120        -3.369339       23091.856344
HLA A*6801      1:148-156       9       RDRNTGLLV       1.155258        0.152236        -4.677089       1.307494        -3.369595       47543.292065
HLA A*0211      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.409253       1.039542        -3.369711       25659.764089
HLA A*0219      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.363882       0.994120        -3.369762       23114.353685
HLA B*0801      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.403050       1.033072        -3.369979       25295.893191
HLA A*0202      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.028718       0.658536        -3.370182       10683.617255
HLA B*4601      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.401344       1.031086        -3.370258       25196.736409
HLA A*2902      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.371795       1.001469        -3.370326       23539.369160
HLA A*3002      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.481704       1.111207        -3.370496       30318.221970
HLA A*0101      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.372190       1.001469        -3.370721       23560.772908
HLA A*0202      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.364984       0.994120        -3.370864       23173.074765
HLA A*2403      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.402061       1.031086        -3.370975       25238.345751
HLA A*0203      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.083753       0.712665        -3.371087       12126.979895
HLA A*2402      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.465753       1.094281        -3.371472       29224.902744
HLA A*2601      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.401657       1.029850        -3.371806       25214.872369
HLA A*0206      1:224-232       9       TILAELPLG       0.771690        -0.564159       -3.580263       0.207531        -3.372732       3804.194563
HLA B*4801      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.374201       1.001469        -3.372732       23670.132689
HLA B*4403      1:33-41 9       VAAAPSPVA       1.399199        -0.116922       -4.655418       1.282277        -3.373141       45229.064061
HLA B*4001      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.412758       1.039542        -3.373217       25867.716396
HLA A*2301      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.484570       1.111207        -3.373363       30518.985997
HLA A*0216      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.406544       1.033072        -3.373472       25500.206833
HLA A*2603      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.308523       0.934977        -3.373546       20348.068395
HLA B*0702      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -3.494671       0.120389        -3.374282       3123.711971
HLA B*0801      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.327173       0.952818        -3.374356       21240.923787
HLA B*1509      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.479566       1.105200        -3.374366       30169.332182
HLA B*4601      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.404316       1.029850        -3.374466       25369.761896
HLA A*0250      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.518722       1.143950        -3.374772       33015.829564
HLA A*0216      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.065445       0.690533        -3.374912       11626.405618
HLA A*3301      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.623669       1.248280        -3.375389       42040.610106
HLA B*4403      1:173-181       9       LLGGAKGPR       0.734546        0.559639        -4.669747       1.294185        -3.375562       46746.285792
HLA A*1101      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.196378       0.820380        -3.375998       15717.286533
HLA A*0250      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.308979       0.932973        -3.376006       20369.435280
HLA B*4402      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.407124       1.031086        -3.376038       25534.304072
HLA B*0802      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.405959       1.029850        -3.376108       25465.879589
HLA A*2301      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.370315       0.994120        -3.376195       23459.278134
HLA B*1801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.470767       1.094281        -3.376486       29564.250645
HLA A*0211      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -3.929514       0.553011        -3.376502       8501.854459
HLA B*5301      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.447890       1.071321        -3.376569       28047.227686
HLA A*2501      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.407686       1.031086        -3.376600       25567.340348
HLA A*8001      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.408390       1.031086        -3.377304       25608.868982
HLA B*5801      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.263742       0.886414        -3.377328       18354.476600
HLA B*1502      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.488729       1.111207        -3.377521       30812.624286
HLA A*2301      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.534858       1.157030        -3.377829       34265.610738
HLA A*8001      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.372027       0.994120        -3.377908       23551.979729
HLA B*4403      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.538009       1.160079        -3.377930       34515.100026
HLA B*3501      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.207453       0.829467        -3.377986       16123.266888
HLA B*4601      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.411224       1.033072        -3.378152       25776.495831
HLA B*4501      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.502074       1.123686        -3.378387       31774.136961
HLA A*2603      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.478967       1.100579        -3.378388       30127.741627
HLA A*0203      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.259407       0.880895        -3.378512       18172.187314
HLA B*3501      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.004509       0.625647        -3.378862       10104.369689
HLA A*2501      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.489640       1.110748        -3.378892       30877.369051
HLA A*8001      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.408795       1.029850        -3.378944       25632.709148
HLA A*0212      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.311415       0.932462        -3.378953       20484.030074
HLA B*5301      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.424910       1.045865        -3.379045       26601.714448
HLA A*0203      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.214074       0.834848        -3.379225       16370.950360
HLA B*1517      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.347311       0.967740        -3.379571       22249.017450
HLA A*3201      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.536618       1.157030        -3.379589       34404.736911
HLA A*2402      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.507818       1.128011        -3.379807       32197.211026
HLA B*5701      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.412920       1.033072        -3.379849       25877.374160
HLA B*5101      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.452767       1.072739        -3.380028       28363.999625
HLA B*1503      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.005773       0.625647        -3.380126       10133.821502
HLA B*5701      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.253078       0.872785        -3.380293       17909.262092
HLA B*1503      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.419856       1.039542        -3.380314       26293.953166
HLA A*3002      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.333303       0.952818        -3.380486       21542.852457
HLA A*2602      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.481405       1.100579        -3.380827       30297.398810
HLA A*2902      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.420394       1.039542        -3.380852       26326.548000
HLA A*3001      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.298517       0.917388        -3.381129       19884.594185
HLA B*4001      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.382602       1.001469        -3.381134       24132.507557
HLA A*2602      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.420850       1.039542        -3.381308       26354.192704
HLA B*5301      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.268011       0.886414        -3.381597       18535.786515
HLA B*5701      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.412688       1.031086        -3.381602       25863.518492
HLA B*5401      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.472595       1.090544        -3.382051       29688.945665
HLA A*2501      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.472249       1.090014        -3.382235       29665.344806
HLA A*6801      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.602108       1.219814        -3.382294       40004.402308
HLA B*1801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.507207       1.124732        -3.382476       32151.955192
HLA A*3001      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.260053       0.877544        -3.382509       18199.242552
HLA B*4601      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.315306       0.932462        -3.382844       20668.366400
HLA B*0803      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.412723       1.029850        -3.382872       25865.617359
HLA A*2902      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.205799       0.822896        -3.382903       16061.977214
HLA A*3201      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.483550       1.100579        -3.382972       30447.414771
HLA A*2402      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.543110       1.160079        -3.383031       34922.865253
HLA B*1517      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.413188       1.029850        -3.383338       25893.338367
HLA B*5301      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.351187       0.967740        -3.383448       22448.508269
HLA B*1502      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.484121       1.100579        -3.383543       30487.467356
HLA A*0219      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.316013       0.932462        -3.383551       20702.049702
HLA A*2601      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.385626       1.001469        -3.384158       24301.117093
HLA A*2902      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.415636       1.031086        -3.384550       26039.714001
HLA B*1502      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.544794       1.160079        -3.384716       35058.590284
HLA B*5301      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.207613       0.822896        -3.384716       16129.199285
HLA A*0301      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.352968       0.967740        -3.385229       22540.751778
HLA B*1503      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.888149       0.502462        -3.385687       7729.450730
HLA B*1509      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.475875       1.090014        -3.385861       29914.011478
HLA A*2301      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.511166       1.124732        -3.386435       32446.381494
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HLA B*0702      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.419511       1.033072        -3.386439       26273.051115
HLA A*0219      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.388286       1.001469        -3.386817       24450.393619
HLA A*0206      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -3.987574       0.600711        -3.386864       9717.938348
HLA A*3101      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.426409       1.039542        -3.386867       26693.689147
HLA B*4403      1:152-160       9       TGLLVMNNV       1.174900        0.079467        -4.641375       1.254367        -3.387008       43789.978201
HLA A*1101      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.460098       1.072739        -3.387359       28846.814657
HLA A*3001      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.216842       0.829467        -3.387375       16475.613108
HLA B*5801      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.340201       0.952818        -3.387384       21887.758841
HLA B*1509      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.342668       0.955042        -3.387627       22012.443501
HLA B*2705      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.268659       0.880895        -3.387764       18563.483515
HLA A*2402      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.516629       1.128647        -3.387982       32857.069228
HLA A*2902      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.441692       1.053156        -3.388536       27649.800280
HLA A*0250      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.045132       0.656423        -3.388709       11095.115385
HLA A*2603      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.479474       1.090544        -3.388930       30162.967557
HLA A*0203      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.390494       1.001469        -3.389026       24575.047785
HLA A*0201      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.322000       0.932973        -3.389027       20989.390848
HLA A*2902      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.422217       1.033072        -3.389146       26437.301109
HLA A*0203      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.262168       0.872785        -3.389383       18288.068916
HLA A*2602      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.500138       1.110748        -3.389390       31632.811076
HLA A*6801      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.079989       0.690533        -3.389456       12022.333816
HLA A*0211      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.391143       1.001469        -3.389674       24611.768920
HLA B*5301      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.490517       1.100579        -3.389938       30939.739051
HLA A*0216      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.102605       0.712665        -3.389939       12664.992158
HLA A*2501      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.435931       1.045865        -3.390066       27285.446277
HLA B*3501      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.443294       1.053156        -3.390138       27752.003872
HLA B*0801      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.384318       0.994120        -3.390198       24228.000553
HLA B*4001      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.343187       0.952818        -3.390370       22038.776998
HLA B*0802      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.450761       1.060336        -3.390425       28233.258908
HLA B*3501      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.385065       0.994120        -3.390945       24269.716940
HLA B*3901      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -3.578350       0.187363        -3.390987       3787.479054
HLA B*4601      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.324086       0.932973        -3.391114       21090.466082
HLA A*0212      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.324361       0.932973        -3.391388       21103.819666
HLA B*5401      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.540876       1.149444        -3.391431       34743.655331
HLA B*4403      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.502269       1.110748        -3.391521       31788.407413
HLA B*4801      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.437625       1.045865        -3.391760       27392.081813
HLA A*0219      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.445080       1.053156        -3.391924       27866.341563
HLA A*2902      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.422029       1.029850        -3.392179       26425.861755
HLA A*0212      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.423296       1.031086        -3.392210       26503.030179
HLA B*1502      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.465116       1.072739        -3.392377       29182.088092
HLA A*0101      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.347506       0.955042        -3.392464       22259.009964
HLA B*5101      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.486772       1.094281        -3.392490       30674.081518
HLA A*3301      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.587539       1.194858        -3.392680       38684.646235
HLA B*5101      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.432365       1.039542        -3.392823       27062.289973
HLA A*6802      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.425929       1.033072        -3.392858       26664.245778
HLA A*0250      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.487166       1.094281        -3.392885       30701.972678
HLA B*4801      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.345972       0.952818        -3.393154       22180.515233
HLA B*4801      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.433309       1.039542        -3.393768       27121.208420
HLA B*0803      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.465123       1.071321        -3.393802       29182.561711
HLA A*2402      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.454412       1.060336        -3.394076       28471.615528
HLA B*5101      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.440205       1.045865        -3.394340       27555.276589
HLA B*0801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.326835       0.932462        -3.394373       21224.383041
HLA B*1502      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -3.896926       0.502462        -3.394464       7887.262756
HLA B*1502      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.465283       1.070235        -3.395049       29193.299147
HLA B*5801      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.350133       0.955042        -3.395091       22394.046111
HLA B*3801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.506098       1.110748        -3.395350       32069.960944
HLA B*0803      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.496040       1.100579        -3.395462       31335.763855
HLA B*0803      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.500723       1.105200        -3.395523       31675.451159
HLA B*7301      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.590739       1.194858        -3.395880       38970.737820
HLA A*3002      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.914115       0.518215        -3.395900       8205.690672
HLA A*0211      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.442051       1.045865        -3.396186       27672.695855
HLA B*1801      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.429310       1.033072        -3.396239       26872.632486
HLA B*0802      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.467654       1.071321        -3.396333       29353.088767
HLA B*7301      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.525127       1.128647        -3.396480       33506.333746
HLA B*7301      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.580993       1.184095        -3.396898       38105.965018
HLA B*1517      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.043360       0.646348        -3.397012       11049.949962
HLA A*2602      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.554185       1.157030        -3.397156       35824.929182
HLA B*4001      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.333578       0.936177        -3.397401       21556.492473
HLA B*0802      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.430884       1.033072        -3.397813       26970.212460
HLA B*0802      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.468281       1.070235        -3.398047       29395.518190
HLA A*0212      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.399573       1.001469        -3.398104       25094.166836
HLA A*8001      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.437656       1.039542        -3.398114       27394.008326
HLA B*5301      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.526410       1.128011        -3.398399       33605.451052
HLA A*6801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.529239       1.130830        -3.398408       33825.054795
HLA B*0803      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.458857       1.060336        -3.398522       28764.533567
HLA A*0216      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.400033       1.001469        -3.398565       25120.789253
HLA B*0803      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.488611       1.090014        -3.398597       30804.290769
HLA B*5801      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.045188       0.646348        -3.398840       11096.556039
HLA A*0101      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.331903       0.932973        -3.398930       21473.503829
HLA A*3101      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.393084       0.994120        -3.398964       24721.994385
HLA A*6801      1:52-60 9       RETMAVVSA       1.427872        -0.179592       -4.647366       1.248280        -3.399086       44398.256485
HLA A*0206      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.430231       1.031086        -3.399145       26929.681117
HLA B*4801      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.432602       1.033072        -3.399530       27077.080816
HLA B*1501      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.335812       0.936177        -3.399636       21667.682194
HLA B*1503      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.334647       0.934977        -3.399670       21609.619129
HLA A*0202      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.543648       1.143950        -3.399698       34966.156765
HLA A*2301      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.543888       1.143950        -3.399937       34985.456719
HLA A*3301      1:122-130       9       EQVLTAPDV       1.040047        0.179767        -4.620079       1.219814        -3.400265       41694.521772
HLA B*0803      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.470518       1.070235        -3.400283       29547.301937
HLA B*6801      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.446245       1.045865        -3.400380       27941.215867
HLA A*3101      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.333148       0.932462        -3.400686       21535.161897
HLA B*3801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.495039       1.094281        -3.400758       31263.630205
HLA A*3101      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.368769       0.967740        -3.401029       23375.918432
HLA A*0250      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.395466       0.994120        -3.401346       24857.982689
HLA B*3501      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.434575       1.033072        -3.401504       27200.407385
HLA B*1517      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.434820       1.033072        -3.401748       27215.715415
HLA B*3501      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.113004       0.710864        -3.402139       12971.904593
HLA A*2902      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -3.662175       0.259962        -3.402214       4593.832603
HLA B*0702      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.319780       0.917388        -3.402392       20882.359659
HLA A*0219      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.433659       1.031086        -3.402573       27143.078920
HLA B*3801      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.533531       1.130830        -3.402701       34161.034810
HLA A*3002      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.492826       1.090014        -3.402812       31104.712408
HLA B*4002      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.503392       1.100579        -3.402813       31870.716291
HLA A*2603      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.559932       1.157030        -3.402903       36302.136118
HLA B*5101      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.493031       1.090014        -3.403017       31119.355609
HLA B*0803      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.497607       1.094281        -3.403326       31449.039951
HLA A*6802      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.371132       0.967740        -3.403393       23503.485142
HLA B*1517      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.356603       0.952818        -3.403785       22730.189154
HLA B*1801      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.449654       1.045865        -3.403789       28161.410508
HLA A*3002      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.560834       1.157030        -3.403805       36377.628469
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HLA B*1509      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.371849       0.967740        -3.404109       23542.298286
HLA A*0250      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.494678       1.090544        -3.404134       31237.594605
HLA A*0201      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.923325       0.518215        -3.405110       8381.565102
HLA B*4402      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.406802       1.001469        -3.405333       25515.386211
HLA A*6801      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.505969       1.100579        -3.405391       32060.420142
HLA A*0301      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.360618       0.955042        -3.405577       22941.315612
HLA A*3002      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.279136       0.872785        -3.406351       19016.729558
HLA B*1501      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.229562       0.822896        -3.406665       16965.305978
HLA B*0702      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.400943       0.994120        -3.406823       25173.437912
HLA B*5401      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.227367       0.820380        -3.406987       16879.799269
HLA B*3801      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.497840       1.090544        -3.407296       31465.887909
HLA A*3201      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.551272       1.143950        -3.407322       35585.410427
HLA B*5401      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.532946       1.124732        -3.408214       34115.048744
HLA A*3201      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.568355       1.160079        -3.408276       37013.067958
HLA B*0702      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.448078       1.039542        -3.408536       28059.368904
HLA B*5401      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.468920       1.060336        -3.408584       29438.805237
HLA A*3101      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.341684       0.932973        -3.408711       21962.603445
HLA A*0250      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.558241       1.149444        -3.408796       36161.009965
HLA B*5101      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.499412       1.090544        -3.408868       31579.976079
HLA B*0802      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.403062       0.994120        -3.408942       25296.577440
HLA A*0101      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.376762       0.967740        -3.409022       23810.122573
HLA A*0211      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.462377       1.053156        -3.409221       28998.588860
HLA B*4402      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.403511       0.994120        -3.409391       25322.729620
HLA A*0301      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.344400       0.934977        -3.409423       22100.384254
HLA A*6801      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.520207       1.110748        -3.409459       33128.905530
HLA A*0212      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.442665       1.033072        -3.409593       27711.796775
HLA B*1517      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.449194       1.039542        -3.409652       28131.565712
HLA A*1101      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.462913       1.053156        -3.409757       29034.379375
HLA A*2902      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.287462       0.877544        -3.409918       19384.848232
HLA A*8001      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.411877       1.001469        -3.410408       25815.291537
HLA B*4002      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.570566       1.160079        -3.410487       37201.971010
HLA B*3801      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.440430       1.029850        -3.410580       27569.591120
HLA A*2301      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.539412       1.128647        -3.410765       34626.753783
HLA A*3002      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.471249       1.060336        -3.410913       29597.056393
HLA B*5701      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.379348       0.967740        -3.411609       23952.365720
HLA A*3002      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.464879       1.053156        -3.411723       29166.147389
HLA A*2402      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.502476       1.090544        -3.411932       31803.544531
HLA B*5701      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.298879       0.886414        -3.412465       19901.167399
HLA B*0801      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.235370       0.822896        -3.412473       17193.711042
HLA A*2601      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.406779       0.994120        -3.412659       25514.005895
HLA A*0101      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.347670       0.934977        -3.412694       22267.440875
HLA A*2501      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.445968       1.033072        -3.412897       27923.384811
HLA B*0802      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.458817       1.045865        -3.412952       28761.888268
HLA A*6901      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.293905       0.880895        -3.413009       19674.544798
HLA A*0216      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.444096       1.031086        -3.413010       27803.247249
HLA B*1509      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.513607       1.100579        -3.413029       32629.272064
HLA B*4801      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.368139       0.955042        -3.413097       23342.051407
HLA B*1502      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.473445       1.060336        -3.413110       29747.144868
HLA A*6801      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.538117       1.124732        -3.413385       34523.690346
HLA A*2301      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.544308       1.130830        -3.413478       35019.352000
HLA A*0202      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.017460       0.603848        -3.413611       10410.212357
HLA B*4801      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.408054       0.994120        -3.413935       25589.065260
HLA B*1502      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.503951       1.090014        -3.413937       31911.777975
HLA A*3001      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -3.932225       0.518215        -3.414010       8555.097665
HLA B*4801      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.381867       0.967740        -3.414127       24091.678672
HLA B*7301      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.504771       1.090544        -3.414227       31972.085964
HLA B*0801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.178366       0.764021        -3.414345       15078.787420
HLA A*6901      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.105030       0.690533        -3.414496       12735.898631
HLA A*2501      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.444739       1.029850        -3.414889       27844.490830
HLA A*2601      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.367977       0.952818        -3.415159       23333.339857
HLA A*2603      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.610028       1.194858        -3.415169       40740.644971
HLA B*5301      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.559187       1.143950        -3.415237       36239.933671
HLA B*4002      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.520839       1.105200        -3.415639       33177.151804
HLA A*6802      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.164688       0.748881        -3.415807       14611.261616
HLA A*3201      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.348937       0.932462        -3.416474       22332.465938
HLA B*2705      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.447608       1.031086        -3.416522       28029.025708
HLA B*1509      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.487342       1.070235        -3.417108       30714.432276
HLA B*5301      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.566875       1.149444        -3.417431       36887.133632
HLA A*2403      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.354279       0.936177        -3.418103       22608.898761
HLA A*0301      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.351350       0.932973        -3.418377       22456.889465
HLA A*2301      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.508984       1.090544        -3.418440       32283.721980
HLA B*1503      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.464473       1.045865        -3.418607       29138.863246
HLA B*4501      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.543354       1.124732        -3.418622       34942.519379
HLA B*5801      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.355128       0.936177        -3.418951       22653.096406
HLA A*0216      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.079392       0.660357        -3.419035       12005.825130
HLA A*3001      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.300034       0.880895        -3.419139       19954.208206
HLA A*0206      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.386930       0.967740        -3.419191       24374.190563
HLA A*1101      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.372403       0.952818        -3.419586       23572.374730
HLA A*8001      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.354658       0.934977        -3.419681       22628.599513
HLA B*3801      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.490207       1.070235        -3.419972       30917.652704
HLA A*0203      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.184423       0.764415        -3.420008       15290.559988
HLA B*4402      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.352482       0.932462        -3.420020       22515.523712
HLA A*6801      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.514409       1.094281        -3.420127       32689.521194
HLA B*0801      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.216090       0.795947        -3.420143       16447.115784
HLA A*0301      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.352874       0.932462        -3.420412       22535.874587
HLA B*5101      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.414776       0.994120        -3.420656       25988.205872
HLA B*1517      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -3.231632       -0.189096       -3.420728       1704.637503
HLA B*4501      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.564939       1.143950        -3.420989       36723.066020
HLA B*5801      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.356034       0.934977        -3.421058       22700.450417
HLA A*0219      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.454147       1.033072        -3.421075       28454.215651
HLA A*2403      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.415542       0.994120        -3.421422       26034.079732
HLA A*2501      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.475203       1.053156        -3.422047       29867.763460
HLA B*5801      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.355066       0.932973        -3.422094       22649.910311
HLA B*0702      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.357099       0.934977        -3.422122       22756.150175
HLA B*4403      1:40-48 9       VAAAFNDEV       1.065598        0.129260        -4.617067       1.194858        -3.422209       41406.350796
HLA A*3001      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.838852       0.416603        -3.422249       6900.042073
HLA B*1503      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.455331       1.033072        -3.422259       28531.904328
HLA A*2301      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.512287       1.090014        -3.422273       32530.218061
HLA B*3901      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.232390       0.809887        -3.422504       17076.170275
HLA A*1101      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.416811       0.994120        -3.422691       26110.245333
HLA B*0802      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.462504       1.039542        -3.422962       29007.061572
HLA B*1801      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.528207       1.105200        -3.423007       33744.817591
HLA A*0250      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.169908       0.746698        -3.423210       14787.960184
HLA B*2705      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.456665       1.033072        -3.423594       28619.712490
HLA A*0219      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.170463       0.746698        -3.423764       14806.852531
HLA B*7301      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.567721       1.143950        -3.423771       36959.043543
HLA B*3801      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.535251       1.111207        -3.424043       34296.582044
HLA A*0211      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.457307       1.033072        -3.424235       28662.012164
HLA A*2403      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.357491       0.932973        -3.424519       22776.718543
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HLA A*0203      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.092056       0.667402        -3.424654       12361.060657
HLA A*0201      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.188995       0.764021        -3.424975       15452.383882
HLA A*0201      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.393147       0.967740        -3.425407       24725.605716
HLA B*3901      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -3.986714       0.561253        -3.425462       9698.715678
HLA B*4402      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.380765       0.955042        -3.425723       24030.629830
HLA A*0216      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.248752       0.822896        -3.425856       17731.778202
HLA A*2301      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.531301       1.105200        -3.426101       33986.102012
HLA A*0202      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.307071       0.880895        -3.426176       20280.152060
HLA B*4601      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.393962       0.967740        -3.426223       24772.064997
HLA B*5301      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.583756       1.157030        -3.426726       38349.169113
HLA A*0206      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.499468       1.072739        -3.426729       31584.076605
HLA A*3101      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.304360       0.877544        -3.426815       20153.937216
HLA B*0803      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.421028       0.994120        -3.426908       26365.030499
HLA A*2402      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.499137       1.071321        -3.427816       31559.993636
HLA B*4002      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.551540       1.123686        -3.427854       35607.363692
HLA A*2902      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.383030       0.955042        -3.427988       24156.280121
HLA B*5401      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.458324       1.029850        -3.428474       28729.231111
HLA A*0216      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.248914       0.820380        -3.428535       17738.398397
HLA B*1509      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.474449       1.045865        -3.428583       29815.940876
HLA A*2601      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.383711       0.955042        -3.428670       24194.207876
HLA B*7301      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.559516       1.130830        -3.428686       36267.391631
HLA B*2705      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.430170       1.001469        -3.428701       26925.893532
HLA B*5101      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.482016       1.053156        -3.428860       30340.044243
HLA B*3801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.459976       1.031086        -3.428890       28838.700778
HLA B*4601      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.381963       0.952818        -3.429146       24097.022931
HLA B*5301      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.589282       1.160079        -3.429203       38840.243819
HLA A*0301      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.365479       0.936177        -3.429303       23199.541622
HLA B*5301      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.553271       1.123686        -3.429585       35749.616795
HLA A*6901      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.365780       0.936177        -3.429604       23215.612075
HLA B*1501      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.316030       0.886414        -3.429616       20702.833688
HLA B*4501      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.193741       0.764021        -3.429721       15622.173200
HLA B*1517      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.483266       1.053156        -3.430110       30427.490519
HLA A*2902      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.055794       0.625647        -3.430146       11370.872399
HLA A*3001      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.281166       0.850740        -3.430426       19105.824554
HLA B*5101      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.316894       0.886414        -3.430481       20744.090755
HLA B*5101      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.432064       1.001469        -3.430595       27043.556749
HLA A*0212      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.398375       0.967740        -3.430635       25025.026363
HLA B*1501      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.311601       0.880895        -3.430706       20492.786435
HLA A*0101      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.363332       0.932462        -3.430870       23085.111412
HLA A*2403      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.384543       0.952818        -3.431725       24240.586618
HLA A*2403      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -3.624151       0.191859        -3.432292       4208.730337
HLA B*3901      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.478205       1.045865        -3.432340       30074.979853
HLA A*3201      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.463523       1.031086        -3.432437       29075.247031
HLA A*2301      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.503892       1.071321        -3.432571       31907.462288
HLA A*3301      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.589686       1.157030        -3.432656       38876.401522
HLA B*0802      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.485834       1.053156        -3.432678       30607.941518
HLA A*2301      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.527006       1.094281        -3.432725       33651.660441
HLA B*1517      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.145906       0.712665        -3.433240       13992.842112
HLA B*7301      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.527530       1.094281        -3.433249       33692.282480
HLA B*4001      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.401098       0.967740        -3.433358       25182.427761
HLA B*5101      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.182267       0.748881        -3.433386       15214.811064
HLA A*2403      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.388751       0.955042        -3.433709       24476.597886
HLA A*2402      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.590957       1.157030        -3.433927       38990.349699
HLA A*6901      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.197515       0.763535        -3.433980       15758.494387
HLA B*4601      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.320670       0.886414        -3.434256       20925.219687
HLA B*3801      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.539875       1.105200        -3.434674       34663.676854
HLA B*4601      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.244664       0.809887        -3.434778       17565.648435
HLA B*5701      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.387901       0.952818        -3.435083       24428.710316
HLA B*3801      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.536216       1.100579        -3.435638       34372.924115
HLA B*1502      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.592762       1.157030        -3.435732       39152.683602
HLA A*8001      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.391002       0.955042        -3.435960       24603.781400
HLA B*7301      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.585408       1.149444        -3.435963       38495.294527
HLA A*2301      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.537248       1.100579        -3.436669       34454.654807
HLA B*1502      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.586300       1.149444        -3.436856       38574.512931
HLA A*2402      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.567779       1.130830        -3.436949       36964.042489
HLA A*2902      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.317914       0.880895        -3.437019       20792.852859
HLA A*1101      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.476634       1.039542        -3.437092       29966.328744
HLA A*2402      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.581132       1.143950        -3.437182       38118.129753
HLA B*5301      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.548854       1.111207        -3.437647       35387.864777
HLA B*5801      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.355273       0.917388        -3.437885       22660.695826
HLA B*4002      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.622445       1.184095        -3.438350       41922.283284
HLA B*4001      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.373660       0.934977        -3.438684       23640.698862
HLA A*0212      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.039507       0.600711        -3.438797       10952.346017
HLA A*3001      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.203337       0.764415        -3.438922       15971.170470
HLA A*0219      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.406668       0.967740        -3.438929       25507.519406
HLA B*1501      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.085552       0.646348        -3.439204       12177.338066
HLA B*1502      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.533822       1.094281        -3.439541       34183.958617
HLA A*3001      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.004580       0.565014        -3.439565       10106.009728
HLA B*5801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.372352       0.932462        -3.439889       23569.569371
HLA B*0803      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.493543       1.053156        -3.440387       31156.078053
HLA A*2501      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.408188       0.967740        -3.440449       25596.957215
HLA A*6802      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.270760       0.830057        -3.440702       18653.482167
HLA A*3301      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.569429       1.128647        -3.440782       37104.689294
HLA A*1101      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.395903       0.955042        -3.440861       24883.008359
HLA B*1503      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.318412       0.877544        -3.440868       20816.713790
HLA A*2402      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.552125       1.111207        -3.440917       35655.361354
HLA A*6802      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.187652       0.746698        -3.440953       15404.641058
HLA A*0206      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.271098       0.830057        -3.441041       18668.019340
HLA B*2705      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.408785       0.967740        -3.441045       25632.154474
HLA B*4501      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.501414       1.060336        -3.441078       31725.871285
HLA A*2601      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.408874       0.967740        -3.441135       25637.424366
HLA A*2301      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.511942       1.070235        -3.441707       32504.358569
HLA A*2601      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.376900       0.934977        -3.441923       23817.723584
HLA B*3901      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.436253       0.994120        -3.442133       27305.676512
HLA B*1801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.495639       1.053156        -3.442483       31306.788825
HLA B*1801      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.444067       1.001469        -3.442599       27801.442358
HLA A*0202      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.237804       0.795128        -3.442676       17290.346242
HLA A*0250      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.488980       1.045865        -3.443115       30830.465588
HLA B*1503      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.207538       0.764021        -3.443517       16126.407297
HLA A*2501      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.483111       1.039542        -3.443570       30416.628241
HLA B*0802      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.445099       1.001469        -3.443630       27867.547619
HLA A*0211      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.411621       0.967740        -3.443881       25800.073317
HLA B*3801      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.534069       1.090014        -3.444055       34203.381932
HLA B*0801      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.330785       0.886414        -3.444371       21418.278390
HLA B*0801      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.274489       0.829467        -3.445022       18814.320980
HLA A*1101      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.476178       1.031086        -3.445092       29934.895026
HLA A*3301      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.605270       1.160079        -3.445191       40296.765958
HLA A*6801      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.535342       1.090014        -3.445328       34303.818895
HLA B*1502      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.142612       0.697019        -3.445593       13887.112566
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HLA A*3101      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.280475       0.834848        -3.445627       19075.460752
HLA A*0202      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.028920       0.583145        -3.445775       10688.588970
HLA B*3901      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.485376       1.039542        -3.445834       30575.669357
HLA B*4601      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.381010       0.934977        -3.446033       24044.153951
HLA A*6802      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -3.943117       0.496962        -3.446155       8772.374914
HLA B*3901      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -3.897659       0.451113        -3.446546       7900.586793
HLA B*5401      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.486203       1.039542        -3.446661       30633.949496
HLA A*0211      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.364248       0.917388        -3.446861       23133.869109
HLA B*7301      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.547508       1.100579        -3.446930       35278.336970
HLA A*2601      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.379414       0.932462        -3.446952       23955.994224
HLA A*0101      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.383446       0.936177        -3.447269       24179.422054
HLA A*2603      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.607594       1.160079        -3.447515       40512.946792
HLA B*1501      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.211381       0.763535        -3.447846       16269.768813
HLA B*4001      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.380847       0.932973        -3.447875       24035.180367
HLA A*3301      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.632031       1.184095        -3.447936       42857.894076
HLA A*1101      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.481189       1.033072        -3.448118       30282.323249
HLA A*0211      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.013503       0.565014        -3.448489       10315.803383
HLA A*2301      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.479582       1.031086        -3.448496       30170.474693
HLA B*0802      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.403654       0.955042        -3.448612       25331.087581
HLA A*0201      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.049629       0.600711        -3.448918       11210.596912
HLA B*3801      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.520310       1.071321        -3.448989       33136.792312
HLA B*5101      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.482535       1.033072        -3.449464       30376.340053
HLA A*0101      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.366877       0.917388        -3.449490       23274.338573
HLA B*1509      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.489668       1.039542        -3.450127       30879.373634
HLA B*1502      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.574981       1.124732        -3.450249       37582.064392
HLA B*2705      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.489802       1.039542        -3.450261       30888.897180
HLA A*2602      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.555525       1.105200        -3.450324       35935.570754
HLA A*0250      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.489939       1.039542        -3.450397       30898.590820
HLA B*7301      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.575378       1.124732        -3.450646       37616.440305
HLA B*0702      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.403708       0.952818        -3.450890       25334.239660
HLA A*0212      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.246067       0.795128        -3.450939       17622.471989
HLA B*4402      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.384329       0.932973        -3.451357       24228.655916
HLA A*0219      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.384372       0.932973        -3.451399       24231.015369
HLA A*6801      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.635776       1.184095        -3.451681       43229.071364
HLA B*5301      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.580443       1.128647        -3.451796       38057.756662
HLA A*0301      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.369274       0.917388        -3.451886       23403.123393
HLA A*2501      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.446208       0.994120        -3.452088       27938.797430
HLA B*3901      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.405421       0.952818        -3.452603       25434.350346
HLA A*0219      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.216785       0.764021        -3.452764       16473.474097
HLA B*1801      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.492542       1.039542        -3.453000       31084.358032
HLA B*4402      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.421080       0.967740        -3.453340       26368.168588
HLA B*1503      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.326349       0.872785        -3.453564       21200.628281
HLA B*3801      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.447714       0.994120        -3.453594       28035.850065
HLA B*4403      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.637721       1.184095        -3.453626       43423.145499
HLA A*0206      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.340105       0.886414        -3.453691       21882.904555
HLA A*3001      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.200447       0.746698        -3.453749       15865.248490
HLA B*0801      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.390175       0.936177        -3.453998       24556.973469
HLA B*4002      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.582083       1.128011        -3.454072       38201.738330
HLA B*1517      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.485216       1.031086        -3.454130       30564.423479
HLA A*6801      1:11-19 9       ELATPYALN       0.932404        -0.621088       -3.765482       0.311316        -3.454166       5827.496498
HLA A*0216      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.421975       0.967740        -3.454235       26422.573857
HLA A*0201      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.390718       0.936177        -3.454541       24587.681118
HLA A*0301      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.055347       0.600711        -3.454637       11359.190524
HLA B*4501      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.410315       0.955042        -3.455273       25722.585914
HLA A*3201      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.566074       1.110748        -3.455326       36819.148002
HLA A*2501      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.390370       0.934977        -3.455393       24568.002536
HLA B*5301      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.580295       1.124732        -3.455563       38044.787913
HLA B*3801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.508965       1.053156        -3.455809       32282.324799
HLA A*0206      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.373442       0.917388        -3.456054       23628.807753
HLA B*3901      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.489137       1.033072        -3.456066       30841.642503
HLA A*3301      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.584132       1.128011        -3.456121       38382.377843
HLA A*0211      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.286424       0.830057        -3.456366       19338.551119
HLA A*2403      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.391568       0.934977        -3.456591       24635.880319
HLA A*2301      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.496172       1.039542        -3.456630       31345.258582
HLA B*5401      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.251978       0.795128        -3.456850       17863.976271
HLA A*2602      1:88-96 9       WRTAAFASA       1.223245        -0.112038       -4.568282       1.111207        -3.457075       37006.861144
HLA A*0216      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.374656       0.917388        -3.457269       23694.987972
HLA B*4402      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.393671       0.936177        -3.457494       24755.452818
HLA A*2601      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.393683       0.936177        -3.457506       24756.122448
HLA A*0201      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.338519       0.880895        -3.457624       21803.141020
HLA A*2601      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.390628       0.932973        -3.457656       24582.627006
HLA A*2603      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.588584       1.130830        -3.457754       38777.887868
HLA B*1517      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.390856       0.932973        -3.457884       24595.530352
HLA B*1801      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.278323       0.820380        -3.457943       18981.166926
HLA B*5401      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.547992       1.090014        -3.457978       35317.674375
HLA A*0250      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.530857       1.072739        -3.458118       33951.370033
HLA A*2402      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.452307       0.994120        -3.458187       28333.940130
HLA A*2902      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.171050       0.712665        -3.458385       14826.891937
HLA B*5701      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.414015       0.955042        -3.458973       25942.693537
HLA B*4403      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.254130       0.795128        -3.459003       17952.720165
HLA B*5401      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.532119       1.072739        -3.459380       34050.145922
HLA A*2402      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.490667       1.031086        -3.459581       30950.453261
HLA B*0801      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.376975       0.917388        -3.459588       23821.847180
HLA A*3201      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.166379       0.706535        -3.459845       14668.285221
HLA A*0212      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.396032       0.936177        -3.459855       24890.413248
HLA A*1101      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.392931       0.932973        -3.459958       24713.302602
HLA A*2501      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.415023       0.955042        -3.459981       26002.972363
HLA B*7301      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.583683       1.123686        -3.459997       38342.738244
HLA B*1503      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.120954       0.660357        -3.460598       13211.569176
HLA B*2705      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.454957       0.994120        -3.460837       28507.372525
HLA A*0202      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.492159       1.031086        -3.461073       31056.959557
HLA B*0803      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.507052       1.045865        -3.461187       32140.477300
HLA B*1501      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.167747       0.706535        -3.461212       14714.541913
HLA B*4002      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.605327       1.143950        -3.461377       40301.998322
HLA A*6801      1:86-94 9       SRWRTAAFA       1.225790        -0.065711       -4.621491       1.160079        -3.461412       41830.305600
HLA A*2602      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.605545       1.143950        -3.461595       40322.280153
HLA A*3301      1:32-40 9       RVAAAPSPV       0.757389        0.366297        -4.585368       1.123686        -3.461681       38491.754350
HLA B*5701      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.397926       0.936177        -3.461749       24999.181638
HLA A*0206      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.296893       0.834848        -3.462045       19810.399696
HLA A*1101      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.394761       0.932462        -3.462299       24817.671730
HLA A*2601      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.339844       0.877544        -3.462300       21869.767866
HLA A*3002      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.274143       0.811766        -3.462377       18799.364769
HLA A*2601      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.379893       0.917388        -3.462506       23982.447070
HLA A*2603      1:181-189       9       RSAGTMGTA       1.257907        -0.163626       -4.556831       1.094281        -3.462550       36043.824024
HLA A*0301      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.340126       0.877544        -3.462582       21883.970038
HLA B*4801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.395088       0.932462        -3.462625       24836.341007
HLA B*5401      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.516319       1.053156        -3.463163       32833.614195
HLA A*2602      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.553737       1.090544        -3.463193       35787.930801
HLA B*7301      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.553227       1.090014        -3.463213       35745.942356
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HLA B*3501      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.160482       0.697019        -3.463463       14470.453392
HLA A*2402      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.493388       1.029850        -3.463537       31144.955677
HLA A*2301      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.493390       1.029850        -3.463540       31145.124168
HLA A*2902      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.396535       0.932973        -3.463562       24919.245971
HLA B*7301      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.591613       1.128011        -3.463602       39049.244573
HLA B*4402      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.416736       0.952818        -3.463918       26105.725611
HLA A*2301      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.524293       1.060336        -3.463957       33442.046228
HLA A*3101      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.350483       0.886414        -3.464069       22412.104635
HLA B*0702      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.465779       1.001469        -3.464310       29226.641934
HLA A*2403      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.293780       0.829467        -3.464313       19668.904440
HLA B*1502      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.569706       1.105200        -3.464506       37128.383262
HLA A*2402      1:97-105        9       AAIAVGLGA       1.149375        -0.048796       -4.565397       1.100579        -3.464819       36761.826666
HLA B*3501      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.345831       0.880895        -3.464935       22173.316753
HLA A*0101      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.287848       0.822896        -3.464951       19402.054524
HLA A*1101      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.433337       0.967740        -3.465598       27122.969150
HLA B*0801      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.295716       0.830057        -3.465659       19756.779189
HLA A*2902      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.433490       0.967740        -3.465750       27132.508424
HLA B*1503      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.296163       0.830057        -3.466105       19777.097206
HLA B*3801      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.526804       1.060336        -3.466469       33636.007632
HLA B*5301      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.536797       1.070235        -3.466562       34418.885382
HLA B*0702      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.287089       0.820380        -3.466709       19368.181090
HLA A*0301      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.353189       0.886414        -3.466776       22552.217332
HLA B*5101      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.399258       0.932462        -3.466796       25075.982035
HLA B*7301      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.577718       1.110748        -3.466970       37819.674120
HLA B*2705      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.422020       0.955042        -3.466978       26425.289917
HLA A*3101      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.287455       0.820380        -3.467076       19384.533625
HLA B*4001      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.399657       0.932462        -3.467195       25099.054551
HLA A*0206      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.403466       0.936177        -3.467289       25320.126883
HLA A*2402      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.537537       1.070235        -3.467302       34477.589128
HLA A*2603      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.595412       1.128011        -3.467401       39392.337658
HLA B*4501      1:217-225       9       GSPQPTGTI       1.015707        0.168388        -4.651813       1.184095        -3.467718       44855.271618
HLA B*0803      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.500819       1.033072        -3.467748       31682.477727
HLA A*0212      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.231946       0.764021        -3.467925       17058.719343
HLA A*3001      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.231850       0.763535        -3.468315       17054.936045
HLA B*1502      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.498463       1.029850        -3.468612       31511.030406
HLA B*3901      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.403670       0.934977        -3.468694       25332.046868
HLA B*0801      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.278753       0.809887        -3.468866       18999.967771
HLA A*0203      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.386298       0.917388        -3.468910       24338.745571
HLA A*0203      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.405310       0.936177        -3.469134       25427.884109
HLA A*6801      1:27-35 9       ADIDRRVAA       1.371750        -0.214720       -4.626282       1.157030        -3.469252       42294.280119
HLA A*3101      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.405477       0.936177        -3.469300       25437.652889
HLA B*5801      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.350422       0.880895        -3.469526       22408.952435
HLA A*0201      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.387027       0.917388        -3.469639       24379.597491
HLA A*0212      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.126480       0.656423        -3.470057       13380.748003
HLA B*4002      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.619553       1.149444        -3.470108       41644.026320
HLA A*0250      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.130587       0.660357        -3.470230       13507.883040
HLA B*1502      1:26-34 9       RADIDRRVA       1.395400        -0.251450       -4.614245       1.143950        -3.470295       41138.194358
HLA B*4501      1:71-79 9       RTAILDATK       0.821937        0.327507        -4.620093       1.149444        -3.470649       41695.875171
HLA B*7301      1:56-64 9       AVVSAATTA       1.129368        -0.059133       -4.541026       1.070235        -3.470791       34755.686810
HLA A*3201      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.542628       1.071321        -3.471307       34884.156311
HLA A*8001      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.404387       0.932973        -3.471414       25373.879659
HLA A*2501      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.349045       0.877544        -3.471500       22338.024173
HLA B*0702      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.306357       0.834848        -3.471508       20246.826605
HLA A*6801      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -3.684007       0.212403        -3.471603       4830.661213
HLA B*1502      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.524974       1.053156        -3.471818       33494.553557
HLA B*3501      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.406842       0.934977        -3.471865       25517.732921
HLA A*0219      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.389411       0.917388        -3.472024       24513.834989
HLA A*0201      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.302158       0.830057        -3.472101       20052.034071
HLA B*4601      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.408313       0.936177        -3.472136       25604.297532
HLA B*4601      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.292580       0.820380        -3.472200       19614.605759
HLA A*0301      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.353610       0.880895        -3.472714       22574.066804
HLA A*2402      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.578131       1.105200        -3.472931       37855.700911
HLA B*5701      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.408231       0.934977        -3.473254       25599.449917
HLA B*4402      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.293775       0.820380        -3.473396       19668.691628
HLA A*6901      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.285618       0.811766        -3.473852       19302.699932
HLA B*5301      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.475377       1.001469        -3.473908       29879.722869
HLA B*1509      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.409079       0.934977        -3.474102       25649.493725
HLA B*1801      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.441932       0.967740        -3.474192       27665.061891
HLA A*8001      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.442178       0.967740        -3.474439       27680.781171
HLA A*0212      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -3.891114       0.416603        -3.474510       7782.402407
HLA B*4601      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.352155       0.877544        -3.474611       22498.598975
HLA A*3301      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.599519       1.124732        -3.474787       39766.617654
HLA A*0301      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.295225       0.820380        -3.474845       19734.453478
HLA A*0202      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.361293       0.886414        -3.474879       22976.962841
HLA A*0219      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.411062       0.936177        -3.474885       25766.875716
HLA B*4501      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.270072       0.795128        -3.474944       18623.938000
HLA B*5401      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.187661       0.712665        -3.474996       15404.974411
HLA A*0301      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.348241       0.872785        -3.475456       22296.732971
HLA B*5801      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.296017       0.820380        -3.475637       19770.464821
HLA B*1501      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.305758       0.830057        -3.475700       20218.914925
HLA B*5801      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.353297       0.877544        -3.475753       22557.830260
HLA B*4403      1:89-97 9       RTAAFASAA       1.280297        -0.151650       -4.604650       1.128647        -3.476003       40239.254763
HLA B*4501      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.522207       1.045865        -3.476341       33281.776529
HLA A*2602      1:74-82 9       ILDATKPEV       0.983482        0.144529        -4.604443       1.128011        -3.476432       40220.102610
HLA B*7301      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.537187       1.060336        -3.476851       34449.808856
HLA B*5101      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.432144       0.955042        -3.477102       27048.531496
HLA B*4403      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.607960       1.130830        -3.477130       40547.151830
HLA A*0250      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.510332       1.033072        -3.477261       32384.127672
HLA B*5401      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.432656       0.955042        -3.477614       27080.450158
HLA B*1801      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.433001       0.955042        -3.477960       27101.994551
HLA B*4001      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.395539       0.917388        -3.478151       24862.151885
HLA B*5101      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.508168       1.029850        -3.478318       32223.174807
HLA A*3301      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.583655       1.105200        -3.478455       38340.249166
HLA B*5301      1:92-100        9       AFASAAAIA       1.132156        -0.021408       -4.589766       1.110748        -3.479018       38883.552959
HLA B*4002      1:131-139       9       RTVSRPLGA       1.205386        -0.080654       -4.603990       1.124732        -3.479258       40178.130371
HLA B*0802      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.447178       0.967740        -3.479438       28001.290431
HLA B*0702      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.302826       0.822896        -3.479929       20082.865866
HLA B*1509      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.513081       1.033072        -3.480010       32589.755365
HLA B*4801      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.415037       0.934977        -3.480060       26003.816416
HLA A*2601      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.353187       0.872785        -3.480402       22552.095328
HLA B*1517      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.416865       0.936177        -3.480688       26113.494366
HLA B*4001      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.361840       0.880895        -3.480945       23005.943660
HLA B*1509      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.331717       0.850740        -3.480977       21464.328417
HLA B*4002      1:189-197       9       AAVTPSTTA       1.238891        -0.108061       -4.612450       1.130830        -3.481620       40968.514709
HLA A*2501      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.483372       1.001469        -3.481903       30434.898841
HLA B*5701      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.414412       0.932462        -3.481950       25966.423042
HLA B*7301      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.555005       1.072739        -3.482266       35892.632380
HLA A*3001      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.128726       0.646348        -3.482378       13450.130542
HLA A*2403      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.363501       0.880895        -3.482606       23094.105092
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HLA B*0702	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.418878	0.936177	-3.482702	26234.844797
HLA B*4403	1:42-50 9	AAFNDEVRA	1.135376	-0.030176	-4.587980	1.105200	-3.482780	38724.010823
HLA A*0301	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.312973	0.830057	-3.482916	20557.633221
HLA A*3101	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.313347	0.830057	-3.483289	20575.323937
HLA B*5801	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.318417	0.834848	-3.483568	20816.939023
HLA B*5301	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.578026	1.094281	-3.483744	37846.486251
HLA B*0702	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.370286	0.886414	-3.483873	23457.755238
HLA A*0211	1:66-74 9	PPAHLRTAI	1.205915	-0.174829	-4.515670	1.031086	-3.484584	32784.625942
HLA A*2403	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.401976	0.917388	-3.484589	25233.430910
HLA A*3002	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.530646	1.045865	-3.484781	33934.843474
HLA A*3002	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.362397	0.877544	-3.484852	23035.459504
HLA A*0201	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.088724	0.603848	-3.484876	12266.598988
HLA B*3801	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.452652	0.967740	-3.484913	28356.481763
HLA A*3301	1:189-197	9	AAVTPSTTA	1.238891	-0.108061	-4.615758	1.130830	-3.484928	41281.768494
HLA A*0201	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.371351	0.886414	-3.484937	23515.313184
HLA B*4002	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.579283	1.094281	-3.485001	37956.183656
HLA A*0203	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.335996	0.850740	-3.485256	21676.827264
HLA B*1801	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.418324	0.932973	-3.485351	26201.371255
HLA B*1509	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.479643	0.994120	-3.485523	30174.718684
HLA B*0802	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.420596	0.934977	-3.485619	26338.799289
HLA A*3002	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.418261	0.932462	-3.485798	26197.544379
HLA A*3001	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-3.743862	0.257963	-3.485899	5544.495818
HLA B*0702	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.182924	0.697019	-3.485905	15237.875451
HLA B*5801	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.359098	0.872785	-3.486313	22861.156826
HLA B*3901	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.250369	0.764021	-3.486348	17797.898921
HLA B*5701	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.419809	0.932973	-3.486836	26291.108373
HLA A*3301	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.630790	1.143950	-3.486840	42735.648542
HLA A*6802	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.322028	0.834848	-3.487180	20990.753495
HLA A*2601	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.368137	0.880895	-3.487241	23341.925129
HLA A*3101	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.404650	0.917388	-3.487262	25389.258543
HLA A*3001	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.200062	0.712665	-3.487396	15851.178738
HLA A*0203	1:28-36 9	DIDRRVAAA	0.875321	-0.322310	-4.040757	0.553011	-3.487746	10983.912941
HLA A*0101	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.374168	0.886414	-3.487754	23668.340018
HLA B*0803	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.527592	1.039542	-3.488050	33697.021873
HLA A*0250	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.541211	1.053156	-3.488056	34770.543914
HLA A*6901	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.323001	0.834848	-3.488152	21037.819049
HLA A*0203	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.144952	0.656423	-3.488529	13962.141751
HLA A*3301	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.561788	1.072739	-3.489049	36457.616649
HLA B*4402	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.424083	0.934977	-3.489106	26551.105512
HLA A*2501	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.238064	0.748881	-3.489184	17300.732173
HLA B*3501	1:59-67 9	SAATTAEPP	0.646418	0.117117	-4.252981	0.763535	-3.489446	17905.290161
HLA B*1501	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.254194	0.764415	-3.489779	17955.342657
HLA B*4403	1:71-79 9	RTAILDATK	0.821937	0.327507	-4.639422	1.149444	-3.489978	43593.557040
HLA B*3501	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.442836	0.952818	-3.490019	27722.742932
HLA A*0202	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.543272	1.053156	-3.490116	34935.903775
HLA B*3901	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.025274	0.534755	-3.490519	10599.221691
HLA A*6802	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.426721	0.936177	-3.490544	26712.902575
HLA A*0212	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.377450	0.886414	-3.491036	23847.893867
HLA B*1517	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.321119	0.830057	-3.491061	20946.852657
HLA A*3101	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.303202	0.811766	-3.491435	20100.256764
HLA A*0101	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.369029	0.877544	-3.491485	23389.959832
HLA A*0216	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.321774	0.830057	-3.491717	20978.492851
HLA A*3301	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.552261	1.060336	-3.491925	35666.550819
HLA B*0801	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.369518	0.877544	-3.491974	23416.294361
HLA A*2603	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-4.562359	1.070235	-3.492125	36505.575460
HLA B*4801	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.425227	0.932973	-3.492254	26621.149709
HLA B*4601	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.409809	0.917388	-3.492422	25692.684694
HLA A*2602	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.241326	0.748881	-3.492445	17431.131058
HLA A*0211	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.199018	0.706535	-3.492484	15813.150043
HLA A*3002	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.139642	0.646348	-3.493294	13792.475043
HLA A*3001	1:203-211	9	GASTALAFT	0.843184	-0.343048	-3.993579	0.500136	-3.493444	9853.248211
HLA B*3501	1:57-65 9	VVSAATTAE	0.760296	-0.525979	-3.728008	0.234317	-3.493690	5345.738809
HLA A*6801	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.605439	1.111207	-3.494232	40312.465090
HLA B*4403	1:131-139	9	RTVSRPLGA	1.205386	-0.080654	-4.619048	1.124732	-3.494316	41595.617222
HLA A*2601	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.381038	0.886414	-3.494624	24045.714916
HLA A*3301	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.605399	1.110748	-3.494651	40308.757799
HLA B*4601	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.317884	0.822896	-3.494987	20791.390579
HLA A*6901	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.367787	0.872785	-3.495002	23323.117403
HLA B*0802	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.447888	0.952818	-3.495070	28047.075954
HLA B*0702	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.324544	0.829467	-3.495077	21112.726753
HLA A*2301	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.541303	1.045865	-3.495438	34777.880774
HLA A*2301	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.548782	1.053156	-3.495626	35381.930498
HLA A*0201	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.242456	0.746698	-3.495757	17476.548658
HLA B*1517	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.376740	0.880895	-3.495845	23808.963311
HLA B*5701	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.413320	0.917388	-3.495932	25901.184041
HLA A*3002	1:54-62 9	TMAVVSAAT	0.831597	-0.329135	-3.998415	0.502462	-3.495953	9963.562819
HLA B*3801	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.542027	1.045865	-3.496162	34835.877579
HLA A*2301	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.529408	1.033072	-3.496336	33838.232627
HLA A*0219	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.383021	0.886414	-3.496607	24155.757395
HLA A*2902	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.326212	0.829467	-3.496745	21193.977128
HLA B*7301	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.537105	1.039542	-3.497563	34443.286535
HLA B*7301	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.568940	1.071321	-3.497619	37062.960467
HLA A*2501	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.450665	0.952818	-3.497847	28226.997311
HLA B*4801	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.210700	0.712665	-3.498035	16244.263708
HLA A*6802	1:28-36 9	DIDRRVAAA	0.875321	-0.322310	-4.051518	0.553011	-3.498507	11259.464172
HLA A*2402	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.433598	0.934977	-3.498621	27139.261322
HLA B*0702	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.308575	0.809887	-3.498688	20350.490317
HLA A*0202	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.145182	0.646348	-3.498834	13969.546010
HLA A*6802	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.212255	0.712665	-3.499590	16302.544346
HLA B*1502	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.311683	0.811766	-3.499917	20496.667032
HLA A*3001	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.190466	0.690533	-3.499933	15504.803492
HLA B*3901	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.432985	0.932973	-3.500012	27100.968239
HLA A*6901	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.206734	0.706535	-3.500199	16096.598092
HLA A*3201	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.125855	0.625647	-3.500208	13361.506546
HLA B*5301	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.590736	1.090014	-3.500722	38970.526993
HLA A*3002	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.540542	1.039542	-3.501000	34716.975356
HLA A*3201	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.331353	0.830057	-3.501296	21446.337417
HLA A*6802	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.313076	0.811766	-3.501310	20562.527242
HLA B*4601	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.382530	0.880895	-3.501634	24128.460716
HLA B*0801	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.382873	0.880895	-3.501977	24147.525960
HLA A*3001	1:7-15  9	FELLELATP	0.903395	-0.108267	-4.297330	0.795128	-3.502203	19830.343733
HLA A*3201	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.613418	1.111207	-3.502211	41059.930219
HLA B*3801	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.541959	1.039542	-3.502417	34830.412719
HLA A*3301	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.613761	1.111207	-3.502554	41092.373962
HLA A*0250	1:53-61 9	ETMAVVSAA	1.064440	-0.244060	-4.323001	0.820380	-3.502621	21037.819049
HLA B*1517	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.380246	0.877544	-3.502701	24001.916326
HLA A*0216	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.389129	0.886414	-3.502716	24497.926098
HLA B*1501	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.140657	0.637921	-3.502736	13824.746747
HLA B*4402	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.420363	0.917388	-3.502976	26324.696557
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HLA B*4403	1:56-64 9	AVVSAATTA	1.129368	-0.059133	-4.573421	1.070235	-3.503186	37447.305546
HLA A*6801	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.631768	1.128011	-3.503757	42831.934018
HLA B*4002	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.614678	1.110748	-3.503929	41179.164510
HLA B*2705	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.436443	0.932462	-3.503981	27317.644510
HLA A*0101	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.385084	0.880895	-3.504188	24270.767334
HLA A*0301	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.334234	0.829467	-3.504767	21589.053528
HLA A*2301	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.439885	0.934977	-3.504908	27535.010390
HLA B*4601	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.339901	0.834848	-3.505052	21872.607563
HLA A*0101	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.334532	0.829467	-3.505065	21603.891511
HLA A*0219	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.328010	0.822896	-3.505113	21281.871537
HLA A*0212	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.422574	0.917388	-3.505186	26459.049525
HLA B*2705	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.438273	0.932973	-3.505301	27433.012285
HLA B*3501	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.335512	0.830057	-3.505454	21652.683258
HLA A*8001	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.441960	0.936177	-3.505783	27666.857928
HLA B*1503	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-3.923208	0.416603	-3.506604	8379.298241
HLA B*1502	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.110480	0.603848	-3.506632	12896.753495
HLA B*5801	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.357392	0.850740	-3.506652	22771.543911
HLA B*4601	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.379713	0.872785	-3.506928	23972.458987
HLA A*2902	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.439472	0.932462	-3.507009	27508.805669
HLA B*5301	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.597620	1.090544	-3.507077	39593.169559
HLA B*4801	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.424696	0.917388	-3.507308	26588.621650
HLA A*3101	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.336834	0.829467	-3.507368	21718.732834
HLA A*0301	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.330423	0.822896	-3.507526	21400.441762
HLA A*0201	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.198276	0.690533	-3.507743	15786.140162
HLA A*2602	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.597787	1.090014	-3.507773	39608.380301
HLA B*1502	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.553678	1.045865	-3.507813	35783.090910
HLA A*2601	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.337351	0.829467	-3.507884	21744.597329
HLA A*2402	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.541045	1.033072	-3.507973	34757.191038
HLA B*3501	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.444246	0.936177	-3.508069	27812.875315
HLA A*8001	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.425664	0.917388	-3.508276	26647.950440
HLA B*1517	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.443435	0.934977	-3.508459	27761.013450
HLA B*2705	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.443492	0.934977	-3.508515	27764.618100
HLA B*5701	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.331459	0.822896	-3.508563	21451.559057
HLA B*4402	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.381517	0.872785	-3.508732	24072.266834
HLA B*0803	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.510842	1.001469	-3.509373	32422.167211
HLA A*0301	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.321156	0.811766	-3.509390	20948.665858
HLA B*3901	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.427064	0.917388	-3.509676	26734.009930
HLA A*6801	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.581153	1.071321	-3.509831	38119.985732
HLA B*1501	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.427816	0.917388	-3.510428	26780.330983
HLA A*0301	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.345351	0.834848	-3.510503	22148.859394
HLA A*0211	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.320719	0.809887	-3.510833	20927.597087
HLA A*2402	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.564091	1.053156	-3.510935	36651.416961
HLA A*2603	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.654887	1.143950	-3.510937	45173.799218
HLA A*2301	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.512548	1.001469	-3.511079	32549.758249
HLA A*2501	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.383902	0.872785	-3.511117	24204.812126
HLA A*3101	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.321152	0.809887	-3.511265	20948.439199
HLA B*4402	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.341134	0.829467	-3.511667	21934.818267
HLA A*0201	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.321575	0.809887	-3.511688	20968.848307
HLA A*0211	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.398215	0.886414	-3.511801	25015.822039
HLA B*5101	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.465631	0.952818	-3.512813	29216.682519
HLA B*0702	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.390600	0.877544	-3.513056	24581.031186
HLA B*4601	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.342546	0.829467	-3.513079	22006.251958
HLA A*0203	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.117797	0.603848	-3.513948	13115.857672
HLA A*3301	1:97-105	9	AAIAVGLGA	1.149375	-0.048796	-4.614600	1.100579	-3.514021	41171.813601
HLA B*5801	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.261019	0.746698	-3.514321	18239.752941
HLA A*8001	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.344343	0.829467	-3.514876	22097.514985
HLA A*0301	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.365735	0.850740	-3.514995	23213.225914
HLA B*4501	1:74-82 9	ILDATKPEV	0.983482	0.144529	-4.643088	1.128011	-3.515076	43963.018514
HLA B*3501	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.227800	0.712665	-3.515134	16896.610118
HLA B*4001	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.393060	0.877544	-3.515516	24720.656989
HLA B*0803	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.470809	0.955042	-3.515767	29567.129693
HLA B*7301	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.548868	1.033072	-3.515797	35389.013462
HLA B*4403	1:88-96 9	WRTAAFASA	1.223245	-0.112038	-4.627088	1.111207	-3.515880	42372.833906
HLA A*0216	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.452166	0.936177	-3.515989	28324.744614
HLA B*1801	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.468833	0.952818	-3.516016	29432.913182
HLA A*2403	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.327911	0.811766	-3.516145	21277.036518
HLA A*0212	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.081187	0.565014	-3.516173	12055.549759
HLA A*2403	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.394228	0.877544	-3.516683	24787.213223
HLA B*4402	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.403308	0.886414	-3.516895	25310.950948
HLA B*3501	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.351749	0.834848	-3.516901	22477.552143
HLA A*0211	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.281232	0.764021	-3.517211	19108.718864
HLA A*0202	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.207838	0.690533	-3.517305	16137.578150
HLA B*5101	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.452302	0.934977	-3.517326	28333.633565
HLA A*2603	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.470205	0.952818	-3.517388	29526.049849
HLA B*4801	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.398311	0.880895	-3.517416	25021.371300
HLA B*3801	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.453632	0.936177	-3.517455	28420.524034
HLA B*3901	1:35-43 9	AAPSPVAAA	1.017695	-0.085233	-4.449960	0.932462	-3.517498	28181.222988
HLA B*5801	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.347130	0.829467	-3.517663	22239.751296
HLA A*3301	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.612215	1.094281	-3.517934	40946.357191
HLA A*2902	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.348011	0.830057	-3.517954	22284.915064
HLA B*0803	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.485825	0.967740	-3.518085	30607.279182
HLA A*2902	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.454487	0.936177	-3.518311	28476.544860
HLA A*3001	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.230946	0.712622	-3.518324	17019.450867
HLA B*0702	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.348399	0.830057	-3.518341	22304.816167
HLA B*5801	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.348486	0.830057	-3.518428	22309.281277
HLA A*0301	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.144144	0.625647	-3.518496	13936.182342
HLA A*3301	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.609013	1.090014	-3.518999	40645.542320
HLA A*1101	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.455629	0.936177	-3.519453	28551.514078
HLA A*0101	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.370897	0.850740	-3.520157	23490.773456
HLA A*2602	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.349646	0.829467	-3.520179	22368.982241
HLA B*1801	1:21-29 9	VSDDERADI	0.727910	0.266210	-4.514618	0.994120	-3.520498	32705.264338
HLA A*6801	1:26-34 9	RADIDRRVA	1.395400	-0.251450	-4.664602	1.143950	-3.520652	46195.719721
HLA A*3002	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.407173	0.886414	-3.520760	25537.205130
HLA A*0203	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.181120	0.660357	-3.520763	15174.696543
HLA B*2705	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.398572	0.877544	-3.521027	25036.401088
HLA B*1502	1:19-27 9	NAVSDDERA	1.177173	-0.137631	-4.560628	1.039542	-3.521086	36360.314284
HLA B*1503	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.212030	0.690533	-3.521497	16294.079829
HLA A*2501	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.454628	0.932973	-3.521656	28485.789657
HLA A*0201	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.394512	0.872785	-3.521727	24803.444160
HLA A*2902	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.408235	0.886414	-3.521822	25599.726899
HLA A*3002	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.454828	0.932973	-3.521855	28498.891592
HLA A*3201	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.476991	0.955042	-3.521949	29990.980285
HLA B*1503	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.403311	0.880895	-3.522415	25311.087878
HLA A*2601	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.286567	0.764021	-3.522546	19344.933957
HLA B*3801	1:64-72 9	AEPPAHLRT	1.338424	-0.305352	-4.555795	1.033072	-3.522723	35957.934567
HLA A*3101	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.235527	0.712665	-3.522862	17199.944249
HLA A*6802	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.160919	0.637921	-3.522998	14485.021460
HLA A*2601	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.220201	0.697019	-3.523182	16603.565070
HLA A*3001	1:72-80 9	TAILDATKP	0.635852	0.144974	-4.304031	0.780826	-3.523205	20138.678716
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HLA A*6802	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.127420	0.603848	-3.523572	13409.734700
HLA B*4002	1:163-171	9	PSRGTVYQM	1.173901	-0.101162	-4.596713	1.072739	-3.523974	39510.576687
HLA B*1503	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.319150	0.795128	-3.524022	20852.105301
HLA B*4501	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.456550	0.932462	-3.524088	28612.126851
HLA A*3301	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.525710	1.001469	-3.524241	33551.317773
HLA B*4403	1:26-34	9	RADIDRRVA	1.395400	-0.251450	-4.668481	1.143950	-3.524531	46610.175424
HLA B*0801	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.397470	0.872785	-3.524685	24972.958298
HLA A*0202	1:64-72	9	AEPPAHLRT	1.338424	-0.305352	-4.557757	1.033072	-3.524685	36120.733239
HLA B*4002	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.615335	1.090544	-3.524792	41241.588698
HLA B*5701	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.405898	0.880895	-3.525002	25462.297884
HLA B*1501	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.272193	0.746698	-3.525495	18715.140944
HLA A*0219	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.355933	0.830057	-3.525876	22695.170334
HLA B*0803	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.478710	0.952818	-3.525893	30109.981200
HLA A*2403	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.412394	0.886414	-3.525980	25846.034559
HLA A*2602	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-4.556023	1.029850	-3.526172	35976.808777
HLA A*0203	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.216757	0.690533	-3.526224	16472.404695
HLA B*5701	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.403901	0.877544	-3.526356	25345.480698
HLA A*8001	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.458883	0.932462	-3.526421	28766.245360
HLA A*3002	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.346820	0.820380	-3.526440	22223.875440
HLA B*3501	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.013954	0.487485	-3.526469	10326.523961
HLA B*4403	1:32-40	9	RVAAAPSPV	0.757389	0.366297	-4.650366	1.123686	-3.526680	44706.040591
HLA B*1502	1:66-74	9	PPAHLRTAI	1.205915	-0.174829	-4.558588	1.031086	-3.527502	36189.974363
HLA A*2501	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.357085	0.829467	-3.527618	22755.411538
HLA B*3501	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.274427	0.746698	-3.527729	18811.674798
HLA A*3002	1:31-39	9	RRVAAAPSP	0.723092	0.213085	-4.464430	0.936177	-3.528254	29136.025900
HLA A*2902	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.446323	0.917388	-3.528935	27946.204555
HLA A*6802	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.175533	0.646348	-3.529185	14980.728722
HLA B*4501	1:170-178	9	QMWLLGGAK	0.777766	0.312778	-4.619952	1.090544	-3.529408	41682.343163
HLA A*6901	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.359798	0.830057	-3.529741	22898.042095
HLA A*2402	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-3.933794	0.403811	-3.529983	8586.070058
HLA B*5101	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.463185	0.932973	-3.530212	29052.605535
HLA B*3501	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.341985	0.811766	-3.530218	21977.817064
HLA B*4001	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.417300	0.886414	-3.530886	26139.642604
HLA A*0101	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.365735	0.834848	-3.530887	23213.225914
HLA A*0212	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.353786	0.822896	-3.530890	22583.227902
HLA A*2602	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.576933	1.045865	-3.531068	37751.399339
HLA A*2603	1:92-100	9	AFASAAAIA	1.132156	-0.021408	-4.641875	1.110748	-3.531127	43840.466756
HLA B*0702	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.381945	0.850740	-3.531205	24095.980056
HLA A*2501	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.463768	0.932462	-3.531306	29091.610196
HLA A*8001	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.417882	0.886414	-3.531469	26174.736458
HLA B*7301	1:66-74	9	PPAHLRTAI	1.205915	-0.174829	-4.562571	1.031086	-3.531485	36523.353988
HLA B*5401	1:64-72	9	AEPPAHLRT	1.338424	-0.305352	-4.564854	1.033072	-3.531783	36715.914678
HLA A*0206	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.295418	0.763535	-3.531883	19743.209838
HLA A*0216	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.238668	0.706535	-3.532134	17324.802828
HLA B*2705	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.093498	0.561253	-3.532246	12402.188313
HLA B*1517	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-3.780725	0.247860	-3.532866	6035.669905
HLA B*0803	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.468262	0.934977	-3.533286	29394.246006
HLA B*2705	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.345459	0.811766	-3.533693	22154.371932
HLA A*0216	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.384498	0.850740	-3.533758	24238.095107
HLA A*3002	1:66-74	9	PPAHLRTAI	1.205915	-0.174829	-4.564967	1.031086	-3.533881	36725.450110
HLA B*5401	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.192590	0.658536	-3.534054	15580.816070
HLA A*0212	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.344207	0.809887	-3.534321	22090.582456
HLA B*4002	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-4.604662	1.070235	-3.534427	40240.343227
HLA A*2403	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.354963	0.820380	-3.534583	22644.519478
HLA B*3901	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.412222	0.877544	-3.534678	25835.829409
HLA A*3301	1:56-64	9	AVVSAATTA	1.129368	-0.059133	-4.605063	1.070235	-3.534829	40277.586432
HLA A*2902	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.407768	0.872785	-3.534983	25572.181883
HLA B*7301	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.581355	1.045865	-3.535490	38137.725200
HLA B*0802	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.468558	0.932973	-3.535586	29414.289308
HLA A*2603	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.625727	1.090014	-3.535713	42240.316037
HLA B*0802	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.422210	0.886414	-3.535796	26436.872044
HLA B*4501	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.607234	1.071321	-3.535913	40479.427572
HLA B*4403	1:181-189	9	RSAGTMGTA	1.257907	-0.163626	-4.630440	1.094281	-3.536159	42701.214349
HLA B*4403	1:74-82	9	ILDATKPEV	0.983482	0.144529	-4.664176	1.128011	-3.536165	46150.507476
HLA A*0301	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.346310	0.809887	-3.536423	22197.801119
HLA A*2402	1:196-204	9	TATLTDLGA	1.275348	-0.229483	-4.582609	1.045865	-3.536744	38248.059837
HLA A*8001	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.414372	0.877544	-3.536828	25964.035069
HLA B*5801	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.348603	0.811766	-3.536837	22315.316630
HLA B*3801	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.491959	0.955042	-3.536918	31042.681589
HLA A*2501	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.423340	0.886414	-3.536926	26505.754509
HLA B*1801	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.417859	0.880895	-3.536963	26173.320472
HLA A*0201	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.387938	0.850740	-3.537198	24430.824914
HLA A*3101	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.360252	0.822896	-3.537355	22921.962623
HLA A*3002	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.284248	0.746698	-3.537550	19241.915791
HLA A*0201	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.198046	0.660357	-3.537689	15777.773056
HLA A*8001	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.418679	0.880895	-3.537783	26222.783724
HLA B*4501	1:185-193	9	TMGTAAVTP	1.086662	0.003352	-4.628330	1.090014	-3.538316	42494.271494
HLA A*6901	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.389059	0.850740	-3.538319	24493.950489
HLA B*4801	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.358755	0.820380	-3.538375	22843.107212
HLA A*2602	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.591537	1.053156	-3.538382	39042.485091
HLA B*1509	1:206-214	9	TALAFTVEP	0.912771	0.088698	-4.540072	1.001469	-3.538603	34679.432672
HLA B*1502	1:64-72	9	AEPPAHLRT	1.338424	-0.305352	-4.571912	1.033072	-3.538841	37317.471078
HLA B*1501	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.334107	0.795128	-3.538979	21582.747552
HLA B*0802	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.471505	0.932462	-3.539042	29614.514270
HLA A*0211	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-3.899990	0.360868	-3.539122	7943.100136
HLA A*0211	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.206612	0.667402	-3.539210	16092.070527
HLA B*1502	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.369654	0.830057	-3.539597	23423.642928
HLA A*6801	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.252629	0.712665	-3.539963	17890.766209
HLA A*0201	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.252678	0.712665	-3.540013	17892.798853
HLA B*1801	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.475144	0.934977	-3.540167	29863.724201
HLA A*2501	1:31-39	9	RRVAAAPSP	0.723092	0.213085	-4.476384	0.936177	-3.540208	29949.149531
HLA A*3201	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.352057	0.811766	-3.540290	22493.487529
HLA A*0101	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.413223	0.872785	-3.540438	25895.439654
HLA A*3101	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.391244	0.850740	-3.540504	24617.494904
HLA B*4801	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.350407	0.809887	-3.540521	22408.225067
HLA A*3201	1:134-142	9	SRPLGAGTA	1.158305	-0.105149	-4.593732	1.053156	-3.540576	39240.259623
HLA A*0203	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.335711	0.795128	-3.540584	21662.642330
HLA A*3001	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.290536	0.748881	-3.541655	19522.504498
HLA A*1101	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.476897	0.934977	-3.541920	29984.491072
HLA A*2602	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.613479	1.071321	-3.542158	41065.705996
HLA B*0702	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.338348	0.795947	-3.542401	21794.532182
HLA B*4001	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.415253	0.872785	-3.542468	26016.761992
HLA B*4801	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.429237	0.886414	-3.542824	26868.126147
HLA A*3301	1:84-92	9	RQSRWRTAA	1.066920	-0.037070	-4.572805	1.029850	-3.542955	37394.265672
HLA B*0802	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.460345	0.917388	-3.542957	28863.205409
HLA B*4002	1:119-127	9	TVAEQVLTA	1.296709	-0.236373	-4.603475	1.060336	-3.543139	40130.556886
HLA B*4002	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.355081	0.811766	-3.543314	22650.645524
HLA B*4002	1:137-145	9	LGAGTATVV	1.105696	-0.034375	-4.614823	1.071321	-3.543502	41192.978859
HLA A*6901	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.108737	0.565014	-3.543723	12845.087916

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HLA B*0802      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.480167       0.936177        -3.543991       30211.143591
HLA A*0219      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.354016       0.809887        -3.544130       22595.204007
HLA A*3002      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.577229       1.033072        -3.544158       37777.141203
HLA B*4402      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.421860       0.877544        -3.544316       26415.570568
HLA A*6901      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.325479       0.780826        -3.544653       21158.234296
HLA B*0801      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.309289       0.764415        -3.544874       20383.986398
HLA B*4601      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.395637       0.850740        -3.544897       24867.801590
HLA B*4001      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.365667       0.820380        -3.545288       23209.584351
HLA B*1517      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.235891       0.690533        -3.545358       17214.373015
HLA B*1509      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.478429       0.932973        -3.545456       30090.440544
HLA A*2603      1:42-50 9       AAFNDEVRA       1.135376        -0.030176       -4.650794       1.105200        -3.545594       44750.079827
HLA B*0803      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.482162       0.936177        -3.545985       30350.222399
HLA A*6802      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.111002       0.565014        -3.545988       12912.251741
HLA A*2402      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.547560       1.001469        -3.546091       35282.535961
HLA A*2402      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.585715       1.039542        -3.546174       38522.585637
HLA A*0201      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.252812       0.706535        -3.546277       17898.317193
HLA A*0250      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.514117       0.967740        -3.546378       32667.599558
HLA B*0702      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.427409       0.880895        -3.546514       26755.278707
HLA A*3002      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.548295       1.001469        -3.546826       35342.330324
HLA B*3901      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.427781       0.880895        -3.546885       26778.157892
HLA A*0250      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.578021       1.031086        -3.546935       37846.076763
HLA B*5301      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.576898       1.029850        -3.547047       37748.336001
HLA B*1502      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.515412       0.967740        -3.547672       32765.122015
HLA A*0250      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.549155       1.001469        -3.547686       35412.378150
HLA B*5401      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.434402       0.886414        -3.547988       27189.520377
HLA B*1509      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.465570       0.917388        -3.548182       29212.573273
HLA B*4601      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.378336       0.830057        -3.548278       23896.581953
HLA A*2403      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.421172       0.872785        -3.548387       26373.732481
HLA B*0803      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.421296       0.872785        -3.548511       26381.295550
HLA A*6801      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.426141       0.877544        -3.548596       26677.231494
HLA A*2902      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.360494       0.811766        -3.548727       22934.738726
HLA A*3002      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.239493       0.690533        -3.548960       17357.731649
HLA A*2601      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.399777       0.850740        -3.549037       25105.980445
HLA A*3201      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.594947       1.045865        -3.549081       39350.164829
HLA A*6801      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.622306       1.072739        -3.549567       41908.904520
HLA A*0203      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -3.901254       0.351592        -3.549662       7966.252367
HLA B*4403      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.622421       1.072739        -3.549682       41920.015396
HLA A*2601      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.359570       0.809887        -3.549684       22886.029288
HLA B*0702      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.422577       0.872785        -3.549792       26459.192666
HLA B*4501      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.603104       1.053156        -3.549948       40096.269448
HLA B*5401      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.361767       0.811766        -3.550001       23002.085735
HLA B*1801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.482540       0.932462        -3.550078       30376.668720
HLA B*5701      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.380255       0.830057        -3.550198       24002.435722
HLA B*1501      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.401034       0.850740        -3.550294       25178.749708
HLA B*1501      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.115396       0.565014        -3.550381       13043.541418
HLA B*2705      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.467790       0.917388        -3.550402       29362.300436
HLA B*1502      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.551998       1.001469        -3.550529       35644.946731
HLA B*4002      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -3.998903       0.448362        -3.550541       9974.780697
HLA B*1801      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.428521       0.877544        -3.550976       26823.829859
HLA B*4501      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.590647       1.039542        -3.551105       38962.516420
HLA B*3801      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.552830       1.001469        -3.551361       35713.275803
HLA B*1801      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.487737       0.936177        -3.551561       30742.360126
HLA A*0201      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.386627       0.834848        -3.551779       24357.186342
HLA A*6901      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.346911       0.795128        -3.551784       22228.564854
HLA B*5301      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.605049       1.053156        -3.551893       40276.279070
HLA A*3002      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.316100       0.764021        -3.552079       20706.193961
HLA A*0212      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.382309       0.830057        -3.552251       24116.193799
HLA B*1517      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -3.810395       0.257963        -3.552432       6462.413998
HLA B*1503      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.265518       0.712622        -3.552896       18429.697855
HLA B*1509      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.489224       0.936177        -3.553048       30847.816566
HLA A*0101      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.364871       0.811766        -3.553104       23167.058085
HLA A*8001      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.376022       0.822896        -3.553125       23769.581937
HLA B*4002      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.599173       1.045865        -3.553308       39735.005675
HLA A*0216      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.363210       0.809887        -3.553323       23078.618155
HLA A*3301      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.599326       1.045865        -3.553461       39748.980661
HLA A*6802      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.213895       0.660357        -3.553538       16364.220802
HLA B*4001      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.404361       0.850740        -3.553621       25372.369735
HLA B*4801      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.432073       0.877544        -3.554529       27044.141966
HLA A*2601      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.384790       0.830057        -3.554732       24254.360112
HLA A*3201      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.588027       1.033072        -3.554956       38728.200902
HLA A*3201      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.432522       0.877544        -3.554978       27072.100818
HLA A*6802      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.427783       0.872785        -3.554998       26778.302759
HLA A*3101      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.435905       0.880895        -3.555010       27283.822601
HLA B*1501      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -3.906851       0.351592        -3.555258       8069.572611
HLA A*2602      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.586350       1.031086        -3.555264       38578.895540
HLA A*2603      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.549573       0.994120        -3.555453       35446.495287
HLA A*0201      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.268180       0.712622        -3.555558       18543.007833
HLA B*4001      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.390506       0.834848        -3.555658       24575.712536
HLA A*2603      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.627391       1.071321        -3.556069       42402.415198
HLA B*4002      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.646163       1.090014        -3.556149       44275.449544
HLA B*0702      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.267078       0.710864        -3.556214       18496.019444
HLA A*6802      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.437301       0.880895        -3.556405       27371.639483
HLA A*8001      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.391303       0.834848        -3.556454       24620.824577
HLA A*6901      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.216978       0.660357        -3.556621       16480.783531
HLA B*5401      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.007775       0.451113        -3.556662       10180.638383
HLA B*1801      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.224069       0.667402        -3.556667       16752.074697
HLA B*4001      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.368529       0.811766        -3.556763       23363.022955
HLA A*2603      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.610152       1.053156        -3.556997       40752.327971
HLA A*2403      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.391850       0.834848        -3.557002       24651.878797
HLA B*0801      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.213487       0.656423        -3.557063       16348.824070
HLA B*5701      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.408141       0.850740        -3.557401       25594.187831
HLA B*1509      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.510262       0.952818        -3.557444       32378.872262
HLA B*0801      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.353088       0.795128        -3.557961       22546.971728
HLA A*1101      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.435550       0.877544        -3.558006       27261.543732
HLA B*1502      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.490958       0.932462        -3.558496       30971.222603
HLA A*3301      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.629916       1.071321        -3.558595       42649.730441
HLA B*5101      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.494837       0.936177        -3.558661       31249.088170
HLA B*0802      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.431547       0.872785        -3.558762       27011.389313
HLA B*2705      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.271648       0.712665        -3.558983       18691.666412
HLA A*1101      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.445501       0.886414        -3.559087       27893.339566
HLA B*1801      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.476793       0.917388        -3.559406       29977.354559
HLA B*4801      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.432308       0.872785        -3.559523       27058.776505
HLA B*5801      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.250089       0.690533        -3.559556       17786.444734
HLA A*0301      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.323588       0.764021        -3.559567       21066.291366
HLA A*2601      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.394634       0.834848        -3.559786       24810.422703
HLA A*6801      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.340657       0.780826        -3.559831       21910.742508
HLA A*2603      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.514954       0.955042        -3.559912       32730.575383
HLA A*0250      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.370101       0.809887        -3.560214       23447.731975
HLA B*3901      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.125367       0.565014        -3.560352       13346.479874
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HLA B*4501      1:163-171       9       PSRGTVYQM       1.173901        -0.101162       -4.633114       1.072739        -3.560375       42964.913297
HLA A*3201      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.493794       0.932973        -3.560822       31174.118223
HLA A*0216      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.395731       0.834848        -3.560883       24873.183454
HLA B*4001      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.390955       0.830057        -3.560897       24601.119469
HLA A*6802      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.411656       0.850740        -3.560916       25802.167035
HLA B*4402      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.384195       0.822896        -3.561299       24221.185830
HLA A*2501      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.478931       0.917388        -3.561544       30125.296910
HLA A*8001      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.391768       0.830057        -3.561710       24647.211501
HLA B*5801      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.356998       0.795128        -3.561870       22750.857136
HLA B*1503      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.479326       0.917388        -3.561938       30152.689075
HLA B*1501      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.222462       0.660357        -3.562105       16690.200469
HLA B*4501      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.563755       1.001469        -3.562286       36623.073871
HLA B*4403      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.391972       0.829467        -3.562505       24658.814697
HLA A*0101      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.392684       0.830057        -3.562627       24699.268484
HLA B*5801      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.358788       0.795947        -3.562841       22844.837379
HLA A*0206      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.368927       -0.194071       -3.562998       2338.441688
HLA A*2301      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.518497       0.955042        -3.563455       32998.687266
HLA B*5401      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.051630       0.487485        -3.564146       11262.388349
HLA B*0702      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.214201       0.649819        -3.564382       16375.733571
HLA B*4403      1:170-178       9       QMWLLGGAK       0.777766        0.312778        -4.655178       1.090544        -3.564634       45204.113155
HLA B*1503      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.180735       0.615847        -3.564888       15161.239192
HLA B*4403      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.594759       1.029850        -3.564908       39333.138112
HLA B*5701      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.277611       0.712665        -3.564946       18950.078553
HLA B*4601      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.376726       0.811766        -3.564960       23808.190500
HLA B*2705      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.387964       0.822896        -3.565068       24432.278805
HLA A*2601      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.388018       0.822896        -3.565122       24435.319041
HLA B*4402      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.446055       0.880895        -3.565159       27928.974680
HLA A*8001      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.437959       0.872785        -3.565174       27413.132611
HLA B*1502      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.451640       0.886414        -3.565226       28290.441048
HLA A*0202      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.533012       0.967740        -3.565272       34120.216777
HLA A*2403      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.388284       0.822896        -3.565387       24450.261345
HLA A*2603      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.611438       1.045865        -3.565572       40873.101250
HLA B*0803      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.498359       0.932462        -3.565897       31503.530566
HLA B*5401      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.560045       0.994120        -3.565925       36311.564088
HLA A*3301      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.605496       1.039542        -3.565954       40317.699493
HLA B*4403      1:185-193       9       TMGTAAVTP       1.086662        0.003352        -4.656698       1.090014        -3.566684       45362.613744
HLA B*4002      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.521795       0.955042        -3.566754       33250.282563
HLA B*3901      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.330604       0.763535        -3.567069       21409.358219
HLA A*0216      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.331212       0.764021        -3.567191       21439.377208
HLA A*2301      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.534971       0.967740        -3.567232       34274.509805
HLA B*3801      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.502356       0.934977        -3.567379       31794.771005
HLA A*0301      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.274343       0.706535        -3.567808       18808.011468
HLA B*5301      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.601144       1.033072        -3.568073       39915.768695
HLA A*6802      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.349176       0.780826        -3.568350       22344.792587
HLA A*8001      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.419153       0.850740        -3.568413       26251.455582
HLA A*2403      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.363656       0.795128        -3.568529       23102.352377
HLA B*5801      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.350064       0.780826        -3.569238       22390.533057
HLA A*2403      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.379214       0.809887        -3.569328       23944.980819
HLA A*2301      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.522312       0.952818        -3.569495       33289.879798
HLA A*2403      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.420356       0.850740        -3.569616       26324.269320
HLA A*0101      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.379508       0.809887        -3.569622       23961.178756
HLA A*0216      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.364869       0.795128        -3.569741       23166.932754
HLA B*4402      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.420493       0.850740        -3.569753       26332.530476
HLA A*3002      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.537495       0.967740        -3.569755       34474.231933
HLA B*2705      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.456188       0.886414        -3.569775       28588.299359
HLA A*2402      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.456289       0.886414        -3.569876       28594.950493
HLA B*0803      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.487347       0.917388        -3.569959       30714.764601
HLA A*0216      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.442770       0.872785        -3.569985       27718.543895
HLA B*4002      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.623263       1.053156        -3.570107       42001.282251
HLA A*1101      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.487639       0.917388        -3.570251       30735.375784
HLA A*0201      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.365484       0.795128        -3.570356       23199.792637
HLA A*0216      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.283092       0.712622        -3.570471       19190.768347
HLA A*3101      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.334617       0.764021        -3.570596       21608.099409
HLA B*4403      1:137-145       9       LGAGTATVV       1.105696        -0.034375       -4.642042       1.071321        -3.570721       43857.309207
HLA B*5701      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.391265       0.820380        -3.570885       24618.693535
HLA A*0212      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.443731       0.872785        -3.570946       27779.943086
HLA B*4002      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.524119       0.952818        -3.571301       33428.660993
HLA A*2602      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.604695       1.033072        -3.571623       40243.391084
HLA A*0301      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.367580       0.795947        -3.571633       23312.016604
HLA B*1501      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.197284       0.625647        -3.571637       15750.141934
HLA A*6802      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -3.791012       0.219167        -3.571844       6180.328012
HLA A*0250      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.125005       0.553011        -3.571994       13335.365246
HLA A*2902      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.381982       0.809887        -3.572096       24098.065851
HLA A*0219      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.422854       0.850740        -3.572114       26476.088732
HLA B*4801      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.423086       0.850740        -3.572346       26490.272568
HLA A*0301      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.367784       0.795128        -3.572657       23322.991228
HLA A*2603      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.407711       0.834848        -3.572863       25568.861875
HLA A*2902      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.407841       0.834848        -3.572992       25576.470866
HLA A*0101      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.369535       0.795947        -3.573588       23417.181135
HLA B*1517      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.403388       0.829467        -3.573921       25315.606977
HLA B*4001      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.383857       0.809887        -3.573970       24202.324292
HLA A*1101      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.397031       0.822896        -3.574134       24947.707198
HLA B*0802      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.451708       0.877544        -3.574163       28294.879792
HLA A*3201      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.613757       1.039542        -3.574215       41091.929354
HLA A*3301      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.605376       1.031086        -3.574290       40306.577199
HLA A*3001      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.285155       0.710864        -3.574291       19282.139073
HLA A*0212      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.425088       0.850740        -3.574348       26612.654034
HLA A*1101      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.447227       0.872785        -3.574442       28004.471773
HLA B*0802      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.409450       0.834848        -3.574602       25671.427323
HLA B*4001      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.397707       0.822896        -3.574811       24986.607221
HLA B*0702      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.321631       0.746698        -3.574933       20971.571023
HLA B*7301      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.576468       1.001469        -3.574999       37710.983274
HLA A*0212      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.409948       0.834848        -3.575100       25700.886683
HLA B*3901      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.387273       0.811766        -3.575507       24393.449972
HLA A*0101      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.339767       0.764021        -3.575746       21865.863885
HLA B*7301      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.104428       0.528496        -3.575932       12718.272491
HLA B*4501      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.543716       0.967740        -3.575976       34971.642923
HLA B*5101      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.266782       0.690533        -3.576249       18483.416002
HLA B*2705      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.397113       0.820380        -3.576733       24952.431397
HLA B*7301      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.397205       0.820380        -3.576825       24957.696558
HLA A*3002      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.407028       0.830057        -3.576970       25528.641052
HLA B*1801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.341296       0.764021        -3.577275       21943.007676
HLA A*3002      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.373289       0.795947        -3.577342       23620.500313
HLA A*0219      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.450322       0.872785        -3.577537       28204.711194
HLA B*5701      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.407239       0.829467        -3.577772       25541.073719
HLA B*4402      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.388025       0.809887        -3.578138       24435.715621
HLA A*0250      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.495993       0.917388        -3.578606       31332.373578
HLA B*5401      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.161779       0.583145        -3.578634       14513.730497
HLA B*5801      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.342198       0.763535        -3.578663       21988.639405
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HLA A*3201      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.515118       0.936177        -3.578941       32742.972545
HLA B*0803      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.511946       0.932973        -3.578974       32504.710261
HLA B*0702      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.390910       0.811766        -3.579144       24598.590902
HLA A*3201      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.452107       0.872785        -3.579322       28320.914030
HLA A*1101      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.408961       0.829467        -3.579494       25642.556618
HLA A*0219      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.292291       0.712622        -3.579669       19601.558221
HLA B*5801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.343765       0.764021        -3.579745       22068.126449
HLA A*3001      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.276958       0.697019        -3.579939       18921.600018
HLA B*4601      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.344294       0.764021        -3.580273       22095.004680
HLA A*3201      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.548013       0.967740        -3.580274       35319.393999
HLA A*0301      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.361156       0.780826        -3.580330       22969.754408
HLA B*4501      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.533207       0.952818        -3.580389       34135.540904
HLA A*6801      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.098648       0.518215        -3.580434       12550.134855
HLA A*6901      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.376529       0.795947        -3.580582       23797.373785
HLA A*0202      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.415902       0.834848        -3.581053       26055.637400
HLA B*3801      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.453862       0.872785        -3.581077       28435.595714
HLA A*3101      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.377105       0.795947        -3.581158       23828.936280
HLA A*2902      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.345217       0.764021        -3.581197       22142.030543
HLA A*0211      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.517630       0.936177        -3.581453       32932.879373
HLA A*0250      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.454297       0.872785        -3.581512       28464.069143
HLA A*2601      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.394061       0.811766        -3.582294       24777.694230
HLA A*0219      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.417370       0.834848        -3.582522       26143.885325
HLA A*2402      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.550299       0.967740        -3.582560       35505.799179
HLA B*4403      1:119-127       9       TVAEQVLTA       1.296709        -0.236373       -4.642979       1.060336        -3.582644       43952.079462
HLA B*4402      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.250364       0.667402        -3.582962       17797.706352
HLA B*1509      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.403363       0.820380        -3.582983       25314.100521
HLA A*2902      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.403534       0.820380        -3.583154       25324.099588
HLA B*4402      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.413226       0.830057        -3.583168       25895.579746
HLA B*1502      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.516290       0.932973        -3.583318       32831.482749
HLA A*2402      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.500859       0.917388        -3.583471       31685.391638
HLA A*2602      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.518490       0.934977        -3.583513       32998.151713
HLA B*1509      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.516244       0.932462        -3.583781       32827.930648
HLA B*3501      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.365188       0.780826        -3.584362       23183.983979
HLA B*0801      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.419790       0.834848        -3.584942       26289.970541
HLA A*2602      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.540121       0.955042        -3.585080       34683.372746
HLA B*4601      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.291886       0.706535        -3.585352       19583.327436
HLA A*0211      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.420255       0.834848        -3.585407       26318.146343
HLA B*2705      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.458364       0.872785        -3.585579       28731.873405
HLA B*5301      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.519152       0.932973        -3.586180       33048.531741
HLA A*0101      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.381355       0.795128        -3.586227       24063.282758
HLA B*0801      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.349996       0.763535        -3.586461       22387.020554
HLA B*5801      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.350955       0.764415        -3.586540       22436.488538
HLA B*0803      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.464202       0.877544        -3.586658       29120.740512
HLA A*0202      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.416900       0.830057        -3.586843       26115.613519
HLA A*0206      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.437587       0.850740        -3.586847       27389.710905
HLA B*3901      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.437968       0.850740        -3.587228       27413.725826
HLA B*0702      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.351660       0.764415        -3.587245       22472.931777
HLA B*4801      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.422755       0.834848        -3.587907       26470.073642
HLA A*0202      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.351533       0.763535        -3.587998       22466.367628
HLA B*1517      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.368980       0.780826        -3.588154       23387.302705
HLA B*2705      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.423195       0.834848        -3.588346       26496.865622
HLA A*2601      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.369398       0.780826        -3.588572       23409.834595
HLA B*5301      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.543810       0.955042        -3.588768       34979.211451
HLA A*2402      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.541663       0.952818        -3.588845       34806.678796
HLA A*2501      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.469747       0.880895        -3.588852       29494.918405
HLA A*3001      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.245919       0.656423        -3.589496       17616.466868
HLA A*3301      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.642681       1.053156        -3.589525       43921.892297
HLA A*0250      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.419600       0.830057        -3.589542       26278.452773
HLA B*4403      1:196-204       9       TATLTDLGA       1.275348        -0.229483       -4.635409       1.045865        -3.589544       43192.603895
HLA A*6901      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.354035       0.764415        -3.589620       22596.181929
HLA A*2603      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.622783       1.033072        -3.589712       41954.954474
HLA B*3801      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.542743       0.952818        -3.589926       34893.404788
HLA B*4002      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.591443       1.001469        -3.589975       39034.037384
HLA B*0801      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.336733       0.746698        -3.590035       21713.681096
HLA B*4002      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.621409       1.031086        -3.590323       41822.385944
HLA B*5401      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.240684       0.649819        -3.590866       17405.406026
HLA A*3301      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.585673       0.994120        -3.591553       38518.834567
HLA A*0212      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.195424       0.603848        -3.591575       15682.802733
HLA A*2902      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.338481       0.746698        -3.591783       21801.253860
HLA A*0250      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.304564       0.712665        -3.591899       20163.425108
HLA A*0202      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.289483       0.697019        -3.592464       19475.246455
HLA B*1502      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.412913       0.820380        -3.592533       25876.954183
HLA B*1501      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.373785       0.780826        -3.592959       23647.478193
HLA B*1503      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.154242       0.561253        -3.592989       14264.018932
HLA A*2902      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.443792       0.850740        -3.593052       27783.850807
HLA A*6901      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.305725       0.712665        -3.593059       20217.383634
HLA A*2601      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.388476       0.795128        -3.593348       24461.110154
HLA B*7301      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.587628       0.994120        -3.593508       38692.599679
HLA B*5701      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.389529       0.795947        -3.593582       24520.466743
HLA A*0201      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.196425       0.602482        -3.593943       15718.987200
HLA A*3001      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.129690       0.535432        -3.594258       13479.996775
HLA B*4403      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.633962       1.039542        -3.594421       43048.904472
HLA B*5401      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.547499       0.952818        -3.594681       35277.573571
HLA A*2603      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.634437       1.039542        -3.594895       43095.973926
HLA B*5401      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.531083       0.936177        -3.594906       33969.007235
HLA B*3501      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -3.184793       -0.410374       -3.595167       1530.356830
HLA B*1801      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.481650       0.886414        -3.595236       30314.449785
HLA A*2602      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.596742       1.001469        -3.595273       39513.141744
HLA A*8001      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.405402       0.809887        -3.595515       25433.249594
HLA A*0301      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.360076       0.764415        -3.595661       22912.664114
HLA A*0203      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.344609       0.748881        -3.595728       22111.027712
HLA B*5101      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.474007       0.877544        -3.596462       29785.631716
HLA B*5401      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.343540       0.746698        -3.596842       22056.668357
HLA A*2602      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.591075       0.994120        -3.596955       39000.897799
HLA B*1517      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.514613       0.917388        -3.597225       32704.910477
HLA A*0211      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.470043       0.872785        -3.597258       29515.030353
HLA B*4403      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.264762       0.667402        -3.597360       18397.621557
HLA B*5401      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.478609       0.880895        -3.597714       30102.977673
HLA B*5401      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.532821       0.934977        -3.597845       34105.268539
HLA B*4601      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.393819       0.795947        -3.597872       24763.891484
HLA A*2603      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.599411       1.001469        -3.597942       39756.722768
HLA A*0301      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.310614       0.712665        -3.597949       20446.276539
HLA A*0250      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.484570       0.886414        -3.598156       30518.985997
HLA B*0802      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.479298       0.880895        -3.598402       30150.731666
HLA A*0201      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.394425       0.795947        -3.598478       24798.479853
HLA B*5701      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.289140       0.690533        -3.598607       19459.870125
HLA B*1509      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.101097       0.502462        -3.598635       12621.081054
HLA A*2301      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.535049       0.936177        -3.598872       34280.629254
HLA B*5701      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.410653       0.811766        -3.598887       25742.632234
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HLA A*0219      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.394284       0.795128        -3.599156       24790.431738
HLA A*0301      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.362869       0.763535        -3.599334       23060.521603
HLA B*3801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.531908       0.932462        -3.599445       34033.571281
HLA B*3501      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.450333       0.850740        -3.599593       28205.474126
HLA B*3901      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.394923       0.795128        -3.599795       24826.937458
HLA A*6901      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.016426       0.416603        -3.599823       10385.461864
HLA A*3301      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.477691       0.877544        -3.600146       30039.369147
HLA B*1509      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.396182       0.795947        -3.600236       24899.032620
HLA B*7301      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.568484       0.967740        -3.600745       37024.082609
HLA B*4403      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.653966       1.053156        -3.600810       45078.101709
HLA A*2601      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.364434       0.763535        -3.600899       23143.758203
HLA B*4601      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.396133       0.795128        -3.601005       24896.204060
HLA A*0219      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.291753       0.690533        -3.601219       19577.289580
HLA B*1517      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.413073       0.811766        -3.601307       25886.475353
HLA A*6802      1:205-213       9       STALAFTVE       0.973168        -0.590501       -3.984224       0.382667        -3.601557       9643.257726
HLA A*0301      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.348427       0.746698        -3.601728       22306.264213
HLA A*2501      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.431960       0.830057        -3.601903       27037.120199
HLA B*4801      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.432036       0.830057        -3.601978       27041.801174
HLA A*1101      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.314684       0.712665        -3.602018       20638.757033
HLA B*4402      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.437087       0.834848        -3.602239       27358.167744
HLA A*0101      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.365780       0.763535        -3.602245       23215.612075
HLA A*2403      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.432353       0.830057        -3.602295       27061.557963
HLA B*4601      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.365848       0.763535        -3.602313       23219.254583
HLA B*1517      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.453223       0.850740        -3.602483       28393.783794
HLA B*3501      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.475386       0.872785        -3.602601       29880.369460
HLA A*0203      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.366168       0.763535        -3.602633       23236.344318
HLA B*4002      1:19-27 9       NAVSDDERA       1.177173        -0.137631       -4.642244       1.039542        -3.602703       43877.718588
HLA B*4601      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.367209       0.764415        -3.602794       23292.098880
HLA A*0211      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.299894       0.697019        -3.602875       19947.732254
HLA B*4801      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.398281       0.795128        -3.603153       25019.611645
HLA B*3801      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.520574       0.917388        -3.603186       33156.876230
HLA A*0101      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.384069       0.780826        -3.603243       24214.111031
HLA A*0211      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.261914       0.658536        -3.603378       18277.386903
HLA A*6801      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.366995       0.763535        -3.603460       23280.635004
HLA B*5101      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.454598       0.850740        -3.603858       28483.786363
HLA B*1502      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.598158       0.994120        -3.604038       39642.250532
HLA B*4002      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.540225       0.936177        -3.604048       34691.629589
HLA B*0801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.242164       0.637921        -3.604243       17464.828862
HLA A*6802      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.399418       0.795128        -3.604290       25085.208496
HLA B*0802      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.414297       0.809887        -3.604410       25959.540657
HLA B*1501      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.400435       0.795947        -3.604488       25144.039023
HLA A*8001      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.400682       0.795947        -3.604735       25158.325859
HLA A*2402      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.560106       0.955042        -3.605064       36316.671927
HLA A*0201      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.302457       0.697019        -3.605438       20065.815674
HLA A*6801      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.428591       0.822896        -3.605695       26828.183630
HLA A*3301      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.638774       1.033072        -3.605702       43528.514788
HLA A*2301      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.492168       0.886414        -3.605755       31057.631623
HLA A*0201      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.370251       0.764415        -3.605836       23455.851757
HLA A*3101      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.312452       0.706535        -3.605917       20532.958419
HLA A*2603      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.637155       1.031086        -3.606069       43366.568018
HLA B*2705      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.436227       0.830057        -3.606170       27304.051633
HLA A*0202      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.542421       0.936177        -3.606245       34867.552955
HLA A*2603      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.636399       1.029850        -3.606548       43291.089897
HLA B*5101      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.427017       0.820380        -3.606637       26731.117526
HLA B*4501      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.416630       0.809887        -3.606743       26099.371076
HLA B*5101      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.370836       0.764021        -3.606815       23487.469544
HLA A*1101      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.313436       0.706535        -3.606901       20579.554160
HLA B*4801      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.429851       0.822896        -3.606954       26906.090228
HLA A*1101      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.371024       0.764021        -3.607003       23497.636913
HLA A*0101      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.371473       0.764415        -3.607058       23521.929307
HLA A*0201      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.274674       0.667402        -3.607272       18822.363586
HLA B*3801      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.540650       0.932973        -3.607677       34725.615921
HLA B*1501      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.320348       0.712622        -3.607726       20909.716605
HLA A*8001      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.428201       0.820380        -3.607821       26804.101620
HLA B*1501      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.320961       0.712665        -3.608296       20939.261583
HLA B*1509      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.486661       0.877544        -3.609117       30666.283170
HLA A*1101      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.439331       0.830057        -3.609273       27499.877943
HLA B*5101      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.439352       0.830057        -3.609294       27501.216917
HLA A*0202      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.526722       0.917388        -3.609334       33629.639387
HLA B*3501      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.404483       0.795128        -3.609356       25379.508348
HLA A*0203      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.405463       0.795947        -3.609516       25436.827213
HLA B*5101      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.490484       0.880895        -3.609588       30937.395812
HLA A*6801      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.112656       0.502462        -3.610194       12961.522618
HLA B*5701      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.391054       0.780826        -3.610228       24606.709856
HLA B*0803      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.406342       0.795947        -3.610395       25488.345609
HLA B*4001      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.391296       0.780826        -3.610470       24620.424993
HLA B*3501      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.266937       0.656423        -3.610514       18490.016734
HLA B*0803      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.491433       0.880895        -3.610537       31005.086381
HLA B*4002      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.543530       0.932973        -3.610558       34956.699893
HLA A*8001      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.422640       0.811766        -3.610874       26463.057764
HLA A*2603      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.543392       0.932462        -3.610930       34945.544073
HLA B*4402      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.422711       0.811766        -3.610944       26467.352978
HLA B*1801      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.420995       0.809887        -3.611109       26363.033728
HLA A*2601      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.407399       0.795947        -3.611452       25550.471306
HLA B*1501      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.308871       0.697019        -3.611852       20364.366877
HLA A*2301      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.545405       0.932973        -3.612433       35107.937384
HLA A*6801      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.309475       0.697019        -3.612456       20392.699993
HLA A*2403      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.376099       0.763535        -3.612564       23773.825813
HLA A*2601      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.361579       0.748881        -3.612698       22992.132791
HLA B*1801      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.359723       0.746698        -3.613025       22894.078410
HLA A*2301      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.545640       0.932462        -3.613178       35126.935527
HLA A*1101      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.464120       0.850740        -3.613380       29115.227135
HLA B*5301      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.545861       0.932462        -3.613399       35144.803156
HLA A*6801      1:134-142       9       SRPLGAGTA       1.158305        -0.105149       -4.666653       1.053156        -3.613497       46414.410414
HLA B*4501      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.644798       1.031086        -3.613712       44136.503838
HLA A*6801      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.443846       0.830057        -3.613789       27787.308096
HLA A*0219      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.310819       0.697019        -3.613800       20455.902055
HLA B*5801      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.320475       0.706535        -3.613940       20915.825937
HLA A*2301      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.531358       0.917388        -3.613970       33990.514963
HLA B*4601      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.395381       0.780826        -3.614555       24853.141919
HLA A*3001      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.282131       0.667402        -3.614730       19148.352938
HLA B*0702      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.275095       0.660357        -3.614738       18840.599430
HLA B*0803      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.501261       0.886414        -3.614847       31714.717073
HLA A*0201      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.395797       0.780826        -3.614971       24876.951452
HLA B*4801      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.426958       0.811766        -3.615192       26727.502461
HLA A*2501      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.466026       0.850740        -3.615286       29243.248504
HLA B*0803      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.466033       0.850740        -3.615293       29243.723116
HLA B*1517      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.411290       0.795947        -3.615343       25780.400670
HLA B*4001      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.362237       0.746698        -3.615539       23026.986951
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HLA B*5101      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.450526       0.834848        -3.615678       28217.989158
HLA A*1101      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.427781       0.811766        -3.616014       26778.157892
HLA A*6901      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.327039       0.710864        -3.616175       21234.374867
HLA B*7301      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.572413       0.955042        -3.617371       37360.497023
HLA A*6801      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.490293       0.872785        -3.617508       30923.841983
HLA B*4801      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.330171       0.712622        -3.617550       21388.057527
HLA B*5801      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.367047       0.748881        -3.618166       23283.405973
HLA A*0202      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.469085       0.850740        -3.618345       29449.955596
HLA B*1509      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.491574       0.872785        -3.618789       31015.152059
HLA A*0301      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.367671       0.748881        -3.618790       23316.935624
HLA B*5701      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.413926       0.795128        -3.618798       25937.360896
HLA B*4001      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.415054       0.795947        -3.619107       26004.801179
HLA B*7301      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.309902       0.690533        -3.619369       20412.788530
HLA B*5801      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.332504       0.712665        -3.619839       21503.263766
HLA A*0216      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.385281       0.764415        -3.620866       24281.799222
HLA B*0802      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.441579       0.820380        -3.621199       27642.621259
HLA B*1503      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.385666       0.764415        -3.621251       24303.352124
HLA A*3001      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.224449       0.602482        -3.621967       16766.762685
HLA B*4001      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.385530       0.763535        -3.621995       24295.727571
HLA A*0216      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.319279       0.697019        -3.622260       20858.310641
HLA B*4801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.386376       0.764021        -3.622355       24343.091067
HLA A*2501      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.386378       0.764021        -3.622357       24343.222760
HLA A*3301      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.452478       0.830057        -3.622421       28345.132033
HLA B*5101      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.452063       0.829467        -3.622596       28318.003132
HLA A*0250      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.313410       0.690533        -3.622877       20578.329532
HLA B*2705      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.432818       0.809887        -3.622931       27090.560699
HLA B*5701      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.386977       0.764021        -3.622956       24376.827939
HLA B*2705      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.418155       0.795128        -3.623027       26191.167494
HLA A*3002      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.433363       0.809887        -3.623476       27124.583253
HLA A*1101      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.504508       0.880895        -3.623612       31952.719702
HLA A*8001      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.418745       0.795128        -3.623617       26226.756170
HLA A*6901      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.270163       0.646348        -3.623815       18627.867799
HLA A*0219      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.388234       0.764415        -3.623819       24447.483765
HLA A*2501      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.459217       0.834848        -3.624368       28788.352202
HLA B*7301      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.454842       0.830057        -3.624785       28499.816662
HLA A*3201      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.127289       0.502462        -3.624827       13405.672785
HLA B*3901      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.497781       0.872785        -3.624996       31461.632523
HLA A*0201      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.388648       0.763535        -3.625113       24470.772290
HLA B*4403      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.656242       1.031086        -3.625156       45315.029816
HLA A*0212      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.178756       0.553011        -3.625745       15092.334880
HLA B*1517      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.389381       0.763535        -3.625846       24512.111027
HLA A*6802      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.421919       0.795947        -3.625972       26419.143443
HLA A*0203      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.406823       0.780826        -3.625997       25516.628560
HLA B*1509      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.421442       0.795128        -3.626314       26390.145667
HLA B*0802      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.477186       0.850740        -3.626446       30004.449882
HLA A*2601      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.390894       0.764415        -3.626479       24597.659390
HLA A*0101      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.339623       0.712622        -3.627002       21858.649270
HLA A*0212      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.392104       0.764415        -3.627689       24666.286310
HLA A*2602      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.560792       0.932973        -3.627819       36374.086261
HLA A*2402      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.564023       0.936177        -3.627846       36645.667289
HLA A*6801      1:84-92 9       RQSRWRTAA       1.066920        -0.037070       -4.657887       1.029850        -3.628036       45486.959655
HLA A*2403      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.424104       0.795947        -3.628157       26552.398290
HLA B*7301      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.509134       0.880895        -3.628238       32294.901602
HLA A*0211      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.479129       0.850740        -3.628389       30138.989881
HLA B*4001      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.392494       0.764021        -3.628473       24688.447611
HLA A*2603      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.506155       0.877544        -3.628610       32074.125092
HLA A*0212      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.341411       0.712665        -3.628746       21948.825200
HLA A*2602      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.597181       0.967740        -3.629441       39553.135412
HLA A*3201      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.342149       0.712665        -3.629484       21986.141469
HLA B*1509      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.459640       0.830057        -3.629582       28816.399379
HLA B*1801      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.464569       0.834848        -3.629720       29145.327122
HLA B*0802      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.459320       0.829467        -3.629853       28795.205657
HLA B*5701      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.393927       0.763535        -3.630392       24770.054867
HLA A*3001      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -3.919054       0.288570        -3.630484       8299.534965
HLA A*6801      1:66-74 9       PPAHLRTAI       1.205915        -0.174829       -4.661630       1.031086        -3.630544       45880.658155
HLA B*4402      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.427036       0.795947        -3.631089       26732.274450
HLA A*2402      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.563668       0.932462        -3.631206       36615.743914
HLA A*2501      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.443130       0.811766        -3.631363       27741.496393
HLA A*0301      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.328393       0.697019        -3.631374       21300.646422
HLA B*4001      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.395938       0.764415        -3.631523       24885.027656
HLA A*3001      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.290841       0.658536        -3.632305       19536.239223
HLA A*0219      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.185673       0.553011        -3.632662       15334.630541
HLA A*6801      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.565491       0.932462        -3.633029       36769.782623
HLA B*4601      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.346023       0.712665        -3.633358       22183.155261
HLA B*0702      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.428530       0.795128        -3.633403       26824.410321
HLA A*0101      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.382551       0.748881        -3.633670       24129.635535
HLA A*3101      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.428892       0.795128        -3.633764       26846.767664
HLA B*1517      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.152057       0.518215        -3.633842       14192.434074
HLA A*2603      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.463319       0.829467        -3.633852       29061.565685
HLA A*2403      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.380551       0.746698        -3.633853       24018.802465
HLA B*4403      1:206-214       9       TALAFTVEP       0.912771        0.088698        -4.635330       1.001469        -3.633861       43184.659941
HLA A*0212      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.340723       0.706535        -3.634188       21914.061730
HLA B*5301      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.383404       0.748881        -3.634523       24177.067625
HLA B*5801      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.260645       0.625647        -3.634998       18224.070355
HLA A*3101      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.325761       0.690533        -3.635228       21171.974400
HLA A*0202      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.508030       0.872785        -3.635245       32212.891344
HLA B*0801      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.416134       0.780826        -3.635308       26069.595990
HLA A*2501      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.341989       0.706535        -3.635455       21978.054860
HLA B*4801      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.431561       0.795947        -3.635614       27012.266099
HLA B*4402      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.399777       0.764021        -3.635756       25105.980445
HLA A*8001      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.399859       0.764021        -3.635838       25110.734615
HLA A*0212      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.326896       0.690533        -3.636363       21227.368611
HLA A*3001      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -3.896391       0.259962        -3.636429       7877.540172
HLA B*1517      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.296865       0.660357        -3.636508       19809.113673
HLA A*0216      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.432590       0.795947        -3.636643       27076.348406
HLA B*4002      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.457262       0.820380        -3.636882       28659.066208
HLA A*3001      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.188587       0.551693        -3.636894       15437.845077
HLA B*1509      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.517954       0.880895        -3.637058       32957.475078
HLA A*3101      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.400672       0.763535        -3.637137       25157.781450
HLA A*2403      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.401208       0.764021        -3.637187       25188.831580
HLA B*4601      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.384047       0.746698        -3.637349       24212.932099
HLA A*3101      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.401908       0.764415        -3.637493       25229.472429
HLA B*4402      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.418322       0.780826        -3.637496       26201.229509
HLA A*2501      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.432757       0.795128        -3.637629       27086.750487
HLA B*5101      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.511002       0.872785        -3.638217       32434.096627
HLA A*3201      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.519331       0.880895        -3.638435       33062.122491
HLA A*3101      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.419276       0.780826        -3.638450       26258.841529
HLA B*0802      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.468671       0.830057        -3.638614       29421.928446
HLA A*6801      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.571755       0.932973        -3.638782       37303.947343
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HLA A*6801      1:64-72 9       AEPPAHLRT       1.338424        -0.305352       -4.672024       1.033072        -3.638952       46991.981786
HLA A*2902      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.434385       0.795128        -3.639257       27188.490750
HLA B*0802      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.435212       0.795947        -3.639266       27240.314604
HLA A*2601      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.345812       0.706535        -3.639277       22172.357133
HLA A*2501      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.462177       0.822896        -3.639281       28985.257198
HLA B*5301      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.592141       0.952818        -3.639324       39096.805232
HLA B*1509      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.403628       0.764021        -3.639607       25329.580204
HLA B*4001      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.352289       0.712665        -3.639624       22505.537795
HLA A*6801      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.633788       0.994120        -3.639668       43031.674076
HLA B*0803      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.474554       0.834848        -3.639706       29823.200302
HLA B*5301      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.574696       0.934977        -3.639720       37557.471351
HLA B*0802      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.462624       0.822896        -3.639727       29015.065850
HLA B*1503      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.352630       0.712665        -3.639965       22523.198829
HLA A*3001      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.289918       0.649819        -3.640099       19494.747613
HLA A*2501      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.450094       0.809887        -3.640207       28189.914394
HLA B*1801      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.513074       0.872785        -3.640289       32589.226449
HLA A*2403      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.421143       0.780826        -3.640317       26372.020389
HLA A*3101      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.387186       0.746698        -3.640488       24388.567724
HLA A*3201      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.057241       0.416603        -3.640638       11408.828947
HLA B*0803      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.470252       0.829467        -3.640785       29529.244675
HLA A*0202      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.301183       0.660357        -3.640827       20007.065668
HLA B*4002      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.635062       0.994120        -3.640942       43158.034991
HLA B*5801      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.353673       0.712622        -3.641051       22577.364371
HLA A*2902      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.347666       0.706535        -3.641131       22267.199948
HLA A*3201      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.298077       0.656423        -3.641654       19864.488122
HLA A*1101      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.476944       0.834848        -3.642095       29987.735502
HLA A*2601      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.388894       0.746698        -3.642196       24484.676576
HLA A*0219      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.348793       0.706535        -3.642259       22325.097367
HLA A*0202      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.355038       0.712622        -3.642417       22648.439956
HLA B*0702      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.243137       0.600711        -3.642426       17503.988573
HLA B*4403      1:21-29 9       VSDDERADI       0.727910        0.266210        -4.637047       0.994120        -3.642927       43355.777378
HLA A*3201      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.472642       0.829467        -3.643175       29692.158117
HLA A*6802      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.299682       0.656423        -3.643259       19938.022266
HLA A*1101      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.453183       0.809887        -3.643297       28391.172591
HLA B*5801      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.354333       0.710864        -3.643469       22611.712104
HLA A*2902      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.424536       0.780826        -3.643710       26578.842227
HLA A*0212      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.440031       0.795947        -3.644084       27544.247543
HLA A*2902      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.282016       0.637921        -3.644095       19143.277678
HLA A*2602      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.580272       0.936177        -3.644095       38042.729787
HLA A*3101      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.269952       0.625647        -3.644304       18618.800284
HLA A*2402      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.577318       0.932973        -3.644346       37784.908067
HLA A*0206      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.197698       0.553011        -3.644687       15765.145423
HLA A*0211      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.439888       0.795128        -3.644760       27535.159352
HLA A*0201      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.393943       0.748881        -3.645062       24770.992907
HLA A*3101      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.394007       0.748881        -3.645126       24774.611396
HLA A*0219      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.249022       0.603848        -3.645174       17742.813234
HLA A*6901      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.295117       0.649819        -3.645298       19729.543073
HLA B*3901      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.441553       0.795947        -3.645607       27640.976330
HLA B*1509      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.475332       0.829467        -3.645865       29876.651753
HLA B*0803      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.246931       0.600711        -3.646221       17657.590443
HLA A*2602      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.532934       0.886414        -3.646521       34114.125963
HLA B*5701      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.411027       0.764415        -3.646612       25764.784861
HLA B*4001      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.395764       0.748881        -3.646883       24875.067382
HLA A*2902      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.442994       0.795947        -3.647047       27732.793210
HLA B*2705      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.411478       0.764415        -3.647063       25791.560614
HLA B*5801      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.344085       0.697019        -3.647066       22084.368935
HLA A*0211      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.359780       0.712622        -3.647158       22897.051109
HLA B*5101      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.459191       0.811766        -3.647425       28786.639093
HLA B*1501      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.337995       0.690533        -3.647462       21776.853455
HLA A*0212      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.411130       0.763535        -3.647595       25770.918515
HLA A*0301      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.360515       0.712622        -3.647893       22935.855423
HLA A*0216      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.304437       0.656423        -3.648014       20157.535546
HLA B*4801      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.412659       0.764415        -3.648244       25861.839522
HLA B*4402      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.412807       0.764415        -3.648393       25870.655334
HLA B*7301      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.581625       0.932462        -3.649163       38161.459482
HLA B*5701      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.000806       0.351592        -3.649214       10018.586196
HLA B*4801      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.430046       0.780826        -3.649220       26918.174335
HLA B*7301      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.584198       0.934977        -3.649221       38388.192327
HLA B*3801      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.535653       0.886414        -3.649239       34328.324184
HLA B*7301      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.444486       0.795128        -3.649358       27828.226936
HLA A*0250      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.585572       0.936177        -3.649395       38509.875157
HLA A*0219      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.445352       0.795947        -3.649406       27883.834494
HLA B*5701      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.396124       0.746698        -3.649425       24895.665323
HLA A*0301      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.360329       0.710864        -3.649465       22926.055163
HLA B*7301      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.582621       0.932973        -3.649649       38249.094440
HLA B*0803      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.470492       0.820380        -3.650112       29545.543666
HLA A*3301      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.585123       0.934977        -3.650147       38470.103884
HLA A*3001      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.247018       0.596633        -3.650385       17661.125244
HLA B*4002      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.618148       0.967740        -3.650408       41509.520847
HLA A*0206      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.523311       0.872785        -3.650526       33366.508044
HLA A*3001      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.266766       0.615847        -3.650919       18482.716063
HLA A*0211      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.415382       0.764415        -3.650968       26024.504272
HLA A*3101      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.363619       0.712622        -3.650997       23100.352765
HLA A*2602      1:102-110       9       GLGAFGLGV       0.937231        0.015587        -4.603893       0.952818        -3.651076       40169.219631
HLA A*2301      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.054901       0.403811        -3.651090       11347.520650
HLA A*8001      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.277061       0.625647        -3.651414       18926.104559
HLA A*3001      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -3.956486       0.305034        -3.651452       9046.607619
HLA A*3101      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.298002       0.646348        -3.651654       19861.049550
HLA B*0801      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.362669       0.710864        -3.651805       23049.919877
HLA A*0216      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.415439       0.763535        -3.651904       26027.883444
HLA A*2403      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.079458       0.427495        -3.651962       12007.643873
HLA B*1509      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.416592       0.764415        -3.652178       26097.112058
HLA A*3101      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.363400       0.710864        -3.652536       23088.733445
HLA A*0301      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.343484       0.690533        -3.652950       22053.804764
HLA B*0803      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.483104       0.830057        -3.653047       30416.134593
HLA B*1501      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.171450       0.518215        -3.653235       14840.534222
HLA B*4501      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.589592       0.936177        -3.653415       38867.989751
HLA A*3101      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.080994       0.427495        -3.653499       12050.202972
HLA B*1501      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.402446       0.748881        -3.653565       25260.747698
HLA B*1801      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.476507       0.822896        -3.653610       29957.575839
HLA A*1101      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.417459       0.763535        -3.653924       26149.260428
HLA A*6901      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.366699       0.712622        -3.654077       23264.771259
HLA B*7301      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.215446       0.561253        -3.654193       16422.754127
HLA B*5301      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.590384       0.936177        -3.654207       38938.915887
HLA A*6802      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.418653       0.764415        -3.654238       26221.223284
HLA B*5101      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.449372       0.795128        -3.654245       28143.134428
HLA A*1101      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.450223       0.795947        -3.654276       28198.303379
HLA A*0301      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.292262       0.637921        -3.654341       19600.285755
HLA B*0801      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.361084       0.706535        -3.654549       22965.902552
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HLA A*2602	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.532178	0.877544	-3.654633	34054.751421
HLA B*4501	1:21-29	9	VSDDERADI	0.727910	0.266210	-4.648762	0.994120	-3.654642	44541.158618
HLA B*5101	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.365851	0.710864	-3.654986	23219.380197
HLA A*2403	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.403962	0.748881	-3.655081	25349.045971
HLA A*2601	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.367852	0.712622	-3.655231	23326.650585
HLA A*0206	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.419797	0.764415	-3.655382	26290.397222
HLA A*3101	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.293320	0.637921	-3.655398	19648.059801
HLA A*0216	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.220535	0.565014	-3.655521	16616.324900
HLA A*3002	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.293820	0.637921	-3.655899	19670.713435
HLA B*5401	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.506940	0.850740	-3.656200	32132.132315
HLA A*2301	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.537114	0.880895	-3.656218	34444.031881
HLA B*5401	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.534219	0.877544	-3.656675	34215.226319
HLA A*0101	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.294852	0.637921	-3.656930	19717.485744
HLA A*0250	1:156-164	9	VMNNVAPPS	0.722767	-0.916838	-3.462939	-0.194071	-3.657010	2903.613704
HLA A*2301	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.534710	0.877544	-3.657166	34253.934219
HLA B*3901	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.404016	0.746698	-3.657317	25352.200285
HLA A*0101	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.370007	0.712665	-3.657341	23442.658539
HLA A*6901	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.315891	0.658536	-3.657355	20696.226740
HLA A*0301	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.313913	0.656423	-3.657490	20602.167195
HLA A*3201	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.543953	0.886414	-3.657540	34990.756609
HLA A*6801	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.222574	0.565014	-3.657560	16694.535054
HLA B*4402	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.421240	0.763535	-3.657705	26377.870495
HLA A*1101	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.422144	0.764415	-3.657729	26432.867771
HLA B*0702	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.009387	0.351592	-3.657795	10218.490800
HLA B*3501	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.304226	0.646348	-3.657878	20147.723432
HLA A*0203	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.304289	0.646348	-3.657941	20150.666565
HLA B*3901	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.481048	0.822896	-3.658152	30272.495404
HLA B*0702	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.422114	0.763535	-3.658579	26431.008851
HLA A*3002	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.086220	0.427495	-3.658724	12196.061812
HLA B*4002	1:35-43	9	AAPSPVAAA	1.017695	-0.085233	-4.591265	0.932462	-3.658803	39017.991777
HLA B*1502	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.493928	0.834848	-3.659080	31183.732671
HLA A*0202	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.423693	0.764415	-3.659278	26527.272218
HLA B*0803	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.482474	0.822896	-3.659578	30372.067705
HLA A*2501	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.406342	0.746698	-3.659643	25488.345609
HLA A*8001	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.423277	0.763535	-3.659742	26501.883176
HLA A*8001	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.424254	0.764415	-3.659839	26561.593196
HLA B*4601	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.408726	0.748881	-3.659845	25628.688031
HLA A*0212	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.372516	0.712622	-3.659894	23578.496674
HLA B*7301	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.612713	0.952818	-3.659896	40993.345365
HLA A*8001	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.406706	0.746698	-3.660007	25509.727387
HLA B*5101	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.406913	0.746698	-3.660214	25521.874700
HLA A*0201	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.225248	0.565014	-3.660234	16797.631217
HLA A*6802	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.318924	0.658536	-3.660388	20841.278585
HLA B*4402	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.407220	0.746698	-3.660522	25539.968348
HLA A*3301	1:183-191	9	AGTMGTAAV	0.865215	0.089827	-4.615603	0.955042	-3.660562	41267.031359
HLA B*1509	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.495519	0.834848	-3.660670	31298.152337
HLA B*4801	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.424459	0.763535	-3.660924	26574.097627
HLA B*4402	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.410150	0.748881	-3.661269	25712.846815
HLA A*2603	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.594474	0.932973	-3.661502	39307.399199
HLA B*1801	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.491666	0.830057	-3.661608	31021.696502
HLA B*1509	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.472205	0.809887	-3.662318	29662.295725
HLA A*8001	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.443196	0.780826	-3.662370	27745.698907
HLA A*3301	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.630396	0.967740	-3.662656	42696.825407
HLA A*0250	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-4.426956	0.764021	-3.662935	26727.357869
HLA A*2601	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.375636	0.712665	-3.662971	23748.502398
HLA B*3501	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.427461	0.764415	-3.663046	26758.463244
HLA B*1509	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.474977	0.811766	-3.663211	29852.255684
HLA A*2403	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.313330	0.649819	-3.663512	20574.544780
HLA A*0216	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.322138	0.658536	-3.663602	20996.091383
HLA A*0101	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.370232	0.706535	-3.663698	23454.836631
HLA A*0219	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.427269	0.763535	-3.663734	26746.595531
HLA A*2902	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.428486	0.764415	-3.664071	26821.653238
HLA A*0219	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.444937	0.780826	-3.664111	27857.147097
HLA A*2402	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.493693	0.829467	-3.664226	31166.867180
HLA A*2603	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.537626	0.872785	-3.664841	34484.677614
HLA A*0212	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.445846	0.780826	-3.665020	27915.530670
HLA A*2403	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.378016	0.712622	-3.665394	23879.006630
HLA A*1101	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.446269	0.780826	-3.665443	27942.727497
HLA B*3901	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.500333	0.834848	-3.665484	31647.018056
HLA A*2301	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.538352	0.872785	-3.665567	34542.372333
HLA A*2403	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.430259	0.764415	-3.665844	26931.429413
HLA A*2902	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.429383	0.763535	-3.665848	26877.139581
HLA B*5801	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.184137	0.518215	-3.665922	15280.471449
HLA B*1801	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.414910	0.748881	-3.666029	25996.220926
HLA A*0219	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.326682	0.660357	-3.666326	21216.920951
HLA A*2902	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.377276	0.710864	-3.666412	23838.348708
HLA A*6802	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.166718	0.500136	-3.666582	14679.716620
HLA B*1501	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.269371	0.602482	-3.666889	18593.937664
HLA B*0802	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.478750	0.811766	-3.666984	30112.750486
HLA A*0211	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.327794	0.660357	-3.667437	21271.281976
HLA B*1502	1:31-39	9	RRVAAAPSP	0.723092	0.213085	-4.603736	0.936177	-3.667559	40154.662430
HLA B*3501	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.084208	0.416603	-3.667605	12139.714065
HLA B*1502	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.585034	0.917388	-3.667646	38462.196175
HLA B*3801	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.518960	0.850740	-3.668220	33033.874303
HLA A*0206	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.417130	0.748881	-3.668250	26129.462882
HLA B*7301	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.585690	0.917388	-3.668302	38520.293273
HLA B*0802	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-4.432506	0.764021	-3.668485	27071.075638
HLA A*0216	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.335975	0.667402	-3.668573	21675.771867
HLA A*2902	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.381416	0.712622	-3.668794	24066.667668
HLA A*0212	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.329389	0.660357	-3.669032	21349.561775
HLA A*0219	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.270133	0.600711	-3.669422	18626.557774
HLA B*4403	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.622349	0.952818	-3.669531	41912.985724
HLA B*3901	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.499814	0.830057	-3.669756	31609.203949
HLA A*0216	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.450597	0.780826	-3.669771	28222.569216
HLA A*3201	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.587414	0.917388	-3.670026	38673.556003
HLA B*0801	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.360795	0.690533	-3.670261	22950.625748
HLA B*5701	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.419316	0.748881	-3.670435	26261.256617
HLA A*3301	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.623349	0.952818	-3.670532	42009.690317
HLA A*2602	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.377093	0.706535	-3.670558	23828.291730
HLA B*1801	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.482441	0.811766	-3.670675	30369.767459
HLA B*3801	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.548316	0.877544	-3.670772	35344.051149
HLA A*2603	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.501139	0.830057	-3.671081	31705.796526
HLA B*1509	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.434707	0.763535	-3.671172	27208.649100
HLA B*1801	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.521974	0.850740	-3.671234	33263.956280
HLA B*1502	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.481123	0.809887	-3.671237	30277.736525
HLA A*2501	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.452096	0.780826	-3.671270	28320.147975
HLA B*2705	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.418867	0.746698	-3.672168	26234.135168
HLA A*6901	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.273175	0.600711	-3.672465	18757.510010
HLA B*1502	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.273288	0.600711	-3.672577	18762.381493
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HLA A*0206      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -3.932624       0.259962        -3.672663       8562.969246
HLA B*5401      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.089528       0.416603        -3.672924       12289.315438
HLA A*2501      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.469071       0.795947        -3.673124       29448.999685
HLA B*3501      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.469174       0.795947        -3.673227       29456.010416
HLA A*2402      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.546061       0.872785        -3.673276       35160.967879
HLA A*0250      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.524112       0.850740        -3.673372       33428.118461
HLA A*3301      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.605841       0.932462        -3.673379       40349.775045
HLA B*4403      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.628730       0.955042        -3.673688       42533.370652
HLA B*0702      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.124822       0.451113        -3.673709       13329.739291
HLA B*3801      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.554815       0.880895        -3.673920       35876.907637
HLA B*5401      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.508887       0.834848        -3.674039       32276.562068
HLA B*0803      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.484037       0.809887        -3.674150       30481.530317
HLA A*0219      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.387010       0.712665        -3.674345       24378.674272
HLA A*0212      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.371912       0.697019        -3.674893       23545.737290
HLA A*2301      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.486804       0.811766        -3.675038       30676.404813
HLA B*0801      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.335608       0.660357        -3.675251       21657.486474
HLA A*2602      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.592740       0.917388        -3.675353       39150.777343
HLA B*4801      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.422201       0.746698        -3.675502       26436.299968
HLA A*1101      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.470642       0.795128        -3.675515       29555.775076
HLA B*1509      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.422269       0.746698        -3.675570       26440.447799
HLA A*3002      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.526360       0.850740        -3.675620       33601.633431
HLA B*5801      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.336069       0.660357        -3.675712       21680.462915
HLA A*2601      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.386655       0.710864        -3.675791       24358.767630
HLA B*0803      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.487624       0.811766        -3.675858       30734.378150
HLA A*2403      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.382516       0.706535        -3.675981       24127.677535
HLA B*0802      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.471180       0.795128        -3.676053       29592.413370
HLA B*5801      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.241361       0.565014        -3.676346       17432.545622
HLA B*1503      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.457375       0.780826        -3.676549       28666.509208
HLA A*3001      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.280903       0.603848        -3.677054       19094.251697
HLA B*0801      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.279850       0.602482        -3.677368       19048.030323
HLA B*4001      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.390386       0.712622        -3.677765       24568.932925
HLA A*3001      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.301839       0.623682        -3.678157       20037.286315
HLA B*5101      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.129582       0.451113        -3.678469       13476.642630
HLA B*5801      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.337149       0.658536        -3.678613       21734.482998
HLA B*4402      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.391716       0.712622        -3.679094       24644.278225
HLA B*5401      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.442808       0.763535        -3.679273       27720.943267
HLA A*3101      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.181736       0.502462        -3.679274       15196.220271
HLA A*2601      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.369920       0.690533        -3.679387       23437.966588
HLA A*3301      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.565801       0.886414        -3.679388       36796.049499
HLA B*1517      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.376914       0.697019        -3.679895       23818.496704
HLA B*4601      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.370517       0.690533        -3.679984       23470.195113
HLA A*0206      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.295965       0.615847        -3.680119       19768.111928
HLA A*8001      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.386665       0.706535        -3.680130       24359.294748
HLA A*2402      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.561036       0.880895        -3.680141       36394.557115
HLA B*4001      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.387005       0.706535        -3.680471       24378.410502
HLA A*1101      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.427219       0.746698        -3.680521       26743.557085
HLA A*0212      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.429623       0.748881        -3.680742       26891.974713
HLA A*2403      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.393419       0.712665        -3.680754       24741.127069
HLA A*2601      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.306526       0.625647        -3.680879       20254.714524
HLA A*0206      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.264705       0.583145        -3.681560       18395.233014
HLA A*0250      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.516511       0.834848        -3.681663       32848.182775
HLA A*2603      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.562773       0.880895        -3.681877       36540.350449
HLA A*3301      1:182-190       9       SAGTMGTAA       1.132034        -0.199061       -4.615192       0.932973        -3.682219       41227.981085
HLA B*5801      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.349818       0.667402        -3.682416       22377.817987
HLA B*4001      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.350217       0.667402        -3.682815       22398.407911
HLA B*2705      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.446903       0.764021        -3.682882       27983.572426
HLA A*3002      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.600296       0.917388        -3.682909       39837.890469
HLA B*4801      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.431937       0.748881        -3.683056       27035.657560
HLA B*5101      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.463888       0.780826        -3.683062       29099.637805
HLA A*2603      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.650848       0.967740        -3.683108       44755.648312
HLA B*4403      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.619381       0.936177        -3.683205       41627.583429
HLA A*0211      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.479249       0.795947        -3.683302       30147.306506
HLA B*1503      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.430083       0.746698        -3.683385       26920.504426
HLA B*2705      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.464252       0.780826        -3.683426       29124.049039
HLA A*6802      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.396152       0.712622        -3.683530       24897.281569
HLA A*2403      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.374114       0.690533        -3.683581       23665.395210
HLA B*5101      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.479547       0.795947        -3.683600       30168.026509
HLA A*0201      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.340114       0.656423        -3.683691       21883.378097
HLA A*2301      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.479829       0.795947        -3.683882       30187.617549
HLA A*0206      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.330380       0.646348        -3.684032       21398.357931
HLA A*2603      1:31-39 9       RRVAAAPSP       0.723092        0.213085        -4.620232       0.936177        -3.684055       41709.185929
HLA A*0219      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.432952       0.748881        -3.684071       27098.915732
HLA A*0101      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.330543       0.646348        -3.684195       21406.347052
HLA B*3801      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.514545       0.830057        -3.684487       32699.779911
HLA A*6802      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.285280       0.600711        -3.684569       19287.668520
HLA A*0101      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.395846       0.710864        -3.684982       24879.777825
HLA A*2902      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.382609       0.697019        -3.685591       24132.899222
HLA A*0101      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.353330       0.667402        -3.685928       22559.538820
HLA A*2301      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.536893       0.850740        -3.686153       34426.520525
HLA A*8001      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.383289       0.697019        -3.686270       24170.659506
HLA B*2705      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.399540       0.712622        -3.686918       25092.266314
HLA A*6901      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.174645       0.487485        -3.687160       14950.125360
HLA A*0206      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.289920       0.602482        -3.687438       19494.853078
HLA A*0101      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.313107       0.625647        -3.687460       20563.973426
HLA A*2301      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.497530       0.809887        -3.687643       31443.425971
HLA A*0301      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.334013       0.646348        -3.687665       21578.077646
HLA B*4501      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.355146       0.667402        -3.687745       22654.076833
HLA B*4001      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.378787       0.690533        -3.688254       23921.416197
HLA A*3101      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.355680       0.667402        -3.688278       22681.914144
HLA A*0201      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.399145       0.710864        -3.688281       25069.471283
HLA B*0802      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.399225       0.710864        -3.688361       25074.082891
HLA B*3901      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.469237       0.780826        -3.688411       29460.313281
HLA A*6801      1:183-191       9       AGTMGTAAV       0.865215        0.089827        -4.643548       0.955042        -3.688506       44009.658908
HLA A*0101      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.379055       0.690533        -3.688522       23936.173740
HLA A*2902      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.356032       0.667402        -3.688630       22700.327611
HLA A*2301      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.518863       0.830057        -3.688806       33026.548022
HLA A*2902      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.291454       0.602482        -3.688972       19563.843507
HLA B*0702      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.254264       0.565014        -3.689250       17958.256986
HLA B*5301      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.567321       0.877544        -3.689777       36925.068633
HLA B*1502      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.396323       0.706535        -3.689789       24907.115992
HLA A*2601      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.001380       0.311316        -3.690064       10031.819592
HLA B*7301      1:188-196       9       TAAVTPSTT       1.185673        -0.299259       -4.577029       0.886414        -3.690616       37759.773734
HLA B*2705      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.454518       0.763535        -3.690983       28478.547645
HLA B*5301      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.403980       0.712665        -3.691315       25350.143079
HLA B*0803      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.486570       0.795128        -3.691442       30659.813706
HLA A*0206      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.472294       0.780826        -3.691468       29668.394201
HLA A*0201      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.191665       0.500136        -3.691529       15547.640986
HLA A*6801      1:113-121       9       RPSPPPTVA       1.222805        -0.255065       -4.659304       0.967740        -3.691564       45635.587831
HLA A*3002      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.514481       0.822896        -3.691585       32695.003901
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HLA A*2902	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.256893	0.565014	-3.691879	18067.299997
HLA B*0801	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.194662	0.502462	-3.692200	15655.337930
HLA A*2402	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.512776	0.820380	-3.692396	32566.843518
HLA B*1801	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.488390	0.795947	-3.692444	30788.629859
HLA B*4001	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.353182	0.660357	-3.692825	22551.851320
HLA A*0216	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.246328	0.553011	-3.693316	17633.057421
HLA B*5401	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.566351	0.872785	-3.693566	36842.659632
HLA B*3801	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.528489	0.834848	-3.693641	33766.731390
HLA A*0301	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.196124	0.502462	-3.693662	15708.106107
HLA A*3001	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-3.824318	0.130576	-3.693742	6672.949292
HLA B*4601	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.340187	0.646348	-3.693839	21887.048391
HLA A*3201	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.440538	0.746698	-3.693840	27576.452802
HLA A*0250	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.489889	0.795947	-3.693943	30895.080702
HLA B*4001	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.404822	0.710864	-3.693957	25399.287298
HLA B*4601	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.352536	0.658536	-3.694000	22518.325436
HLA B*4402	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.407004	0.712665	-3.694339	25527.260019
HLA A*0203	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.353123	0.658536	-3.694587	22548.801451
HLA A*3002	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.355393	0.660357	-3.695036	22666.948873
HLA B*5401	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.333104	0.637921	-3.695182	21532.948457
HLA A*2301	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.524720	0.829467	-3.695253	33474.989476
HLA B*1517	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.490942	0.795128	-3.695814	30970.049769
HLA B*5701	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.402463	0.706535	-3.695928	25261.704321
HLA B*4403	1:182-190	9	SAGTMGTAA	1.132034	-0.199061	-4.629129	0.932973	-3.696157	42572.505784
HLA A*3002	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.577123	0.880895	-3.696228	37767.945666
HLA B*2705	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-4.022628	0.326268	-3.696360	10534.852412
HLA A*0206	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.492319	0.795947	-3.696372	31068.386659
HLA A*0301	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.363945	0.667402	-3.696543	23117.730176
HLA A*2402	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.574255	0.877544	-3.696710	37519.292599
HLA B*4403	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.518107	0.820380	-3.697727	32969.066375
HLA B*3801	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.520672	0.822896	-3.697776	33164.410837
HLA B*0802	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.478701	0.780826	-3.697875	30109.329641
HLA B*4501	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.509670	0.811766	-3.697903	32334.760478
HLA B*5701	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.263014	0.565014	-3.697999	18323.720735
HLA A*0211	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.114644	0.416603	-3.698040	13020.980435
HLA A*2501	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.080839	0.382667	-3.698173	12045.901182
HLA A*8001	1:65-73	9	EPPAHLRTA	1.140501	-0.391620	-4.447519	0.748881	-3.698638	28023.264211
HLA B*0801	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.357456	0.658536	-3.698920	22774.870325
HLA B*5801	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.355482	0.656423	-3.699059	22671.609128
HLA B*3901	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.463549	0.764415	-3.699134	29076.977315
HLA B*4601	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.410007	0.710864	-3.699142	25704.362892
HLA A*0301	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.359542	0.660357	-3.699185	22884.543605
HLA A*3001	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.282510	0.583145	-3.699365	19165.038269
HLA B*0702	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.480193	0.780826	-3.699367	30212.941473
HLA B*1801	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.480233	0.780826	-3.699407	30215.720228
HLA B*5101	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.412131	0.712665	-3.699465	25830.378994
HLA B*4002	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.495486	0.795947	-3.699539	31295.781954
HLA B*4501	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.550405	0.850740	-3.699665	35514.443941
HLA B*0801	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.412347	0.712622	-3.699725	25843.238226
HLA B*1503	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.410592	0.710864	-3.699728	25739.011604
HLA B*4601	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.412443	0.712622	-3.699822	25848.971033
HLA B*3801	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.520266	0.820380	-3.699886	33133.386426
HLA A*0101	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.397118	0.697019	-3.700099	24952.701378
HLA B*0801	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.412986	0.712665	-3.700321	25881.294282
HLA B*4403	1:113-121	9	RPSPPPTVA	1.222805	-0.255065	-4.668074	0.967740	-3.700335	46566.572863
HLA A*0101	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.356970	0.656423	-3.700546	22749.380229
HLA B*1502	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-4.464682	0.764021	-3.700661	29152.896408
HLA B*1501	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.411550	0.710864	-3.700686	25795.886391
HLA B*0802	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.464238	0.763535	-3.700703	29123.103707
HLA B*0702	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.413585	0.712665	-3.700920	25917.022728
HLA A*2403	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.359798	0.658536	-3.701262	22898.042095
HLA B*2705	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.128792	0.427495	-3.701297	13452.168080
HLA A*6801	1:102-110	9	GLGAFGLGV	0.937231	0.015587	-4.654236	0.952818	-3.701418	45106.155201
HLA B*5701	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.398668	0.697019	-3.701649	25041.954914
HLA B*5701	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.412521	0.710864	-3.701656	25853.586167
HLA A*3101	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.358309	0.656423	-3.701885	22819.639326
HLA B*5101	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.465478	0.763535	-3.701943	29206.410489
HLA B*1503	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.236984	0.534755	-3.702229	17257.731979
HLA B*1501	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.369847	0.667402	-3.702445	23434.036217
HLA B*5401	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.359251	0.656423	-3.702828	22869.197201
HLA A*6901	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.359686	0.656423	-3.703262	22892.096825
HLA B*4001	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.400529	0.697019	-3.703510	25149.480670
HLA A*2501	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.467978	0.764415	-3.703563	29375.010929
HLA A*2601	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.371485	0.667402	-3.704083	23522.565570
HLA A*0301	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.363330	0.658536	-3.704794	23084.986525
HLA B*4601	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.401849	0.697019	-3.704830	25226.060443
HLA B*4402	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.411576	0.706535	-3.705042	25797.421518
HLA A*2603	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.591559	0.886414	-3.705145	39044.386077
HLA B*1503	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.233699	0.528496	-3.705203	17127.703644
HLA A*2301	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.540100	0.834848	-3.705252	34681.684088
HLA A*3301	1:77-85	9	ATKPEVRRQ	0.927767	-0.054982	-4.578105	0.872785	-3.705320	37853.448232
HLA A*2602	1:90-98	9	TAAFASAAA	0.917226	-0.153205	-4.469566	0.764021	-3.705545	29482.634517
HLA B*5301	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.586531	0.880895	-3.705635	38594.969369
HLA B*4501	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.640801	0.934977	-3.705825	43732.212996
HLA A*0201	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.364526	0.658536	-3.705989	23148.641720
HLA B*4002	1:121-129	9	AEQVLTAPD	0.414330	-0.778826	-3.341766	-0.364496	-3.706262	2196.678493
HLA A*3101	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.366659	0.660357	-3.706302	23262.631740
HLA A*3301	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.516206	0.809887	-3.706319	32825.089243
HLA B*3901	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.419036	0.712665	-3.706370	26244.355669
HLA A*0301	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.308901	0.602482	-3.706419	20365.799123
HLA B*5401	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.487246	0.780826	-3.706420	30707.620403
HLA B*0803	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.453832	0.746698	-3.707133	28433.595950
HLA B*1509	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.530293	0.822896	-3.707397	33907.317083
HLA B*1509	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.488282	0.780826	-3.707456	30780.968911
HLA A*2301	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.530963	0.822896	-3.708067	33959.636331
HLA B*4501	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.594643	0.886414	-3.708230	39322.712886
HLA A*6901	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.060225	0.351592	-3.708633	11487.483874
HLA A*0211	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-3.519613	-0.189096	-3.708709	3308.362692
HLA B*4402	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.419626	0.710864	-3.708761	26280.016618
HLA A*3001	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.211339	0.502462	-3.708877	16268.184573
HLA B*4402	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.157592	0.448362	-3.709230	14374.484278
HLA A*6801	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.538702	0.829467	-3.709235	34570.227248
HLA B*4801	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.400280	0.690533	-3.709747	25135.062879
HLA B*5301	1:53-61	9	ETMAVVSAA	1.064440	-0.244060	-4.530249	0.820380	-3.709869	33903.832000
HLA A*0203	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.326036	0.615847	-3.710190	21185.379592
HLA B*5401	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.540321	0.830057	-3.710264	34699.325235
HLA A*3101	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.314153	0.603848	-3.710304	20613.538787
HLA A*3301	1:31-39	9	RRVAAAPSP	0.723092	0.213085	-4.646574	0.936177	-3.710398	44317.386315
HLA A*8001	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.401199	0.690533	-3.710666	25188.286510
HLA A*0203	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.293860	0.583145	-3.710715	19672.522597

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HLA B*5301      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.401281       0.690533        -3.710748       25193.056266
HLA B*4002      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.646001       0.934977        -3.711024       44258.925384
HLA A*2301      1:53-61 9       ETMAVVSAA       1.064440        -0.244060       -4.531454       0.820380        -3.711074       33998.055081
HLA B*0802      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.457929       0.746698        -3.711231       28703.132084
HLA A*2402      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.562345       0.850740        -3.711605       36504.390533
HLA A*2902      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.402200       0.690533        -3.711666       25246.402699
HLA B*7301      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.589226       0.877544        -3.711681       38835.201233
HLA B*4403      1:35-43 9       AAPSPVAAA       1.017695        -0.085233       -4.644239       0.932462        -3.711777       44079.712291
HLA B*5701      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.424404       0.712622        -3.711783       26570.791286
HLA A*2403      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.372288       0.660357        -3.711931       23566.126886
HLA A*3201      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.521861       0.809887        -3.711974       33255.319595
HLA B*5301      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.542142       0.830057        -3.712084       34845.113257
HLA A*0101      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.370693       0.658536        -3.712157       23479.719882
HLA A*8001      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.423054       0.710864        -3.712189       26488.266311
HLA A*2601      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.230729       0.518215        -3.712515       17010.982227
HLA B*1509      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.409549       0.697019        -3.712530       25677.260928
HLA B*4601      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.373176       0.660357        -3.712819       23614.367464
HLA B*3901      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.362890       0.649819        -3.713072       23061.644424
HLA A*2902      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.462060       0.748881        -3.713179       28977.417907
HLA A*2601      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.373658       0.660357        -3.713301       23640.570969
HLA B*5301      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.494325       0.780826        -3.713499       31212.256099
HLA B*1801      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.477101       0.763535        -3.713566       29998.606904
HLA B*4402      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.404323       0.690533        -3.713790       25370.173643
HLA B*0801      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.411081       0.697019        -3.714062       25767.990907
HLA A*3002      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.478483       0.764415        -3.714068       30094.184854
HLA B*4001      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.337859       0.623682        -3.714177       21770.021526
HLA A*0212      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.232440       0.518215        -3.714225       17078.110369
HLA B*5101      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.364493       0.649819        -3.714674       23146.888544
HLA B*3901      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.463963       0.748881        -3.715082       29104.675867
HLA B*0702      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.405663       0.690533        -3.715130       25448.526788
HLA B*1501      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.374034       0.658536        -3.715498       23661.042687
HLA A*6802      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.426392       0.710864        -3.715528       26692.678297
HLA A*2403      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.426493       0.710864        -3.715629       26698.888410
HLA A*0216      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.464545       0.748881        -3.715664       29143.750435
HLA B*0702      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.428436       0.712622        -3.715814       26818.606265
HLA A*3001      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.268840       0.553011        -3.715829       18571.217958
HLA A*0216      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.077132       0.360868        -3.716264       11943.505361
HLA A*3301      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.551227       0.834848        -3.716379       35581.752866
HLA A*0301      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.366234       0.649819        -3.716415       23239.864354
HLA B*2705      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.245071       0.528496        -3.716574       17582.096011
HLA B*5101      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.481053       0.764415        -3.716638       30272.822947
HLA B*7301      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.551646       0.834848        -3.716797       35616.033182
HLA B*4501      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.539722       0.822896        -3.716826       34651.489765
HLA A*0101      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.377441       0.660357        -3.717084       23847.377815
HLA A*6801      1:136-144       9       PLGAGTATV       1.012784        -0.077807       -4.652095       0.934977        -3.717119       44884.400517
HLA B*3501      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.429771       0.712622        -3.717149       26901.141679
HLA B*2705      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.466362       0.748881        -3.717481       29265.880247
HLA B*4601      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.384924       0.667402        -3.717522       24261.840429
HLA B*5801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.355816       0.637921        -3.717895       22689.032246
HLA B*4801      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.424444       0.706535        -3.717910       26573.235063
HLA A*2601      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.374494       0.656423        -3.718071       23686.144702
HLA A*0101      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.320555       0.602482        -3.718073       20919.673469
HLA A*2501      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.415187       0.697019        -3.718168       26012.821352
HLA A*2403      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.415472       0.697019        -3.718453       26029.854830
HLA A*0250      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.283520       0.565014        -3.718506       19209.672879
HLA A*3001      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.279763       0.561253        -3.718510       19044.217939
HLA B*5301      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.591523       0.872785        -3.718738       39041.217818
HLA A*0212      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.386150       0.667402        -3.718748       24330.451780
HLA A*2602      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.553751       0.834848        -3.718902       35789.092472
HLA A*0212      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.377572       0.658536        -3.719036       23854.603563
HLA B*4001      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.375500       0.656423        -3.719077       23741.051915
HLA B*4801      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.253888       0.534755        -3.719134       17942.719362
HLA B*7301      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.431888       0.712622        -3.719266       27032.586276
HLA B*7301      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.529220       0.809887        -3.719333       33823.590908
HLA B*4501      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.592245       0.872785        -3.719460       39106.112752
HLA B*1517      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.484034       0.764415        -3.719620       30481.365416
HLA B*5701      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.366050       0.646348        -3.719702       23230.059866
HLA B*1509      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.430661       0.710864        -3.719797       26956.354964
HLA B*1502      1:77-85 9       ATKPEVRRQ       0.927767        -0.054982       -4.592700       0.872785        -3.719915       39147.176886
HLA B*3501      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.357982       0.637921        -3.720061       22802.485987
HLA B*5801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.370582       0.649819        -3.720764       23473.750575
HLA B*1517      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.469794       0.748881        -3.720913       29498.109862
HLA B*4601      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.377427       0.656423        -3.721003       23846.603758
HLA A*2402      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.543951       0.822896        -3.721055       34990.567313
HLA B*0702      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.377542       0.656423        -3.721118       23852.925962
HLA B*0801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.370940       0.649819        -3.721121       23493.061052
HLA B*3801      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.531036       0.809887        -3.721149       33965.332063
HLA B*2705      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.379861       0.658536        -3.721325       23980.630746
HLA A*0219      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.432355       0.710864        -3.721491       27061.704363
HLA B*1502      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.485919       0.764415        -3.721504       30613.903179
HLA A*2301      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.516784       0.795128        -3.721656       32868.803028
HLA B*3801      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.517773       0.795947        -3.721826       32943.749123
HLA A*0212      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.432780       0.710864        -3.721916       27088.215889
HLA B*4403      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -3.357832       -0.364496       -3.722328       2279.461579
HLA A*3101      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.372213       0.649819        -3.722394       23562.047554
HLA A*0250      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.419666       0.697019        -3.722647       26282.433653
HLA A*2603      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.325141       0.602482        -3.722659       21141.757942
HLA B*0802      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.487100       0.764415        -3.722686       30697.322391
HLA B*4601      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.348427       0.625647        -3.722779       22306.264213
HLA A*3301      1:116-124       9       PPPTVAEQV       1.105805        -0.188417       -4.640357       0.917388        -3.722970       43687.521014
HLA A*6901      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.348645       0.625647        -3.722998       22317.489757
HLA A*2402      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.534795       0.811766        -3.723029       34260.606029
HLA A*0203      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.434160       0.710864        -3.723295       27174.374091
HLA B*4002      1:198-206       9       TLTDLGAST       1.133749        -0.256205       -4.600851       0.877544        -3.723306       39888.785334
HLA B*0801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.140042       0.416603        -3.723438       13805.165557
HLA A*8001      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.436159       0.712622        -3.723537       27299.768324
HLA A*1101      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -3.983594       0.259962        -3.723633       9629.286577
HLA A*0219      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.242261       0.518215        -3.724046       17468.703086
HLA B*3801      1:169-177       9       YQMWLLGGA       0.988610        -0.159143       -4.553560       0.829467        -3.724093       35773.413091
HLA B*0802      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.430891       0.706535        -3.724357       26970.650181
HLA A*8001      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.437524       0.712665        -3.724859       27385.710464
HLA B*1501      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.329041       0.603848        -3.725193       21332.474799
HLA B*0803      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.488729       0.763535        -3.725194       30812.624286
HLA B*5401      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.489617       0.764415        -3.725202       30875.698665
HLA A*2602      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.555261       0.830057        -3.725204       35913.803714
HLA A*6802      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.375220       0.649819        -3.725402       23725.772895
HLA B*0803      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.489438       0.764021        -3.725417       30863.006682
HLA A*2501      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.488997       0.763535        -3.725462       30831.633136
HLA A*2602      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.535434       0.809887        -3.725547       34311.057273
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HLA B*4001	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.384198	0.658536	-3.725662	24221.316865
HLA A*2601	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.384334	0.658536	-3.725798	24228.918066
HLA B*4801	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.422830	0.697019	-3.725811	26474.656444
HLA A*2402	1:55-63 9	MAVVSAATT	1.035754	-0.225867	-4.535902	0.809887	-3.726015	34348.015347
HLA A*2403	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.393603	0.667402	-3.726201	24751.569319
HLA B*3501	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.330169	0.603848	-3.726321	21387.941820
HLA B*4801	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.437414	0.710864	-3.726549	27378.748128
HLA A*3002	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.433156	0.706535	-3.726622	27111.673119
HLA B*1509	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.475985	0.748881	-3.727104	29921.618525
HLA B*0803	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.476159	0.748881	-3.727278	29933.599498
HLA A*3101	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.324039	0.596633	-3.727406	21088.184263
HLA B*3501	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.329981	0.602482	-3.727499	21378.687312
HLA A*3201	1:59-67 9	SAATTAEPP	0.646418	0.117117	-4.491043	0.763535	-3.727508	30977.255022
HLA B*1501	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.111030	0.382667	-3.728363	12913.090015
HLA A*6901	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.263209	0.534755	-3.728454	18331.950315
HLA A*6802	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.216616	0.488141	-3.728475	16467.058730
HLA B*1801	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.263296	0.534755	-3.728541	18335.620113
HLA B*5401	1:38-46 9	SPVAAAFND	0.902542	-0.927500	-3.703611	-0.024958	-3.728568	5053.714262
HLA B*1801	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.492998	0.764415	-3.728583	31116.998767
HLA A*0301	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.332521	0.603848	-3.728672	21504.078094
HLA A*1101	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.375056	0.646348	-3.728708	23716.789830
HLA B*4402	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.425831	0.697019	-3.728812	26658.187940
HLA A*3101	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.331435	0.602482	-3.728953	21450.398582
HLA B*1502	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.579694	0.850740	-3.728954	37992.134952
HLA B*4001	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.367126	0.637921	-3.729205	23287.689029
HLA B*5401	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.281201	0.551693	-3.729508	19107.375023
HLA A*6801	1:31-39 9	RRVAAAPSP	0.723092	0.213085	-4.666000	0.936177	-3.729823	46344.657964
HLA B*2705	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.436368	0.706535	-3.729833	27312.915785
HLA A*0211	1:59-67 9	SAATTAEPP	0.646418	0.117117	-4.493378	0.763535	-3.729843	31144.281722
HLA A*2602	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.610754	0.880895	-3.729858	40808.806259
HLA A*2603	1:82-90 9	VRRQSRWRT	1.037980	-0.242033	-4.525806	0.795947	-3.729859	33558.760464
HLA B*3901	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.436429	0.706535	-3.729894	27316.757812
HLA B*7301	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.602686	0.872785	-3.729901	40057.676918
HLA B*5801	1:46-54 9	DEVRAVRET	1.031728	-0.408046	-4.353671	0.623682	-3.729989	22577.242230
HLA A*2902	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.386794	0.656423	-3.730371	24366.543786
HLA B*4001	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.376820	0.646348	-3.730472	23813.343044
HLA A*2601	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.368625	0.637921	-3.730704	23368.205576
HLA A*3101	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.427879	0.697019	-3.730860	26784.242992
HLA B*1503	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.479787	0.748881	-3.730906	30184.678082
HLA A*0201	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.377513	0.646348	-3.731165	23851.377512
HLA A*3301	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.495389	0.764021	-3.731369	31288.841148
HLA A*0206	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.266693	0.534755	-3.731938	18479.616650
HLA B*3501	1:6-14  9	DFELLELAT	0.874861	-0.429715	-4.177394	0.445146	-3.732248	15045.053340
HLA B*1517	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.336280	0.603848	-3.732432	21691.021487
HLA B*5801	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.348901	0.615847	-3.733055	22330.653769
HLA A*2902	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.379713	0.646348	-3.733365	23972.458987
HLA B*4002	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.650996	0.917388	-3.733608	44770.904667
HLA A*3101	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-4.334426	0.600711	-3.733716	21598.632792
HLA A*6801	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.440414	0.706535	-3.733879	27568.547101
HLA B*5301	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.498009	0.764021	-3.733988	31478.146638
HLA B*4403	1:136-144	9	PLGAGTATV	1.012784	-0.077807	-4.669085	0.934977	-3.734108	46675.024556
HLA B*0802	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.483219	0.748881	-3.734338	30424.198510
HLA A*2603	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.360379	0.625647	-3.734731	22928.659886
HLA B*0802	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.447671	0.712665	-3.735006	28033.120123
HLA A*0219	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.393582	0.658536	-3.735046	24750.364219
HLA A*0212	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.381585	0.646348	-3.735237	24076.043751
HLA A*3001	1:68-76 9	AHLRTAILD	1.193151	-0.778234	-4.150487	0.414917	-3.735570	14141.237933
HLA B*4002	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.448315	0.712665	-3.735650	28074.704699
HLA B*7301	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.448515	0.712665	-3.735849	28087.617556
HLA A*2402	1:144-152	9	VVFSRDRNT	0.997060	-0.167003	-4.566316	0.830057	-3.736258	36839.670032
HLA B*1501	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.386162	0.649819	-3.736343	24331.109914
HLA A*3301	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.339090	0.602482	-3.736608	21831.822344
HLA B*5701	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.397026	0.660357	-3.736669	24947.437271
HLA B*0801	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.404077	0.667402	-3.736675	25355.766503
HLA A*3001	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.272043	0.534755	-3.737288	18708.662268
HLA B*4501	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.353448	0.615847	-3.737601	22565.641876
HLA B*4402	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.363351	0.625647	-3.737703	23086.110537
HLA A*3002	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.237853	0.500136	-3.737717	17292.310669
HLA A*1101	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.486635	0.748881	-3.737754	30664.458311
HLA A*3002	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.302887	0.565014	-3.737872	20085.690863
HLA A*2603	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.655324	0.917388	-3.737936	45219.277751
HLA B*3901	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.448818	0.710864	-3.737954	28107.226064
HLA B*4403	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.610907	0.872785	-3.738122	40823.158905
HLA B*1501	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.290171	0.551693	-3.738478	19506.141099
HLA A*3301	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.568132	0.829467	-3.738665	36994.050369
HLA A*6801	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.385114	0.646348	-3.738766	24272.474322
HLA A*2501	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.364460	0.625647	-3.738812	23145.135501
HLA B*5301	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.589881	0.850740	-3.739141	38893.861755
HLA A*0219	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.385765	0.646348	-3.739417	24308.874846
HLA A*2403	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.385962	0.646348	-3.739614	24319.924055
HLA B*1517	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.239805	0.500136	-3.739670	17370.225296
HLA B*4402	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.400148	0.660357	-3.739792	25127.449269
HLA B*2705	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.400249	0.660357	-3.739893	25133.295228
HLA A*0101	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.389773	0.649819	-3.739955	24534.266537
HLA A*2403	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.132636	0.392663	-3.739973	13571.755982
HLA B*5101	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.407507	0.667402	-3.740105	25556.830457
HLA A*2402	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.575251	0.834848	-3.740402	37605.452868
HLA B*3801	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.489330	0.748881	-3.740449	30855.327227
HLA B*0803	1:72-80 9	TAILDATKP	0.635852	0.144974	-4.521323	0.780826	-3.740497	33214.146265
HLA B*5701	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.399115	0.658536	-3.740579	25067.708245
HLA A*2403	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-3.860476	0.119790	-3.740686	7252.310653
HLA B*5301	1:169-177	9	YQMWLLGGA	0.988610	-0.159143	-4.570181	0.829467	-3.740714	37168.979248
HLA A*2402	1:7-15  9	FELLELATP	0.903395	-0.108267	-4.535857	0.795128	-3.740729	34344.484968
HLA A*0101	1:28-36 9	DIDRRVAAA	0.875321	-0.322310	-4.293869	0.553011	-3.740858	19672.948306
HLA B*5801	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.344867	0.603848	-3.741019	22124.189631
HLA B*4801	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.338016	0.596633	-3.741383	21777.913774
HLA A*2902	1:54-62 9	TMAVVSAAT	0.831597	-0.329135	-4.243877	0.502462	-3.741415	17533.842814
HLA B*4002	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.628683	0.886414	-3.742269	42528.768884
HLA B*0803	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.506766	0.764415	-3.742351	32119.271375
HLA A*2403	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.339137	0.596633	-3.742504	21834.184627
HLA A*0219	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.409976	0.667402	-3.742574	25702.555205
HLA A*3301	1:28-36 9	DIDRRVAAA	0.875321	-0.322310	-4.295681	0.553011	-3.742670	19755.176024
HLA B*5301	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.392515	0.649819	-3.742696	24689.649696
HLA B*4501	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.660131	0.917388	-3.742743	45722.573610
HLA A*2501	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.453881	0.710864	-3.743017	28436.826408
HLA A*2601	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.393105	0.649819	-3.743286	24723.198103
HLA A*2403	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.369065	0.625647	-3.743417	23391.857966
HLA A*6901	1:46-54 9	DEVRAVRET	1.031728	-0.408046	-4.367206	0.623682	-3.743524	23291.972873
HLA A*2501	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.456264	0.712622	-3.743642	28593.248893
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HLA A*3201	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.507666	0.764021	-3.743645	32185.891099
HLA B*1509	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.456461	0.712665	-3.743795	28606.245495
HLA B*1502	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.400242	0.656423	-3.743819	25132.887326
HLA B*3801	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.555635	0.811766	-3.743869	35944.709066
HLA B*4601	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.393807	0.649819	-3.743989	24763.221643
HLA B*3901	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.456618	0.712622	-3.743997	28616.616068
HLA A*3301	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.624895	0.880895	-3.744000	42159.498987
HLA B*4501	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.621627	0.877544	-3.744083	41843.432904
HLA B*0802	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.441459	0.697019	-3.744440	27634.995592
HLA A*6802	1:70-78 9	LRTAILDAT	0.824289	-0.241144	-4.327711	0.583145	-3.744566	21267.254723
HLA B*7301	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.556603	0.811766	-3.744837	36024.914656
HLA A*0219	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.401347	0.656423	-3.744923	25196.872721
HLA A*0301	1:46-54 9	DEVRAVRET	1.031728	-0.408046	-4.368607	0.623682	-3.744925	23367.194242
HLA A*2601	1:46-54 9	DEVRAVRET	1.031728	-0.408046	-4.369069	0.623682	-3.745388	23392.111062
HLA B*5701	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.412951	0.667402	-3.745549	25879.194143
HLA A*2902	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.404244	0.658536	-3.745708	25365.507578
HLA A*3001	1:96-104	9	AAAIAVGLG	0.855432	-0.489259	-4.112172	0.366173	-3.745999	12947.085862
HLA A*2602	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.311021	0.565014	-3.746006	20465.421388
HLA A*3201	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.580979	0.834848	-3.746130	38104.728144
HLA A*3001	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.243191	0.496962	-3.746229	17506.166685
HLA A*1101	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.264889	0.518215	-3.746674	18402.996913
HLA A*3001	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.236206	0.489218	-3.746988	17226.856671
HLA A*0201	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.396906	0.649819	-3.747088	24940.555114
HLA A*1101	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.312372	0.565014	-3.747357	20529.182011
HLA B*4002	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.628265	0.880895	-3.747369	42487.835082
HLA B*4801	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.407975	0.660357	-3.747618	25584.358937
HLA B*0702	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.385605	0.637921	-3.747684	24299.933925
HLA A*1101	1:60-68 9	AATTAEPPA	0.798576	-0.138219	-4.408054	0.660357	-3.747698	25589.065260
HLA A*0301	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.363809	0.615847	-3.747962	23110.477581
HLA A*0211	1:65-73 9	EPPAHLRTA	1.140501	-0.391620	-4.497354	0.748881	-3.748473	31430.670650
HLA B*3501	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.243957	0.495365	-3.748592	17537.068219
HLA A*0101	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-4.349447	0.600711	-3.748736	22358.698440
HLA B*1503	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.300636	0.551693	-3.748943	19981.862565
HLA B*5301	1:7-15  9	FELLELATP	0.903395	-0.108267	-4.544341	0.795128	-3.749213	35022.004412
HLA B*1801	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.461912	0.712665	-3.749246	28967.543419
HLA B*4501	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.584233	0.834848	-3.749384	38391.307592
HLA A*1101	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.462184	0.712622	-3.749562	28985.727623
HLA B*1501	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.365531	0.615847	-3.749685	23202.302939
HLA A*2902	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-4.350431	0.600711	-3.749720	22409.437360
HLA B*0702	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.268260	0.518215	-3.750045	18546.418877
HLA A*2601	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.396399	0.646348	-3.750051	24911.428197
HLA B*3801	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.496764	0.746698	-3.750066	31388.020466
HLA B*4403	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.667656	0.917388	-3.750268	46521.752688
HLA A*2501	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.441018	0.690533	-3.750485	27606.903455
HLA B*1801	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.461555	0.710864	-3.750690	28943.733107
HLA B*4801	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.418108	0.667402	-3.750706	26188.333821
HLA A*3101	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.409368	0.658536	-3.750832	25666.566998
HLA A*2501	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.240524	0.489218	-3.751306	17399.004234
HLA A*6801	1:116-124	9	PPPTVAEQV	1.105805	-0.188417	-4.669005	0.917388	-3.751617	46666.440118
HLA B*0802	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.442230	0.690533	-3.751697	27684.075866
HLA A*3001	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.280278	0.528496	-3.751781	19066.794247
HLA B*4402	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.367695	0.615847	-3.751848	23318.197079
HLA A*0216	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.252002	0.500136	-3.751866	17864.942719
HLA A*0203	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.402390	0.649819	-3.752571	25257.468123
HLA B*5101	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.465483	0.712622	-3.752861	29206.726498
HLA A*8001	1:58-66 9	VSAATTAEP	0.530485	0.115863	-4.399281	0.646348	-3.752933	25077.338655
HLA B*5801	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.349707	0.596633	-3.753074	22372.128819
HLA B*7301	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.420490	0.667402	-3.753088	26332.388020
HLA A*2902	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.271354	0.518215	-3.753139	18679.030705
HLA A*2601	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.355948	0.602482	-3.753466	22695.907016
HLA B*1509	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.403344	0.649819	-3.753525	25313.004973
HLA A*2601	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.318664	0.565014	-3.753649	20828.767202
HLA B*5801	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-4.354543	0.600711	-3.753832	22622.601815
HLA B*7301	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.518076	0.764021	-3.754055	32966.747789
HLA B*5801	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.356815	0.602482	-3.754332	22741.258951
HLA B*4001	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.202698	0.448362	-3.754335	15947.686337
HLA B*1502	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.577307	0.822896	-3.754410	37783.886020
HLA B*4001	1:61-69 9	ATTAEPPAH	0.752441	-0.126794	-4.380143	0.625647	-3.754495	23996.203707
HLA B*5301	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.589397	0.834848	-3.754549	38850.541133
HLA A*2603	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.451985	0.697019	-3.754966	28312.948074
HLA A*2602	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.251945	0.496962	-3.754983	17862.623333
HLA B*4002	1:77-85 9	ATKPEVRRQ	0.927767	-0.054982	-4.627769	0.872785	-3.754984	42439.363457
HLA B*1517	1:69-77 9	HLRTAILDA	0.775000	-0.174289	-4.355720	0.600711	-3.755009	22684.000253
HLA B*7301	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.578155	0.822896	-3.755258	37857.748918
HLA B*4801	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.413815	0.658536	-3.755279	25930.766776
HLA A*8001	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.422720	0.667402	-3.755318	26467.925726
HLA A*2501	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.405204	0.649819	-3.755386	25421.694570
HLA A*0301	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.352358	0.596633	-3.755724	22509.068894
HLA B*1503	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.423380	0.667402	-3.755978	26508.192306
HLA B*4801	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.412483	0.656423	-3.756060	25851.348424
HLA B*5401	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-4.004115	0.247860	-3.756255	10095.190390
HLA B*4001	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.406147	0.649819	-3.756328	25476.903381
HLA B*4001	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.353290	0.596633	-3.756657	22557.464157
HLA A*0301	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.321734	0.565014	-3.756720	20976.563587
HLA B*5701	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.413388	0.656423	-3.756964	25905.247913
HLA B*3501	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.424379	0.667402	-3.756977	26569.210137
HLA B*7301	1:72-80 9	TAILDATKP	0.635852	0.144974	-4.537979	0.780826	-3.757153	34512.672714
HLA A*3301	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.580798	0.822896	-3.757902	38088.858488
HLA B*3501	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.416743	0.658536	-3.758207	26106.149301
HLA B*4601	1:9-17  9	LLELATPYA	0.993939	-0.356018	-4.396253	0.637921	-3.758332	24903.073978
HLA A*6801	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.505163	0.746698	-3.758465	32000.984245
HLA A*3101	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.323706	0.565014	-3.758691	21071.990451
HLA A*6801	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.361264	0.602482	-3.758782	22975.471255
HLA A*2301	1:72-80 9	TAILDATKP	0.635852	0.144974	-4.539635	0.780826	-3.758809	34644.554412
HLA A*2301	1:90-98 9	TAAFASAAA	0.917226	-0.153205	-4.522996	0.764021	-3.758975	33342.328588
HLA A*2602	1:48-56 9	VRAVRETMA	1.031036	-0.180296	-4.609786	0.850740	-3.759046	40717.949850
HLA A*1101	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.449887	0.690533	-3.759354	28176.497209
HLA A*3001	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.247500	0.488141	-3.759359	17680.722779
HLA B*3501	1:70-78 9	LRTAILDAT	0.824289	-0.241144	-4.342983	0.583145	-3.759838	22028.406660
HLA A*6901	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.356500	0.596633	-3.759867	22724.779215
HLA A*0301	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.278194	0.518215	-3.759979	18975.520036
HLA A*0211	1:72-80 9	TAILDATKP	0.635852	0.144974	-4.540984	0.780826	-3.760158	34752.302536
HLA A*2501	1:5-13  9	TDFELLELA	1.003059	-0.335657	-4.427597	0.667402	-3.760196	26766.860660
HLA A*2902	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.364049	0.603848	-3.760200	23123.233662
HLA A*2902	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.410237	0.649819	-3.760419	25717.994165
HLA A*3201	1:12-20 9	LATPYALNA	1.117892	-0.294996	-4.583570	0.822896	-3.760674	38332.782899
HLA B*5401	1:82-90 9	VRRQSRWRT	1.037980	-0.242033	-4.556666	0.795947	-3.760720	36030.177092
HLA A*0216	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.471594	0.710864	-3.760730	29620.602923
HLA B*1517	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.472080	0.710864	-3.761216	29653.792048
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HLA A*0212	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.377288	0.615847	-3.761441	23838.993531
HLA A*3001	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.263850	0.502118	-3.761732	18359.044770
HLA B*1503	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.411666	0.649819	-3.761847	25802.725389
HLA A*6901	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.365719	0.603848	-3.761871	23212.346863
HLA B*0702	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.387651	0.625647	-3.762004	24414.705731
HLA A*2501	1:104-112	9	GAFGLGVLT	1.005157	-0.292492	-4.474705	0.712665	-3.762039	29833.527863
HLA A*0216	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.378261	0.615847	-3.762414	23892.445420
HLA A*8001	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.422826	0.660357	-3.762469	26474.369995
HLA A*3101	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.262828	0.500136	-3.762692	18315.891194
HLA A*2403	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.400654	0.637921	-3.762732	25156.692667
HLA A*3201	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.613564	0.850740	-3.762824	41073.704568
HLA A*2501	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.400919	0.637921	-3.762998	25172.076094
HLA B*2705	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.430647	0.667402	-3.763245	26955.479993
HLA A*0201	1:46-54	9	DEVRAVRET	1.031728	-0.408046	-4.387078	0.623682	-3.763396	24382.499264
HLA B*3901	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.346601	0.583145	-3.763456	22212.696983
HLA A*1101	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.430891	0.667402	-3.763490	26970.650181
HLA A*0202	1:72-80	9	TAILDATKP	0.635852	0.144974	-4.544329	0.780826	-3.763503	35021.057099
HLA A*3301	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.614252	0.850740	-3.763512	41138.862022
HLA A*2601	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.364323	0.600711	-3.763613	23137.874309
HLA B*3801	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.528301	0.764415	-3.763886	33752.120611
HLA A*2403	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.420681	0.656423	-3.764257	26343.929428
HLA A*0201	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.317282	0.553011	-3.764271	20762.615855
HLA A*3002	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.527817	0.763535	-3.764282	33714.526945
HLA B*3901	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.179334	0.414917	-3.764417	15112.433625
HLA B*1502	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.367054	0.602482	-3.764572	23283.783858
HLA B*4402	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.414574	0.649819	-3.764756	25976.117659
HLA B*4501	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.560834	0.795947	-3.764888	36377.628469
HLA A*0250	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.477627	0.712622	-3.765006	30034.981707
HLA B*0702	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.380864	0.615847	-3.765017	24036.090578
HLA B*0802	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.477670	0.712622	-3.765048	30037.906596
HLA B*4002	1:48-56	9	VRAVRETMA	1.031036	-0.180296	-4.615878	0.850740	-3.765138	41293.159885
HLA B*4002	1:133-141	9	VSRPLGAGT	1.072243	-0.237395	-4.600130	0.834848	-3.765281	39822.591589
HLA A*2603	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.512045	0.746698	-3.765347	32512.096669
HLA A*2402	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.561758	0.795947	-3.765811	36455.052728
HLA B*5301	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.529643	0.763535	-3.766108	33856.543688
HLA A*0101	1:46-54	9	DEVRAVRET	1.031728	-0.408046	-4.389968	0.623682	-3.766286	24545.285407
HLA A*0201	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.392043	0.625647	-3.766395	24662.817066
HLA B*1502	1:82-90	9	VRRQSRWRT	1.037980	-0.242033	-4.562392	0.795947	-3.766445	36508.340440
HLA B*4403	1:188-196	9	TAAVTPSTT	1.185673	-0.299259	-4.653085	0.886414	-3.766671	44986.744085
HLA A*0101	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.370646	0.603848	-3.766798	23477.179566
HLA B*3901	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.413317	0.646348	-3.766969	25901.043919
HLA B*1801	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.464050	0.697019	-3.767031	29110.502214
HLA B*5701	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.392686	0.625647	-3.767039	24699.402105
HLA B*2705	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.368256	0.600711	-3.767546	23348.366156
HLA B*4501	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.474470	0.706535	-3.767935	29817.392620
HLA A*6802	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.027971	0.259962	-3.768010	10665.253551
HLA B*5101	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.474691	0.706535	-3.768156	29832.559502
HLA B*1517	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.424621	0.656423	-3.768197	26584.019120
HLA B*4801	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.394719	0.625647	-3.769071	24815.255153
HLA B*2705	1:208-216	9	LAFTVEPGT	0.857007	-0.166474	-4.459940	0.690533	-3.769407	28836.360661
HLA A*0201	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.385288	0.615847	-3.769441	24282.193311
HLA A*6901	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.385295	0.615847	-3.769448	24282.587406
HLA B*0801	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.415935	0.646348	-3.769587	26057.610888
HLA B*5401	1:5-13	9	TDFELLELA	1.003059	-0.335657	-4.437005	0.667402	-3.769603	27352.988071
HLA B*5701	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.419654	0.649819	-3.769835	26281.722738
HLA B*0803	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.476373	0.706535	-3.769838	29948.339434
HLA B*3901	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.466921	0.697019	-3.769902	29303.585906
HLA B*1517	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.419832	0.649819	-3.770014	26292.530731
HLA B*3801	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.565416	0.795128	-3.770288	36763.417719
HLA A*8001	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.408221	0.637921	-3.770300	25598.895962
HLA A*0216	1:115-123	9	SPPPTVAEQ	0.875652	-0.225833	-4.420420	0.649819	-3.770601	26328.114708
HLA B*4402	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.427059	0.656423	-3.770636	26733.720676
HLA B*4501	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.651776	0.880895	-3.770880	44851.389193
HLA A*2403	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.305645	0.534755	-3.770890	20213.665266
HLA A*2301	1:175-183	9	GGAKGPRSA	1.161451	-0.397036	-4.535521	0.764415	-3.771106	34317.925864
HLA B*4601	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.336402	0.565014	-3.771388	21697.124338
HLA B*1509	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.478182	0.706535	-3.771647	30073.352874
HLA B*3801	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.535841	0.763535	-3.772306	34343.184394
HLA B*1801	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.325686	0.553011	-3.772675	21168.309500
HLA B*4402	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.410604	0.637921	-3.772682	25739.707840
HLA B*5101	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.469747	0.697019	-3.772728	29494.918405
HLA A*8001	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.429348	0.656423	-3.772925	26874.958634
HLA A*3001	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.133811	0.360868	-3.772943	13608.516525
HLA B*1501	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.007460	0.234317	-3.773143	10173.260857
HLA B*5701	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.411217	0.637921	-3.773295	25776.077491
HLA A*2301	1:59-67	9	SAATTAEPP	0.646418	0.117117	-4.536884	0.763535	-3.773349	34425.775558
HLA A*0250	1:7-15	9	FELLELATP	0.903395	-0.108267	-4.568517	0.795128	-3.773390	37026.886862
HLA B*4601	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.275966	0.502462	-3.773504	18878.451784
HLA B*1503	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.411456	0.637921	-3.773535	25790.304879
HLA B*1503	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.470645	0.697019	-3.773626	29555.934970
HLA B*1503	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.134577	0.360868	-3.773709	13632.538006
HLA B*4002	1:12-20	9	LATPYALNA	1.117892	-0.294996	-4.596826	0.822896	-3.773930	39520.837916
HLA A*2402	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.486661	0.712622	-3.774039	30666.283170
HLA B*4402	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.420547	0.646348	-3.774199	26335.807169
HLA A*6901	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.263580	0.489218	-3.774362	18347.626477
HLA B*2705	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.471399	0.697019	-3.774380	29607.305642
HLA B*1502	1:199-207	9	LTDLGASTA	1.057727	-0.311029	-4.521342	0.746698	-3.774644	33215.583775
HLA A*1101	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.271679	0.496962	-3.774717	18692.981017
HLA B*1501	1:46-54	9	DEVRAVRET	1.031728	-0.408046	-4.398483	0.623682	-3.774801	25031.254739
HLA B*5801	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.358067	0.583145	-3.774922	22806.927341
HLA B*3801	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.485905	0.710864	-3.775040	30612.909488
HLA A*6901	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.226169	0.451113	-3.775056	16833.291358
HLA B*4403	1:55-63	9	MAVVSAATT	1.035754	-0.225867	-4.585069	0.809887	-3.775183	38465.317445
HLA B*4801	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.421639	0.646348	-3.775291	26402.140884
HLA A*1101	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.486299	0.710864	-3.775435	30640.745026
HLA A*2601	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.391479	0.615847	-3.775632	24630.816299
HLA B*1503	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.203139	0.427495	-3.775644	15963.914329
HLA B*4403	1:198-206	9	TLTDLGAST	1.133749	-0.256205	-4.653204	0.877544	-3.775660	44999.157835
HLA B*1503	1:156-164	9	VMNNVAPPS	0.722767	-0.916838	-3.581696	-0.194071	-3.775767	3816.769265
HLA A*2403	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.341167	0.565014	-3.776153	21936.479639
HLA B*1517	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.488825	0.712622	-3.776203	30819.459452
HLA B*0801	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.392078	0.615847	-3.776231	24664.818493
HLA B*1801	1:190-198	9	AVTPSTTAT	0.839277	-0.132742	-4.482848	0.706535	-3.776313	30398.204158
HLA A*0101	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.392170	0.615847	-3.776323	24670.022966
HLA A*2902	1:60-68	9	AATTAEPPA	0.798576	-0.138219	-4.436925	0.660357	-3.776568	27347.957328
HLA B*1503	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.312043	0.535432	-3.776611	20513.639414
HLA A*6801	1:172-180	9	WLLGGAKGP	0.816481	0.064414	-4.657668	0.880895	-3.776773	45464.080026
HLA B*5301	1:153-161	9	GLLVMNNVA	1.100376	-0.288610	-4.588631	0.811766	-3.776865	38782.083776
HLA A*2501	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.329997	0.553011	-3.776986	21379.496921

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HLA A*2403      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.392849       0.615847        -3.777002       24708.623677
HLA B*5101      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.435586       0.658536        -3.777050       27263.756050
HLA B*1501      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.373717       0.596633        -3.777084       23643.768507
HLA B*2705      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.487998       0.710864        -3.777134       30760.826387
HLA B*5101      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.437557       0.660357        -3.777200       27387.784694
HLA A*0250      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.541724       0.764415        -3.777309       34811.574948
HLA A*6802      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.401192       0.623682        -3.777510       25187.877716
HLA B*2705      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.342567       0.565014        -3.777553       22007.323446
HLA B*2705      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.403363       0.625647        -3.777715       25314.100521
HLA A*8001      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.393624       0.615847        -3.777777       24752.774478
HLA A*2501      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.438140       0.660357        -3.777783       27424.554245
HLA A*0101      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.360947       0.583145        -3.777802       22958.697590
HLA A*6801      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.628655       0.850740        -3.777915       42526.008063
HLA B*4403      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.600816       0.822896        -3.777919       39885.548557
HLA B*5701      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.374581       0.596633        -3.777948       23690.886335
HLA B*0803      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.488849       0.710864        -3.777984       30821.126796
HLA B*0702      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.424407       0.646348        -3.778059       26570.935031
HLA B*1509      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.490728       0.712622        -3.778106       30954.806969
HLA B*0801      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.313180       0.534755        -3.778425       20567.422429
HLA B*4403      1:172-180       9       WLLGGAKGP       0.816481        0.064414        -4.659482       0.880895        -3.778587       45654.354833
HLA A*2402      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.542746       0.764021        -3.778725       34893.593558
HLA B*4601      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.379597       0.600711        -3.778887       23966.105101
HLA B*5401      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.491557       0.712622        -3.778936       31013.977562
HLA A*0250      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.297206       0.518215        -3.778991       19824.658710
HLA B*3801      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.559913       0.780826        -3.779087       36300.565028
HLA A*1101      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.437688       0.658536        -3.779152       27396.083184
HLA A*2602      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.560369       0.780826        -3.779543       36338.683142
HLA B*1509      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.426197       0.646348        -3.779849       26680.695420
HLA A*2603      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.589930       0.809887        -3.780044       38898.280647
HLA B*3801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.429945       0.649819        -3.780126       26911.913217
HLA A*3101      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.396279       0.615847        -3.780432       24904.555974
HLA A*8001      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.439213       0.658536        -3.780677       27492.440384
HLA A*0203      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.406577       0.625647        -3.780929       25502.138252
HLA A*2602      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.477992       0.697019        -3.780973       30060.177587
HLA B*0801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.332706       0.551693        -3.781013       21513.270497
HLA B*4801      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.346305       0.565014        -3.781291       22197.560945
HLA B*3501      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.382121       0.600711        -3.781410       24105.758783
HLA A*6901      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.364944       0.583145        -3.781799       23170.943679
HLA B*3901      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.438285       0.656423        -3.781862       27433.754343
HLA B*1801      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.382586       0.600711        -3.781875       24131.593695
HLA B*0801      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.385814       0.603848        -3.781966       24311.636677
HLA B*4801      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.365489       0.583145        -3.782344       23200.043655
HLA A*8001      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.383061       0.600711        -3.782350       24157.979057
HLA B*4001      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.398346       0.615847        -3.782500       25023.401825
HLA B*0803      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.495147       0.712622        -3.782526       31271.411281
HLA A*2602      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.578500       0.795947        -3.782554       37887.867407
HLA A*0212      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.432550       0.649819        -3.782732       27073.858360
HLA B*5301      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.578702       0.795947        -3.782756       37905.498857
HLA B*4801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.432583       0.649819        -3.782764       27075.908969
HLA A*3301      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.594705       0.811766        -3.782938       39328.244294
HLA B*3901      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.408625       0.625647        -3.782978       25622.726844
HLA B*1801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.433095       0.649819        -3.783277       27107.859938
HLA B*3801      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.547424       0.764021        -3.783403       35271.466971
HLA A*2602      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.494638       0.710864        -3.783773       31234.721875
HLA A*0202      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.032012       0.247860        -3.784153       10764.956986
HLA A*0301      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.367467       0.583145        -3.784322       23305.963849
HLA A*6801      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.619268       0.834848        -3.784420       41616.775203
HLA B*3901      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.475250       0.690533        -3.784717       29870.995261
HLA A*8001      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.387330       0.602482        -3.784848       24396.617358
HLA A*3201      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.381564       0.596633        -3.784931       24074.871541
HLA A*0216      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.431566       0.646348        -3.785218       27012.558368
HLA A*0203      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.409001       0.623682        -3.785319       25644.915024
HLA B*0803      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.498383       0.712665        -3.785717       31505.234918
HLA B*4601      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.409612       0.623682        -3.785930       25681.011802
HLA B*1801      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.498709       0.712622        -3.786088       31528.934964
HLA A*8001      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.435933       0.649819        -3.786115       27285.593888
HLA B*4402      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -3.421691       -0.364496       -3.786187       2640.531050
HLA B*0702      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.288849       0.502462        -3.786387       19446.820311
HLA A*1101      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.424597       0.637921        -3.786676       26582.580993
HLA A*3001      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.282157       0.495365        -3.786792       19149.492467
HLA B*2705      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.424724       0.637921        -3.786803       26590.347804
HLA A*0212      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.592781       -0.194071       -3.786852       3915.441834
HLA A*0101      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.383540       0.596633        -3.786907       24184.654940
HLA A*6901      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.275161       0.488141        -3.787020       18843.453561
HLA B*4601      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.390884       0.603848        -3.787036       24597.127113
HLA A*2602      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.610002       0.822896        -3.787106       40738.220617
HLA B*5701      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.387922       0.600711        -3.787211       24429.899755
HLA B*0702      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.391561       0.603848        -3.787713       24635.480490
HLA B*5701      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.391582       0.603848        -3.787734       24636.679996
HLA B*1517      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.425859       0.637921        -3.787937       26659.918610
HLA A*2602      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.551892       0.763535        -3.788357       35636.270203
HLA B*1801      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.478995       0.690533        -3.788462       30129.697544
HLA A*2501      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.444981       0.656423        -3.788558       27860.010622
HLA A*1101      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.485839       0.697019        -3.788820       30608.272690
HLA A*0202      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.584804       0.795947        -3.788857       38441.810110
HLA B*0801      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.414527       0.625647        -3.788880       25973.307253
HLA A*3301      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.585227       0.795947        -3.789280       38479.262210
HLA B*4001      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.391798       0.602482        -3.789316       24648.944965
HLA A*2902      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.277494       0.488141        -3.789353       18944.953355
HLA B*0801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.350835       0.561253        -3.789582       22430.299067
HLA A*2501      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.448355       0.658536        -3.789819       28077.286796
HLA B*2705      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.446562       0.656423        -3.790139       27961.629770
HLA B*4601      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.406086       0.615847        -3.790239       25473.320125
HLA A*3001      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.194484       0.403811        -3.790673       15648.902536
HLA A*0201      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.387511       0.596633        -3.790877       24406.782166
HLA B*0801      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.374088       0.583145        -3.790943       23663.986953
HLA A*3002      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.503655       0.712665        -3.790990       31890.032851
HLA B*0702      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.449584       0.658536        -3.791048       28156.840376
HLA A*0219      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.207937       0.416603        -3.791334       16141.245272
HLA B*4601      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.287084       0.495365        -3.791719       19367.971532
HLA A*6801      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.417666       0.625647        -3.792019       26161.712276
HLA A*2301      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.540932       0.748881        -3.792051       34748.166648
HLA A*0202      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.345107       0.553011        -3.792096       22136.401320
HLA B*1503      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.118389       0.326268        -3.792121       13133.750610
HLA A*2603      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.541096       0.748881        -3.792215       34761.328001
HLA B*1501      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.240663       0.448362        -3.792301       17404.558595
HLA B*1801      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.449203       0.656423        -3.792780       28132.174474
HLA A*6801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.209389       0.416603        -3.792786       16195.300795
HLA A*3101      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.416762       0.623682        -3.793080       26107.279177
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HLA B*5301      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.539908       0.746698        -3.793209       34666.302327
HLA B*3901      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.453707       0.660357        -3.793350       28425.444520
HLA B*1502      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.556927       0.763535        -3.793392       36051.819627
HLA B*3901      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.460852       0.667402        -3.793450       28896.952819
HLA A*2601      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.397357       0.603848        -3.793509       24966.474295
HLA A*0201      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.376665       0.583145        -3.793520       23804.841944
HLA A*2402      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.557127       0.763535        -3.793592       36068.401529
HLA B*4601      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.377027       0.583145        -3.793882       23824.682567
HLA A*6802      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.283196       0.489218        -3.793978       19195.336968
HLA B*4402      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.452901       0.658536        -3.794365       28372.747401
HLA B*0801      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.418223       0.623682        -3.794541       26195.276864
HLA A*2602      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.606522       0.811766        -3.794756       40413.128193
HLA B*1502      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.243151       0.448362        -3.794789       17504.556750
HLA B*7301      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.559345       0.764415        -3.794930       36253.071672
HLA B*0802      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.444944       0.649819        -3.795125       27857.599213
HLA B*0803      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.492194       0.697019        -3.795175       31059.479880
HLA A*2603      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.607284       0.811766        -3.795517       40484.026607
HLA B*4403      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.508300       0.712665        -3.795634       32232.938419
HLA A*2402      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.542384       0.746698        -3.795686       34864.535012
HLA A*1101      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.452302       0.656423        -3.795879       28333.633565
HLA B*1502      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.591086       0.795128        -3.795959       39001.952766
HLA B*4002      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.626037       0.830057        -3.795980       42270.490846
HLA B*1509      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.486530       0.690533        -3.795996       30656.994111
HLA A*0216      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.421837       0.625647        -3.796189       26414.141554
HLA A*6801      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.463749       0.667402        -3.796347       29090.351164
HLA B*4801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.434420       0.637921        -3.796499       27190.697140
HLA A*2402      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.577325       0.780826        -3.796499       37785.521309
HLA A*0211      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.446696       0.649819        -3.796878       27970.253450
HLA A*3201      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.592137       0.795128        -3.797009       39096.382215
HLA B*4801      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.299727       0.502462        -3.797265       19940.071759
HLA A*1101      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.179973       0.382667        -3.797307       15134.687787
HLA A*3002      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.592435       0.795128        -3.797307       39123.252846
HLA B*7301      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.544014       0.746698        -3.797316       34995.678654
HLA A*0219      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.447516       0.649819        -3.797698       28023.112609
HLA A*6802      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.394411       0.596633        -3.797778       24797.674924
HLA A*3201      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.578655       0.780826        -3.797829       37901.397787
HLA A*2301      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.544555       0.746698        -3.797856       35039.249986
HLA B*0802      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.458662       0.660357        -3.798305       28751.620592
HLA B*1509      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.465880       0.667402        -3.798478       29233.441579
HLA B*2705      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.414452       0.615847        -3.798606       25968.811235
HLA B*5701      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.422328       0.623682        -3.798646       26444.024038
HLA B*1801      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.457300       0.658536        -3.798764       28661.546993
HLA B*4001      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.399505       0.600711        -3.798794       25090.230201
HLA B*4403      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.247430       0.448362        -3.799067       17677.853489
HLA A*2603      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.649845       0.850740        -3.799105       44652.381071
HLA A*2601      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.395778       0.596633        -3.799145       24875.874823
HLA A*6901      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.299311       0.500136        -3.799175       19920.987274
HLA B*3501      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.299513       0.500136        -3.799377       19930.257679
HLA A*0206      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -3.865932       0.066377        -3.799555       7343.987060
HLA A*2601      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.352839       0.553011        -3.799828       22534.045913
HLA A*6901      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.111152       0.311316        -3.799837       12916.723162
HLA B*1502      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.512510       0.712665        -3.799845       32546.940921
HLA B*5701      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.415749       0.615847        -3.799902       26046.476733
HLA A*2403      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.383587       0.583145        -3.800442       24187.271807
HLA B*3501      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.424202       0.623682        -3.800521       26558.432088
HLA B*4601      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.397545       0.596633        -3.800912       24977.281902
HLA A*3002      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.401652       0.600711        -3.800942       25214.599551
HLA A*0219      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.416870       0.615847        -3.801023       26113.776910
HLA B*0803      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.439674       0.637921        -3.801752       27521.607131
HLA A*2602      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.596897       0.795128        -3.801769       39527.252537
HLA B*0702      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.469291       0.667402        -3.801890       29463.979181
HLA A*3002      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.582748       0.780826        -3.801922       38260.269934
HLA B*3501      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.367030       0.565014        -3.802016       23282.524266
HLA A*2301      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.514768       0.712622        -3.802146       32716.589938
HLA B*5301      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.337008       0.534755        -3.802254       21727.429274
HLA B*4403      1:48-56 9       VRAVRETMA       1.031036        -0.180296       -4.653070       0.850740        -3.802330       44985.283869
HLA B*4403      1:133-141       9       VSRPLGAGT       1.072243        -0.237395       -4.637284       0.834848        -3.802436       43379.473396
HLA B*4801      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.418625       0.615847        -3.802778       26219.521093
HLA A*2902      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.399617       0.596633        -3.802984       25096.746345
HLA A*0301      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.356100       0.553011        -3.803089       22703.889271
HLA A*0212      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.428944       0.625647        -3.803296       26849.963091
HLA A*0203      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.331825       0.528496        -3.803329       21469.670585
HLA A*3101      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.386803       0.583145        -3.803658       24367.071073
HLA B*0801      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.400362       0.596633        -3.803729       25139.822556
HLA A*0206      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.453773       0.649819        -3.803954       28429.750645
HLA A*6802      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.429627       0.625647        -3.803980       26892.265679
HLA B*5101      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.441918       0.637921        -3.803996       27664.163916
HLA B*4601      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.406492       0.602482        -3.804010       25497.172041
HLA A*3301      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.517202       0.712665        -3.804537       32900.469624
HLA A*2402      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.553650       0.748881        -3.804769       35780.767995
HLA A*3101      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.323012       0.518215        -3.804798       21038.388118
HLA A*0301      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.366680       0.561253        -3.805427       23263.764402
HLA B*1509      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.388598       0.583145        -3.805453       24467.992380
HLA A*0250      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.586338       0.780826        -3.805512       38577.852017
HLA A*3001      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.198252       0.392663        -3.805589       15785.286172
HLA A*6802      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.421491       0.615847        -3.805645       26393.143960
HLA B*0802      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.462118       0.656423        -3.805695       28981.337287
HLA B*5801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.366957       0.561253        -3.805705       23278.619961
HLA A*0212      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.388948       0.583145        -3.805803       24487.723331
HLA B*0802      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.421799       0.615847        -3.805952       26411.855292
HLA B*1517      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.473412       0.667402        -3.806011       29744.891951
HLA A*2601      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.308533       0.502462        -3.806071       20348.508723
HLA A*8001      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.429768       0.623682        -3.806086       26900.996147
HLA B*1502      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.555008       0.748881        -3.806127       35892.826555
HLA A*2301      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.517016       0.710864        -3.806152       32886.411584
HLA B*0802      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.473650       0.667402        -3.806248       29761.148965
HLA A*0211      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.422344       0.615847        -3.806497       26445.025472
HLA B*5801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.358238       0.551693        -3.806545       22815.936075
HLA A*8001      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.410749       0.603848        -3.806901       25748.342724
HLA A*3201      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.453329       0.646348        -3.806981       28400.696960
HLA B*4001      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.411062       0.603848        -3.807213       25766.875716
HLA A*3002      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.518172       0.710864        -3.807308       32974.060805
HLA B*1503      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.372619       0.565014        -3.807605       23584.109852
HLA A*0212      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.308067       0.500136        -3.807932       20326.723924
HLA B*1517      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.466754       0.658536        -3.808218       29292.332498
HLA A*2603      1:12-20 9       LATPYALNA       1.117892        -0.294996       -4.631298       0.822896        -3.808401       42785.615877
HLA B*5401      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.515656       0.706535        -3.809121       32783.561792
HLA B*1801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.447223       0.637921        -3.809301       28004.168773
HLA B*4801      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.433034       0.623682        -3.809352       27104.047292
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HLA A*0219      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.309491       0.500136        -3.809356       20393.472263
HLA A*0250      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.572941       0.763535        -3.809406       37406.000845
HLA B*3901      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.468175       0.658536        -3.809639       29388.362869
HLA B*4001      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.375129       0.565014        -3.810114       23720.767624
HLA B*0803      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.500659       0.690533        -3.810126       31670.824759
HLA B*0802      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.456498       0.646348        -3.810150       28608.721708
HLA B*1517      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.307229       0.496962        -3.810267       20287.504189
HLA A*0101      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.371847       0.561253        -3.810594       23542.170925
HLA A*3001      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.193262       0.382667        -3.810595       15604.941808
HLA B*5801      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.298768       0.488141        -3.810627       19896.107876
HLA B*5401      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.306218       0.495365        -3.810853       20240.365185
HLA B*2705      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.345810       0.534755        -3.811055       22172.237183
HLA A*2602      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.227696       0.416603        -3.811093       16892.588610
HLA B*1501      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.394418       0.583145        -3.811273       24798.077385
HLA A*1101      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.408031       0.596633        -3.811398       25587.680957
HLA A*2403      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.415681       0.603848        -3.811832       26042.390706
HLA A*6801      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.071850       0.259962        -3.811889       11799.134902
HLA A*0216      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.346839       0.534755        -3.812084       22224.837290
HLA B*4002      1:55-63 9       MAVVSAATT       1.035754        -0.225867       -4.622069       0.809887        -3.812182       41886.011799
HLA A*0202      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.561170       0.748881        -3.812289       36405.781606
HLA A*2501      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.458662       0.646348        -3.812314       28751.620592
HLA A*0219      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.438062       0.625647        -3.812415       27419.658676
HLA B*5801      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.347424       0.534755        -3.812669       22254.795706
HLA B*1502      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.525590       0.712622        -3.812968       33542.062095
HLA A*0206      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.164880       0.351592        -3.813288       14617.744769
HLA A*0212      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.410066       0.596633        -3.813432       25707.839571
HLA B*5701      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.416092       0.602482        -3.813610       26067.057509
HLA A*0301      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.365341       0.551693        -3.813648       23192.137894
HLA A*2601      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.396831       0.583145        -3.813686       24936.237867
HLA A*0212      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.437399       0.623682        -3.813718       27377.859446
HLA A*3001      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.208844       0.394780        -3.814064       16174.986916
HLA B*1501      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.174936       0.360868        -3.814068       14960.157662
HLA B*0802      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.452006       0.637921        -3.814085       28314.326637
HLA B*2705      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.460439       0.646348        -3.814091       28869.451954
HLA A*0101      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.379395       0.565014        -3.814381       23954.957453
HLA B*4402      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.397597       0.583145        -3.814452       24980.254814
HLA B*4501      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.527328       0.712665        -3.814663       33676.610776
HLA A*3001      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.125696       0.310721        -3.814974       13356.592120
HLA B*0802      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.438748       0.623682        -3.815066       27463.007402
HLA A*2603      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.527707       0.712622        -3.815085       33705.955617
HLA B*5801      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.368557       0.553011        -3.815546       23364.539701
HLA A*0219      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.439364       0.623682        -3.815682       27501.960820
HLA A*2603      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.522448       0.706535        -3.815914       33300.326921
HLA A*0206      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.311420       0.495365        -3.816055       20484.251708
HLA A*2403      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.416780       0.600711        -3.816070       26108.409101
HLA A*0206      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.063965       0.247860        -3.816106       11586.847602
HLA B*1801      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.419224       0.602482        -3.816742       26255.716452
HLA B*1501      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.352400       0.535432        -3.816968       22511.260889
HLA B*1509      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.473492       0.656423        -3.817069       29750.363617
HLA B*5701      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.400762       0.583145        -3.817617       25162.953812
HLA B*5101      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.474225       0.656423        -3.817802       29800.621224
HLA B*1517      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.183991       0.366173        -3.817818       15275.347038
HLA B*5801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.317959       0.500136        -3.817823       20794.990223
HLA A*2402      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.582412       0.764415        -3.817997       38230.682694
HLA B*0802      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.418714       0.600711        -3.818003       26224.911745
HLA B*4403      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.648141       0.830057        -3.818084       44477.589862
HLA B*3801      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.524695       0.706535        -3.818160       33472.997480
HLA A*0203      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.306512       0.488141        -3.818371       20254.057080
HLA B*1501      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.371579       0.553011        -3.818567       23527.656300
HLA B*1501      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.318774       0.500136        -3.818638       20834.063898
HLA A*6901      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.370376       0.551693        -3.818683       23462.578080
HLA A*2301      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.531668       0.712665        -3.819002       34014.796441
HLA B*4001      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.380570       0.561253        -3.819317       24019.842000
HLA A*1101      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.235990       0.416603        -3.819387       17218.284829
HLA A*0101      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.371219       0.551693        -3.819526       23508.190209
HLA B*0801      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.384607       0.565014        -3.819592       24244.127626
HLA A*2602      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.443374       0.623682        -3.819692       27757.108941
HLA B*1517      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.354517       0.534755        -3.819762       22621.255612
HLA A*0203      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.416412       0.596633        -3.819778       26086.243271
HLA A*3301      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.615021       0.795128        -3.819893       41211.702467
HLA A*0206      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.531085       0.710864        -3.820221       33969.191004
HLA A*2501      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.444088       0.623682        -3.820407       27802.796015
HLA B*3501      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.373510       0.553011        -3.820499       23632.515091
HLA A*2403      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.444208       0.623682        -3.820526       27810.467986
HLA A*3201      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.616475       0.795947        -3.820528       41349.940307
HLA A*0211      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.531534       0.710864        -3.820670       34004.309130
HLA A*6901      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.317651       0.496962        -3.820689       20780.258128
HLA B*4501      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.585213       0.764415        -3.820798       38478.013219
HLA A*3002      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.533475       0.712622        -3.820853       34156.599720
HLA A*2501      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.339452       0.518215        -3.821237       21850.018515
HLA B*4501      1:144-152       9       VVFSRDRNT       0.997060        -0.167003       -4.651405       0.830057        -3.821347       44813.068288
HLA A*0211      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.467764       0.646348        -3.821416       29360.553173
HLA A*6802      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.373129       0.551693        -3.821436       23611.812580
HLA A*3301      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.568160       0.746698        -3.821462       36996.452052
HLA A*3001      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.309360       0.487485        -3.821875       20387.294919
HLA B*0803      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.489495       0.667402        -3.822093       30867.014113
HLA B*4001      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.356955       0.534755        -3.822201       22748.641811
HLA A*3101      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.239023       0.416603        -3.822420       17338.961125
HLA B*1517      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.438640       0.615847        -3.822793       27456.173948
HLA B*1503      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.426792       0.603848        -3.822943       26717.238342
HLA B*3801      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.535998       0.712622        -3.823376       34355.634769
HLA B*3801      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.520409       0.697019        -3.823390       33144.322355
HLA B*1801      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.268615       0.445146        -3.823469       18561.575512
HLA B*4001      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.406640       0.583145        -3.823495       25505.863545
HLA A*6802      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.002789       0.179262        -3.823528       10064.435116
HLA B*4402      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.424308       0.600711        -3.823598       26564.898393
HLA B*1503      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.482254       0.658536        -3.823717       30356.626536
HLA B*4501      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.388981       0.565014        -3.823967       24489.578064
HLA A*0250      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.473831       0.649819        -3.824012       29773.548895
HLA B*2705      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.427893       0.603848        -3.824045       26785.112404
HLA A*0250      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.573092       0.748881        -3.824211       37418.954276
HLA B*5101      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.470560       0.646348        -3.824212       29550.179335
HLA B*4002      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.588431       0.764021        -3.824411       38764.254300
HLA B*4402      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.421150       0.596633        -3.824517       26372.448401
HLA B*1509      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.389580       0.565014        -3.824566       24523.385282
HLA A*2501      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.425316       0.600711        -3.824606       26626.622935
HLA B*4402      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.427386       0.602482        -3.824904       26753.831315
HLA A*0301      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.359747       0.534755        -3.824992       22895.316988
HLA B*5801      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.353770       0.528496        -3.825273       22582.372709
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HLA A*3002      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.427861       0.602482        -3.825379       26783.083818
HLA B*4801      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.427945       0.602482        -3.825463       26788.300493
HLA A*8001      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.408945       0.583145        -3.825800       25641.585572
HLA A*6901      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.387088       0.561253        -3.825835       24383.026896
HLA A*2403      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.428394       0.602482        -3.825912       26815.994850
HLA B*1501      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.360787       0.534755        -3.826033       22950.253270
HLA A*3301      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.606873       0.780826        -3.826047       40445.717277
HLA A*0202      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.314279       0.488141        -3.826138       20619.561583
HLA B*7301      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.589686       0.763535        -3.826151       38876.401522
HLA B*0802      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.484720       0.658536        -3.826184       30529.554503
HLA A*6801      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.638118       0.811766        -3.826352       43462.864187
HLA A*2501      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.428920       0.602482        -3.826438       26848.510577
HLA B*1503      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.429244       0.602482        -3.826762       26868.562211
HLA A*0219      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.409967       0.583145        -3.826822       25701.999019
HLA A*3101      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.379861       0.553011        -3.826849       23980.630746
HLA A*0201      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.243795       0.416603        -3.827192       17530.523163
HLA B*0802      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.453454       0.625647        -3.827806       28408.841293
HLA B*5701      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.346153       0.518215        -3.827938       22189.756705
HLA B*4601      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.245010       0.416603        -3.828406       17579.623138
HLA A*0202      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.040813       0.212403        -3.828410       10985.339156
HLA A*2602      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.488802       0.660357        -3.828445       30817.792199
HLA B*5801      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.330996       0.502462        -3.828534       21428.709275
HLA A*3101      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.389858       0.561253        -3.828605       24539.045198
HLA A*0301      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.364295       0.535432        -3.828864       23136.372277
HLA B*5301      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.593349       0.764415        -3.828934       39205.672346
HLA A*2301      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.496379       0.667402        -3.828977       31360.184679
HLA B*1509      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.455075       0.625647        -3.829427       28515.084654
HLA B*1502      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.610380       0.780826        -3.829554       40773.718744
HLA A*6901      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.358128       0.528496        -3.829632       22810.135523
HLA A*2602      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.576527       0.746698        -3.829828       37716.083925
HLA B*5801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.365580       0.535432        -3.830149       23204.939049
HLA B*5401      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -3.950603       0.120389        -3.830213       8924.885302
HLA B*1501      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.636204       -0.194071       -3.830275       4327.170009
HLA A*3301      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.332749       0.502462        -3.830287       21515.365519
HLA B*4801      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.434296       0.603848        -3.830447       27182.902029
HLA B*4601      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.391885       0.561253        -3.830633       24653.879337
HLA B*1501      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.319876       0.489218        -3.830658       20886.991994
HLA A*3002      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.480574       0.649819        -3.830755       30239.431763
HLA B*1503      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.454774       0.623682        -3.831092       28495.345768
HLA A*0211      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.456860       0.625647        -3.831213       28632.566222
HLA A*2301      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.538181       0.706535        -3.831646       34528.733487
HLA A*3002      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.528759       0.697019        -3.831740       33787.745468
HLA B*5401      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.478189       0.646348        -3.831841       30073.840958
HLA B*1517      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.428657       0.596633        -3.832024       26832.247788
HLA A*2601      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.393295       0.561253        -3.832042       24734.034208
HLA B*4601      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.367526       0.535432        -3.832094       23309.116130
HLA B*1801      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.492584       0.660357        -3.832227       31087.385113
HLA B*5101      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.367096       0.534755        -3.832341       23286.051297
HLA A*0219      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.367136       0.534755        -3.832381       23288.192970
HLA B*5301      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.538930       0.706535        -3.832395       34588.373055
HLA B*5401      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.529469       0.697019        -3.832450       33842.992550
HLA B*1509      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.247770       0.414917        -3.832853       17691.726038
HLA B*0801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.368386       0.535432        -3.832954       23355.314354
HLA B*0702      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.429604       0.596633        -3.832971       26890.810877
HLA A*2602      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.482874       0.649819        -3.833055       30400.013171
HLA B*2705      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.483010       0.649819        -3.833191       30409.553389
HLA A*1101      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.483057       0.649819        -3.833238       30412.843813
HLA A*3001      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.282037       0.448362        -3.833675       19144.209768
HLA B*4801      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.434430       0.600711        -3.833719       27191.285541
HLA A*6801      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.171318       0.337522        -3.833795       14836.038907
HLA B*7301      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.583533       0.748881        -3.834652       38329.465025
HLA B*0702      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.396323       0.561253        -3.835071       24907.115992
HLA B*0702      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.437569       0.602482        -3.835087       27388.525529
HLA A*0201      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.396636       0.561253        -3.835383       24925.043491
HLA A*0219      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.364161       0.528496        -3.835665       23129.238960
HLA B*4501      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.599657       0.763535        -3.836122       39779.312526
HLA A*0301      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.365040       0.528496        -3.836544       23176.083690
HLA A*3101      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.219262       0.382667        -3.836595       16567.674539
HLA B*5801      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.094659       0.257963        -3.836696       12435.377307
HLA A*3101      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.371482       0.534755        -3.836728       23522.438316
HLA B*4001      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.390196       0.553011        -3.837185       24558.169152
HLA A*2902      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.453035       0.615847        -3.837189       28381.497875
HLA B*0803      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.487286       0.649819        -3.837468       30710.444655
HLA A*0301      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.337929       0.500136        -3.837794       21773.555015
HLA B*0702      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.421179       0.583145        -3.838034       26374.160521
HLA A*0206      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.199023       0.360868        -3.838155       15813.321139
HLA A*3002      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.442073       0.603848        -3.838224       27674.043243
HLA B*1501      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.204516       0.366173        -3.838343       16014.603355
HLA A*3201      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.602794       0.764415        -3.838379       40067.646708
HLA A*0203      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.373329       0.534755        -3.838574       23622.672746
HLA B*4402      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.442930       0.603848        -3.839082       27728.742660
HLA A*6801      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.489074       0.649819        -3.839255       30837.137886
HLA B*3501      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.455171       0.615847        -3.839324       28521.410157
HLA A*0202      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.455237       0.615847        -3.839390       28525.730819
HLA B*5701      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.087611       0.247860        -3.839751       12235.184197
HLA B*4403      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.635729       0.795947        -3.839782       43224.394328
HLA B*0803      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.496433       0.656423        -3.840009       31364.086990
HLA A*0206      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.741137       -0.098967       -3.840103       5509.810440
HLA B*1801      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.486929       0.646348        -3.840581       30685.201739
HLA B*1517      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.443106       0.602482        -3.840624       27739.995650
HLA A*0211      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.192318       0.351592        -3.840726       15571.041441
HLA A*0250      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.508133       0.667402        -3.840731       32220.560056
HLA A*0101      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.343256       0.502462        -3.840794       22042.234862
HLA A*0301      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.100768       0.259962        -3.840806       12611.525662
HLA A*3001      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.292053       0.451113        -3.840940       19590.850878
HLA A*1101      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.444847       0.603848        -3.840999       27851.420931
HLA B*4403      1:153-161       9       GLLVMNNVA       1.100376        -0.288610       -4.652824       0.811766        -3.841057       44959.737758
HLA B*0702      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.464802       0.623682        -3.841120       29160.940929
HLA B*1509      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.369906       0.528496        -3.841410       23437.205819
HLA A*6901      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.377008       0.535432        -3.841577       23823.651478
HLA A*3101      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.393286       0.551693        -3.841593       24733.498980
HLA A*0219      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.438238       0.596633        -3.841605       27430.786232
HLA A*2601      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.258301       0.416603        -3.841697       18125.942473
HLA A*3301      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.532657       0.690533        -3.842124       34092.355583
HLA A*2601      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.339503       0.496962        -3.842542       21852.619205
HLA A*2601      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.394533       0.551693        -3.842840       24804.651844
HLA A*0101      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.371344       0.528496        -3.842847       23514.931541
HLA A*3002      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.591848       0.748881        -3.842967       39070.375496
HLA A*0101      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.378554       0.535432        -3.843123       23908.607819
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HLA B*0803      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.503923       0.660357        -3.843566       31909.706373
HLA A*2501      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.346498       0.502462        -3.844036       22207.410210
HLA A*0212      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.379151       0.534755        -3.844396       23941.483502
HLA A*2603      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.639707       0.795128        -3.844579       43622.102575
HLA A*2402      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.555463       0.710864        -3.844599       35930.516515
HLA A*6801      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.555553       0.710864        -3.844688       35937.903719
HLA A*0101      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.379706       0.534755        -3.844951       23972.069926
HLA A*2902      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.249116       0.403811        -3.845305       17746.653115
HLA A*0201      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.397284       0.551693        -3.845591       24962.287605
HLA B*1501      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.406859       0.561253        -3.845606       25518.699276
HLA A*2402      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.558504       0.712665        -3.845838       36182.926835
HLA B*4402      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.410895       0.565014        -3.845881       25756.980504
HLA B*3801      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.558656       0.712665        -3.845991       36195.652537
HLA A*0250      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.504879       0.658536        -3.846343       31980.043364
HLA A*0101      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.364589       0.518215        -3.846374       23152.023220
HLA A*6802      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.220699       0.373896        -3.846804       16622.618565
HLA A*3001      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.292323       0.445146        -3.847178       19603.042869
HLA A*0216      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.430377       0.583145        -3.847232       26938.715200
HLA A*0202      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.558147       0.710864        -3.847282       36153.185730
HLA B*4002      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.430708       0.583145        -3.847563       26959.271740
HLA A*0216      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.471265       0.623682        -3.847583       29598.177232
HLA A*2301      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.544693       0.697019        -3.847674       35050.435720
HLA A*0211      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.348100       0.500136        -3.847965       22289.496774
HLA B*0803      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.506620       0.658536        -3.848084       32108.499957
HLA A*0203      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.409344       0.561253        -3.848092       25665.178503
HLA A*0101      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.343573       0.495365        -3.848208       22058.338958
HLA B*4601      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.366504       0.518215        -3.848289       23254.327238
HLA B*5301      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.508864       0.660357        -3.848507       32274.815989
HLA B*3501      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.445428       0.596633        -3.848795       27888.662062
HLA A*2403      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.400501       0.551693        -3.848808       25147.848052
HLA A*2301      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.505253       0.656423        -3.848829       32007.563549
HLA B*2705      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.451360       0.602482        -3.848878       28272.234179
HLA B*7301      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.507611       0.658536        -3.849075       32181.886540
HLA A*0250      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.464961       0.615847        -3.849115       29171.670409
HLA B*1501      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.345067       0.495365        -3.849702       22134.365570
HLA A*3101      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.385208       0.535432        -3.849776       24277.727346
HLA B*1501      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.352292       0.502118        -3.850174       22505.659548
HLA A*2403      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.368501       0.518215        -3.850286       23361.506308
HLA A*8001      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.447129       0.596633        -3.850496       27998.109451
HLA B*5701      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.385309       0.534755        -3.850554       24283.375615
HLA B*4601      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.403724       0.553011        -3.850713       25335.199066
HLA A*2301      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.541392       0.690533        -3.850859       34785.031000
HLA A*0101      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.339243       0.488141        -3.851102       21839.500697
HLA B*3901      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.379710       0.528496        -3.851214       23972.329299
HLA A*2501      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.467257       0.615847        -3.851410       29326.264346
HLA A*0216      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.448144       0.596633        -3.851511       28063.619572
HLA B*4501      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.632639       0.780826        -3.851813       42917.986988
HLA A*3301      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.558398       0.706535        -3.851863       36174.119354
HLA A*0206      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.475738       0.623682        -3.852057       29904.626724
HLA A*6802      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.303192       0.451113        -3.852079       20099.821808
HLA B*1509      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.468020       0.615847        -3.852174       29377.871548
HLA A*0206      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.256022       0.403811        -3.852210       18031.074047
HLA B*1503      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.300692       0.448362        -3.852330       19984.457126
HLA A*2902      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.476039       0.623682        -3.852357       29925.341827
HLA A*2301      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.510903       0.658536        -3.852367       32426.727940
HLA B*4001      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.404088       0.551693        -3.852395       25356.452372
HLA B*4402      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.387933       0.535432        -3.852502       24430.560579
HLA B*0702      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.405909       0.553011        -3.852898       25462.986634
HLA B*5701      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.414151       0.561253        -3.852899       25950.834946
HLA B*3901      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.490977       0.637921        -3.853056       30972.563039
HLA A*3201      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.602143       0.748881        -3.853262       40007.648731
HLA A*0250      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.564356       0.710864        -3.853492       36673.829463
HLA B*3801      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.479155       0.625647        -3.853507       30140.783469
HLA A*0201      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.388286       0.534755        -3.853531       24450.393619
HLA B*5101      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.437082       0.583145        -3.853937       27357.871736
HLA B*5801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.356298       0.502118        -3.854180       22714.208960
HLA B*1503      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.372417       0.518215        -3.854203       23573.139886
HLA A*2601      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.342610       0.488141        -3.854469       22009.466580
HLA A*0301      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.351434       0.496962        -3.854472       22461.263505
HLA B*4002      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.618909       0.764415        -3.854494       41582.342708
HLA B*1517      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.478191       0.623682        -3.854509       30074.003655
HLA A*3201      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.545114       0.690533        -3.854581       35084.393956
HLA A*0301      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.356725       0.502118        -3.854607       22736.584380
HLA B*4002      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.635870       0.780826        -3.855044       43238.426956
HLA B*3501      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.206720       0.351592        -3.855128       16096.075615
HLA A*6802      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.416393       0.561253        -3.855140       26085.114306
HLA A*2403      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.250101       0.394780        -3.855321       17786.925854
HLA B*4601      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.407166       0.551693        -3.855473       25536.790673
HLA B*1517      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.357989       0.502462        -3.855527       22802.856067
HLA B*5701      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.407300       0.551693        -3.855607       25544.666506
HLA B*2705      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.479310       0.623682        -3.855628       30151.547238
HLA B*4001      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.351037       0.495365        -3.855672       22440.737202
HLA A*0212      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.416945       0.561253        -3.855692       26118.298026
HLA B*5801      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.352740       0.496962        -3.855779       22528.926413
HLA B*4002      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.456529       0.600711        -3.855818       28610.733789
HLA A*0301      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.345044       0.489218        -3.855826       22133.168158
HLA B*3501      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -3.831352       -0.024958       -3.856310       6781.912508
HLA B*7301      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.516969       0.660357        -3.856613       32882.853540
HLA B*3501      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.359173       0.502118        -3.857055       22865.114811
HLA B*5701      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.357569       0.500136        -3.857433       22780.785150
HLA B*0803      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.503819       0.646348        -3.857471       31902.111646
HLA B*1502      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.568428       0.710864        -3.857564       37019.275813
HLA B*3501      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.232022       0.373896        -3.858126       17061.672743
HLA A*2403      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.360616       0.502462        -3.858154       22941.191502
HLA A*8001      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.386801       0.528496        -3.858305       24366.939250
HLA A*8001      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.423505       0.565014        -3.858490       26515.793934
HLA A*2601      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.358718       0.500136        -3.858582       22841.130038
HLA B*4001      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.376980       0.518215        -3.858765       23822.104929
HLA A*0201      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.394366       0.535432        -3.858935       24795.126154
HLA A*3101      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.356006       0.496962        -3.859044       22698.976782
HLA B*3901      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.475038       0.615847        -3.859192       29856.454911
HLA B*4601      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.394113       0.534755        -3.859358       24780.643386
HLA A*1101      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.461959       0.602482        -3.859477       28970.677812
HLA A*2601      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.348784       0.489218        -3.859566       22324.614267
HLA B*1502      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.394439       0.534755        -3.859685       24799.284808
HLA A*2601      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.395186       0.535432        -3.859755       24841.984846
HLA B*3801      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.550304       0.690533        -3.859771       35506.183346
HLA A*2501      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.424851       0.565014        -3.859837       26598.116884
HLA A*0201      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.388533       0.528496        -3.860036       24464.286325
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HLA A*3002      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.516676       0.656423        -3.860253       32860.624483
HLA A*2902      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.443478       0.583145        -3.860333       27763.716894
HLA A*6802      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.118370       0.257963        -3.860407       13133.182206
HLA A*2602      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.624830       0.764415        -3.860415       42153.113281
HLA B*0802      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.413515       0.553011        -3.860503       25912.816823
HLA B*4501      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.609483       0.748881        -3.860602       40689.543695
HLA A*2603      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.641457       0.780826        -3.860631       43798.270448
HLA B*3901      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.461808       0.600711        -3.861098       28960.648946
HLA A*6901      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.363304       0.502118        -3.861186       23083.612806
HLA B*5101      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.348869       0.487485        -3.861384       22328.962544
HLA B*3501      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.379621       0.518215        -3.861406       23967.401676
HLA B*1517      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.244361       0.382667        -3.861694       17553.394072
HLA A*2403      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.422960       0.561253        -3.861707       26482.534988
HLA A*0206      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.413435       0.551693        -3.861742       25908.050955
HLA B*1801      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.487559       0.625647        -3.861911       30729.722955
HLA B*1501      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.122045       0.259962        -3.862083       13244.774364
HLA A*2902      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.415328       0.553011        -3.862317       26021.266311
HLA A*6901      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.358034       0.495365        -3.862669       22805.200045
HLA A*3301      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.307948       0.445146        -3.862802       20321.116466
HLA B*0802      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.466688       0.603848        -3.862840       29287.895722
HLA A*2902      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.352214       0.489218        -3.862996       22501.642054
HLA B*5101      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.486720       0.623682        -3.863038       30670.430980
HLA B*0801      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.358508       0.495365        -3.863144       22830.135135
HLA A*2601      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.391676       0.528496        -3.863180       24642.011841
HLA A*3201      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.576113       0.712622        -3.863491       37680.190005
HLA B*5701      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.398971       0.535432        -3.863540       25059.437185
HLA A*0301      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.351777       0.488141        -3.863636       22479.011403
HLA B*4402      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.424971       0.561253        -3.863718       26605.456432
HLA B*4001      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.353048       0.489218        -3.863830       22544.898220
HLA A*2602      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.246769       0.382667        -3.864103       17651.000406
HLA B*5301      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.351601       0.487485        -3.864116       22469.892581
HLA B*1509      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.524525       0.660357        -3.864169       33459.961884
HLA A*0101      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.364516       0.500136        -3.864381       23148.140799
HLA B*5401      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -3.840553       -0.023878       -3.864431       6927.120876
HLA B*4801      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.382891       0.518215        -3.864677       24148.571066
HLA B*5101      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.465443       0.600711        -3.864732       29204.040534
HLA B*3901      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.461414       0.596633        -3.864780       28934.339689
HLA A*6801      1:7-15  9       FELLELATP       0.903395        -0.108267       -4.659997       0.795128        -3.864869       45708.476602
HLA A*6802      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.393410       0.528496        -3.864914       24740.591688
HLA B*4002      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.611781       0.746698        -3.865082       40905.397369
HLA A*3101      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.216968       0.351592        -3.865376       16480.426898
HLA B*5301      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.578164       0.712622        -3.865542       37858.568152
HLA A*3201      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.562568       0.697019        -3.865549       36523.156402
HLA A*0211      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.400421       0.534755        -3.865666       25143.222877
HLA B*3501      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.427226       0.561253        -3.865974       26743.991127
HLA B*4501      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.612878       0.746698        -3.866179       41008.872166
HLA A*8001      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.384400       0.518215        -3.866185       24232.588465
HLA A*2601      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.401257       0.534755        -3.866503       25191.693387
HLA A*0203      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.401946       0.535432        -3.866514       25231.656342
HLA B*7301      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.577596       0.710864        -3.866731       37809.036403
HLA B*0802      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.469381       0.602482        -3.866899       29470.036884
HLA B*5801      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.362449       0.495365        -3.867084       23038.201291
HLA A*0301      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.362535       0.495365        -3.867171       23042.813215
HLA B*4801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.418876       0.551693        -3.867183       26234.702869
HLA A*6802      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.199413       0.332159        -3.867254       15827.528537
HLA B*5801      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.354798       0.487485        -3.867311       22635.823340
HLA A*2501      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.471359       0.603848        -3.867511       29604.582839
HLA A*2301      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.514580       0.646348        -3.868232       32702.433551
HLA B*4001      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.403760       0.535432        -3.868328       25337.255059
HLA B*1509      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.492154       0.623682        -3.868472       31056.623529
HLA A*0206      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.494187       0.625647        -3.868539       31202.295253
HLA B*5801      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.357822       0.489218        -3.868604       22794.099124
HLA A*2603      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.632804       0.764021        -3.868783       42934.242774
HLA B*4402      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.387661       0.518215        -3.869446       24415.234060
HLA B*4402      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.421197       0.551693        -3.869504       26375.301996
HLA A*2402      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.297015       0.427495        -3.869520       19815.973427
HLA A*0211      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.452704       0.583145        -3.869559       28359.856883
HLA B*0801      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.357261       0.487485        -3.869776       22764.646230
HLA A*3301      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.566882       0.697019        -3.869863       36887.732303
HLA B*4002      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.576409       0.706535        -3.869874       37705.883313
HLA B*1509      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.528451       0.658536        -3.869915       33763.808729
HLA A*2602      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.516361       0.646348        -3.870013       32836.811622
HLA A*0202      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.181552       0.311316        -3.870237       15189.809254
HLA B*5701      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.423328       0.553011        -3.870317       26505.037553
HLA B*4801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.431648       0.561253        -3.870395       27017.673575
HLA A*2601      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.372568       0.502118        -3.870450       23581.303096
HLA A*3301      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.619687       0.748881        -3.870806       41656.869806
HLA A*8001      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.373439       0.502462        -3.870977       23628.679924
HLA A*0301      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.287815       0.416603        -3.871212       19400.585098
HLA B*1501      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.368315       0.496962        -3.871353       23351.524172
HLA A*3301      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.635456       0.763535        -3.871921       43197.277492
HLA B*0801      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.400548       0.528496        -3.872052       25150.569141
HLA B*1503      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.468923       0.596633        -3.872289       29438.964499
HLA B*4001      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.374910       0.502462        -3.872448       23708.836241
HLA B*0803      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.488357       0.615847        -3.872511       30786.298064
HLA A*6801      1:82-90 9       VRRQSRWRT       1.037980        -0.242033       -4.668716       0.795947        -3.872769       46635.397834
HLA A*2402      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.569990       0.697019        -3.872971       37152.695331
HLA B*1502      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.498721       0.625647        -3.873074       31529.787816
HLA A*1101      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.375577       0.502462        -3.873116       23745.290696
HLA A*1101      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.489076       0.615847        -3.873230       30837.304712
HLA A*0203      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.424931       0.551693        -3.873238       26603.009691
HLA B*3901      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.497372       0.623682        -3.873691       31432.030971
HLA A*0201      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.361953       0.488141        -3.873812       23011.918496
HLA A*3002      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.363128       0.489218        -3.873910       23074.248722
HLA B*3901      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.392198       0.518215        -3.873983       24671.624563
HLA A*0219      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.435292       0.561253        -3.874039       27245.325545
HLA B*4403      1:72-80 9       TAILDATKP       0.635852        0.144974        -4.655244       0.780826        -3.874418       45210.961053
HLA A*6801      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.530930       0.656423        -3.874507       33957.064378
HLA A*2402      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.581186       0.706535        -3.874651       38122.872990
HLA A*0216      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.403210       0.528496        -3.874713       25305.200565
HLA A*1101      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.475663       0.600711        -3.874953       29899.450189
HLA A*2403      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.403722       0.528496        -3.875226       25335.062006
HLA B*5101      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.479150       0.603848        -3.875301       30140.457354
HLA B*1502      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.565855       0.690533        -3.875322       36800.628223
HLA B*1502      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.525226       0.649819        -3.875407       33513.947765
HLA A*0219      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.681479       -0.194071       -3.875550       4802.623421
HLA A*2603      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.476448       0.600711        -3.875737       29953.524433
HLA A*3002      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.681666       -0.194071       -3.875738       4804.702403
HLA B*4002      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.536151       0.660357        -3.875794       34367.717805
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HLA B*4403      1:90-98 9       TAAFASAAA       0.917226        -0.153205       -4.640021       0.764021        -3.876000       43653.736799
HLA A*6801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.208351       0.332159        -3.876192       16156.621324
HLA A*3201      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.476967       0.600711        -3.876257       29989.357850
HLA B*4002      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.639801       0.763535        -3.876266       43631.543226
HLA A*2402      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.526088       0.649819        -3.876269       33580.553437
HLA B*1801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.411713       0.535432        -3.876281       25805.517337
HLA B*0801      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.394507       0.518215        -3.876292       24803.175793
HLA B*4001      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.376529       0.500136        -3.876393       23797.373785
HLA A*2402      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.522907       0.646348        -3.876559       33335.474917
HLA B*1502      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.514531       0.637921        -3.876609       32698.718515
HLA B*1801      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.473610       0.596633        -3.876977       29758.412014
HLA B*3801      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.537354       0.660357        -3.876997       34463.043642
HLA A*3301      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.588112       0.710864        -3.877248       38735.744186
HLA A*6901      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.209460       0.332159        -3.877301       16197.929451
HLA A*0202      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.473979       0.596633        -3.877346       29783.698135
HLA A*2902      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.322597       0.445146        -3.877451       21018.252443
HLA B*7301      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.574635       0.697019        -3.877616       37552.188996
HLA A*3001      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.085176       0.207531        -3.877646       12166.802139
HLA B*0702      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.406283       0.528496        -3.877787       25484.898614
HLA B*1509      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.478762       0.600711        -3.878052       30113.565030
HLA A*2603      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.642545       0.764415        -3.878130       43908.112930
HLA B*3501      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.430013       0.551693        -3.878320       26916.135672
HLA B*2705      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.380916       0.502462        -3.878454       24038.951465
HLA B*0801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.378987       0.500136        -3.878851       23932.418765
HLA B*1801      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.381714       0.502462        -3.879252       24083.208497
HLA B*3901      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.482113       0.602482        -3.879630       30346.774576
HLA B*4601      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.408172       0.528496        -3.879676       25595.987896
HLA B*3801      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.526299       0.646348        -3.879951       33596.907455
HLA A*3301      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.644777       0.764415        -3.880362       44134.354928
HLA A*3201      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.547830       0.667402        -3.880428       35304.493371
HLA A*0301      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.368125       0.487485        -3.880640       23341.293752
HLA B*1501      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.128581       0.247860        -3.880721       13445.619948
HLA A*0203      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.284575       0.403811        -3.880764       19256.390664
HLA A*0212      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.416374       0.535432        -3.880942       26083.985390
HLA B*4002      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.629888       0.748881        -3.881007       42646.961767
HLA A*6901      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.068462       0.187363        -3.881099       11707.447236
HLA B*0702      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.432802       0.551693        -3.881108       27089.534820
HLA B*3801      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.537645       0.656423        -3.881222       34486.170113
HLA B*4801      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.434806       0.553011        -3.881794       27214.832025
HLA A*0203      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.247986       0.366173        -3.881813       17700.533575
HLA A*2402      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.572518       0.690533        -3.881985       37369.593357
HLA A*2602      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.594662       0.712622        -3.882041       39324.414775
HLA B*4402      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.435250       0.553011        -3.882238       27242.672579
HLA A*3101      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.411017       0.528496        -3.882521       25764.227329
HLA B*5101      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.508192       0.625647        -3.882544       32224.918092
HLA A*8001      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.417333       0.534755        -3.882578       26141.622455
HLA A*0202      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.140638       0.257963        -3.882675       13824.148438
HLA B*4001      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.411222       0.528496        -3.882725       25776.356384
HLA A*1101      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.382887       0.500136        -3.882751       24148.309785
HLA A*0206      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.265499       0.382667        -3.882833       18428.900251
HLA B*0801      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.265631       0.382667        -3.882964       18434.484202
HLA B*5101      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.499036       0.615847        -3.883189       31552.652839
HLA A*8001      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.444448       0.561253        -3.883195       27825.818279
HLA A*0212      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.434982       0.551693        -3.883289       27225.876457
HLA B*4601      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.383425       0.500136        -3.883289       24178.244811
HLA B*0802      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.480299       0.596633        -3.883666       30220.297558
HLA B*0803      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.487580       0.603848        -3.883731       30731.219191
HLA B*1501      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.412410       0.528496        -3.883914       25847.013346
HLA A*8001      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.435764       0.551693        -3.884071       27274.967891
HLA B*5301      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.581094       0.697019        -3.884075       38114.830459
HLA A*6802      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -3.473751       -0.410374       -3.884125       2976.810353
HLA A*0206      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.480957       0.596633        -3.884324       30266.109015
HLA B*5701      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.386832       0.502462        -3.884370       24368.653002
HLA B*7301      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.541103       0.656423        -3.884680       34761.892170
HLA B*7301      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.591601       0.706535        -3.885066       39048.188326
HLA B*0803      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.510800       0.625647        -3.885152       32419.010159
HLA A*0101      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.382187       0.496962        -3.885225       24109.410525
HLA A*2501      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.481948       0.596633        -3.885315       30335.284664
HLA A*0202      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.246217       0.360868        -3.885349       17628.574525
HLA A*3101      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.381261       0.495365        -3.885896       24058.076134
HLA A*6801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.386047       0.500136        -3.885911       24324.660967
HLA A*1101      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.509620       0.623682        -3.885938       32331.087210
HLA B*1517      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.302591       0.416603        -3.885988       20072.004196
HLA B*3901      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.489838       0.603848        -3.885989       30891.403864
HLA A*2301      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.546383       0.660357        -3.886026       35187.037259
HLA A*0203      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.375368       0.489218        -3.886150       23733.860562
HLA A*2501      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.420913       0.534755        -3.886159       26358.042463
HLA B*5301      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.544809       0.658536        -3.886273       35059.728281
HLA A*6802      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.134191       0.247860        -3.886332       13620.448284
HLA A*2301      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.536167       0.649819        -3.886349       34369.019309
HLA A*1101      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.469623       0.583145        -3.886478       29486.462713
HLA B*5801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.303143       0.416603        -3.886540       20097.538444
HLA A*2301      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.524678       0.637921        -3.886757       33471.729907
HLA B*3501      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.422208       0.535432        -3.886776       26436.729023
HLA B*0702      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.376123       0.489218        -3.886905       23775.111985
HLA A*3201      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.597865       0.710864        -3.887000       39615.452071
HLA B*7301      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.510835       0.623682        -3.887153       32421.641014
HLA A*2603      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -3.698207       -0.189096       -3.887302       4991.221779
HLA A*0201      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.389832       0.502118        -3.887714       24537.584953
HLA A*0219      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.439429       0.551693        -3.887736       27506.127047
HLA A*2602      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.440924       0.553011        -3.887913       27600.930090
HLA B*3901      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.441140       0.553011        -3.888129       27614.670762
HLA A*0250      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.239798       0.351592        -3.888206       17369.943386
HLA A*0203      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -3.699151       -0.189096       -3.888247       5002.088378
HLA B*5701      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.416851       0.528496        -3.888355       26112.646753
HLA A*2902      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.449645       0.561253        -3.888392       28160.801114
HLA B*4402      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.417105       0.528496        -3.888608       26127.907996
HLA A*6801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.526856       0.637921        -3.888935       33640.011146
HLA A*0101      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.391077       0.502118        -3.888959       24608.041088
HLA A*1101      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.440952       0.551693        -3.889259       27602.721963
HLA A*6802      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.255474       0.366173        -3.889301       18008.360122
HLA A*6802      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.425011       0.535432        -3.889579       26607.903398
HLA A*3101      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.377819       0.488141        -3.889678       23868.157742
HLA B*0803      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.492345       0.602482        -3.889863       31070.235555
HLA B*4601      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.392303       0.502118        -3.890185       24677.631478
HLA A*0211      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.486950       0.596633        -3.890317       30686.695808
HLA A*2602      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.378627       0.488141        -3.890486       23912.617786
HLA A*3201      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.494410       0.603848        -3.890561       31218.335465
HLA B*4403      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.654541       0.763535        -3.891006       45137.888868
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HLA A*3002      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.294819       0.403811        -3.891007       19715.992429
HLA A*6801      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.639909       0.748881        -3.891028       43642.402501
HLA A*2902      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.419757       0.528496        -3.891261       26287.979455
HLA B*4501      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.604107       0.712622        -3.891485       40188.999802
HLA B*1517      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.379940       0.488141        -3.891800       23985.042058
HLA B*4002      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.582407       0.690533        -3.891874       38230.269048
HLA A*0101      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.379546       0.487485        -3.892061       23963.252883
HLA B*5301      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.559545       0.667402        -3.892143       36269.746139
HLA A*6802      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.426925       0.534755        -3.892171       26725.478238
HLA A*3001      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.218467       0.326268        -3.892199       16537.407522
HLA A*2403      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.445540       0.553011        -3.892529       27895.904982
HLA A*0202      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.542365       0.649819        -3.892547       34863.026138
HLA A*3001      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.140714       0.247860        -3.892854       13826.541832
HLA B*0802      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.457927       0.565014        -3.892913       28702.976804
HLA B*5101      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.495436       0.602482        -3.892954       31292.226715
HLA B*0803      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.489720       0.596633        -3.893087       30883.049041
HLA B*1501      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.381338       0.488141        -3.893197       24062.371518
HLA B*1517      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.454565       0.561253        -3.893312       28481.629127
HLA B*1801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.445162       0.551693        -3.893469       27871.618446
HLA B*0802      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.476720       0.583145        -3.893575       29972.327581
HLA A*0212      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.422579       0.528496        -3.894083       26459.335808
HLA B*4801      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.422797       0.528496        -3.894301       26472.651370
HLA A*2402      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.561800       0.667402        -3.894398       36458.602821
HLA B*4601      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.383634       0.489218        -3.894416       24189.888958
HLA B*4402      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.429214       0.534755        -3.894459       26866.672650
HLA A*2601      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.382210       0.487485        -3.894725       24110.714853
HLA A*2902      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.395238       0.500136        -3.895102       24844.941655
HLA A*2403      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.430642       0.535432        -3.895211       26955.188342
HLA A*2501      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.478515       0.583145        -3.895370       30096.464227
HLA B*4001      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.382950       0.487485        -3.895465       24151.837314
HLA B*2705      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.448785       0.553011        -3.895774       28105.097347
HLA A*0203      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.398081       0.502118        -3.895963       25008.109257
HLA B*1509      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.449022       0.553011        -3.896011       28120.458134
HLA B*0702      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.431516       0.535432        -3.896085       27009.489708
HLA A*2603      1:59-67 9       SAATTAEPP       0.646418        0.117117        -4.659741       0.763535        -3.896206       45681.531268
HLA A*8001      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.449452       0.553011        -3.896441       28148.311446
HLA B*3801      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.563929       0.667402        -3.896527       36637.738187
HLA A*0211      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.520320       0.623682        -3.896638       33137.509385
HLA A*2601      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.392047       0.495365        -3.896682       24663.083913
HLA B*4403      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.661176       0.764415        -3.896761       45832.778765
HLA A*2603      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.564168       0.667402        -3.896766       36657.960789
HLA B*4801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.432273       0.535432        -3.896841       27056.580819
HLA B*1517      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.480123       0.583145        -3.896977       30208.038411
HLA A*2402      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.555783       0.658536        -3.897247       35956.961938
HLA B*0802      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.432153       0.534755        -3.897399       27049.116821
HLA A*1101      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.458756       0.561253        -3.897504       28757.842988
HLA A*0101      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.386822       0.489218        -3.897604       24368.125681
HLA B*0802      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.400289       0.502462        -3.897827       25135.606796
HLA B*0801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.202942       0.305034        -3.897908       15956.661484
HLA B*4001      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.400104       0.502118        -3.897986       25124.866605
HLA A*6802      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.393387       0.495365        -3.898022       24739.253286
HLA B*1509      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.535958       0.637921        -3.898037       34352.475292
HLA B*5701      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.395438       0.496962        -3.898476       24856.368994
HLA A*0201      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.393873       0.495365        -3.898508       24766.972984
HLA A*2403      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.399498       0.500136        -3.899362       25089.822999
HLA B*0702      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.401694       0.502118        -3.899576       25217.055018
HLA B*3901      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.387121       0.487485        -3.899636       24384.873699
HLA B*5701      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.387830       0.488141        -3.899689       24424.745939
HLA A*2902      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.451666       0.551693        -3.899973       28292.124628
HLA A*0216      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.461395       0.561253        -3.900142       28933.087463
HLA B*0801      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.397327       0.496962        -3.900365       24964.718501
HLA B*1509      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.502950       0.602482        -3.900468       31838.318365
HLA B*5101      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.452222       0.551693        -3.900529       28328.422462
HLA B*7301      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.516551       0.615847        -3.900705       32851.203900
HLA A*3201      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.801814       -0.098967       -3.900781       6335.989623
HLA A*0202      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.526755       0.625647        -3.901108       33632.186540
HLA A*2402      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.557843       0.656423        -3.901420       36127.964102
HLA B*1502      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.560106       0.658536        -3.901570       36316.671927
HLA A*2902      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.399547       0.496962        -3.902585       25092.673557
HLA B*5801      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.353760       0.451113        -3.902647       22581.884042
HLA B*0801      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.353887       0.451113        -3.902774       22588.481942
HLA B*0803      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.526588       0.623682        -3.902906       33619.270827
HLA B*4402      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.405026       0.502118        -3.902908       25411.244549
HLA A*6901      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.285667       0.382667        -3.903001       19304.892991
HLA A*2603      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.615857       0.712665        -3.903192       41291.149411
HLA B*3501      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.392508       0.489218        -3.903290       24689.248994
HLA A*6801      1:175-183       9       GGAKGPRSA       1.161451        -0.397036       -4.668119       0.764415        -3.903704       46571.359589
HLA A*0201      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.401271       0.496962        -3.904310       25192.511105
HLA B*2705      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.422525       0.518215        -3.904310       26456.043745
HLA B*3801      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.542306       0.637921        -3.904385       34858.311330
HLA A*8001      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.439817       0.535432        -3.904386       27530.690850
HLA A*2602      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.595146       0.690533        -3.904613       39368.263793
HLA B*5101      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.501371       0.596633        -3.904738       31722.782034
HLA B*1517      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.457835       0.553011        -3.904824       28696.921526
HLA B*5401      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.440318       0.535432        -3.904886       27562.432925
HLA B*5801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.353800       0.448362        -3.905438       22583.960951
HLA B*4403      1:199-207       9       LTDLGASTA       1.057727        -0.311029       -4.652147       0.746698        -3.905449       44889.742867
HLA B*4403      1:65-73 9       EPPAHLRTA       1.140501        -0.391620       -4.654461       0.748881        -3.905580       45129.587138
HLA B*2705      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.457936       0.551693        -3.906243       28703.597930
HLA B*0802      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.434763       0.528496        -3.906267       27212.182028
HLA A*3002      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.289532       0.382667        -3.906866       19477.459118
HLA A*0201      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.396100       0.489218        -3.906882       24894.318531
HLA B*1502      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.471951       0.565014        -3.906937       29644.970056
HLA B*4601      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.404143       0.496962        -3.907181       25359.607607
HLA B*0801      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.396699       0.489218        -3.907481       24928.684483
HLA A*0203      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.358685       0.451113        -3.907572       22839.400152
HLA A*0201      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.395071       0.487485        -3.907586       24835.400492
HLA B*1801      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.490735       0.583145        -3.907590       30955.309359
HLA A*0219      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.395149       0.487485        -3.907664       24839.834661
HLA A*2902      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.442439       0.534755        -3.907685       27697.408408
HLA A*0301      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.290369       0.382667        -3.907702       19515.007302
HLA A*0202      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -3.931078       0.023284        -3.907795       8532.541773
HLA A*0301      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.268761       0.360868        -3.907893       18567.802352
HLA B*1502      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.554296       0.646348        -3.907948       35834.039358
HLA A*0216      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.259565       0.351592        -3.907973       18178.775246
HLA B*4001      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.405202       0.496962        -3.908240       25421.557042
HLA A*0301      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.359613       0.451113        -3.908500       22888.257992
HLA B*0803      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.491804       0.583145        -3.908659       31031.599695
HLA A*2403      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.398088       0.489218        -3.908870       25008.515133
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HLA A*2403      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.396486       0.487485        -3.909001       24916.415115
HLA A*2602      1:104-112       9       GAFGLGVLT       1.005157        -0.292492       -4.621853       0.712665        -3.909187       41865.169908
HLA A*0250      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.326081       0.416603        -3.909478       21187.557305
HLA B*5801      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.354824       0.445146        -3.909679       22637.292875
HLA A*3001      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.283710       0.373896        -3.909815       19218.092422
HLA B*1801      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.475210       0.565014        -3.910195       29868.248208
HLA B*4002      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.622952       0.712622        -3.910331       41971.299616
HLA B*3801      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.568926       0.658536        -3.910390       37061.757447
HLA A*3101      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.170641       0.259962        -3.910680       14812.941643
HLA B*5101      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.475752       0.565014        -3.910738       29905.597424
HLA B*0801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.412958       0.502118        -3.910840       25879.614157
HLA B*4402      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.413538       0.502462        -3.911076       25914.218715
HLA A*3002      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.578707       0.667402        -3.911305       37905.908988
HLA B*1517      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.446889       0.535432        -3.911458       27982.664112
HLA B*3801      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.527483       0.615847        -3.911637       33688.637247
HLA B*0802      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.473093       0.561253        -3.911840       29723.015346
HLA A*2301      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.535629       0.623682        -3.911947       34326.467110
HLA B*4001      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.357132       0.445146        -3.911986       22757.873756
HLA B*1801      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.516025       0.603848        -3.912177       32811.418424
HLA A*2602      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.132067       0.219167        -3.912900       13553.999558
HLA B*4601      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.361354       0.448362        -3.912991       22980.194941
HLA B*4801      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.401142       0.488141        -3.913001       25185.016342
HLA B*7301      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.448435       0.535432        -3.913003       28082.451701
HLA A*2603      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.624209       0.710864        -3.913345       42092.952723
HLA B*3501      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.442254       0.528496        -3.913757       27685.573585
HLA A*0250      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.414271       0.500136        -3.914136       25957.995882
HLA A*0216      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.402406       0.488141        -3.914265       25258.424622
HLA A*3301      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.581721       0.667402        -3.914319       38169.924840
HLA B*0702      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.342302       0.427495        -3.914806       21993.874096
HLA A*2403      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.411959       0.496962        -3.914997       25820.180025
HLA A*2301      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.540756       0.625647        -3.915108       34734.070728
HLA A*1101      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.468168       0.553011        -3.915157       29387.885910
HLA B*1517      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.466989       0.551693        -3.915296       29308.183612
HLA A*8001      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.412312       0.496962        -3.915350       25841.141175
HLA B*4403      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.628006       0.712622        -3.915384       42462.558611
HLA A*0203      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.410836       0.495365        -3.915471       25753.497180
HLA B*5401      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.516276       0.600711        -3.915566       32830.417078
HLA A*3002      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.512212       0.596633        -3.915579       32524.587033
HLA B*1503      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.330780       0.414917        -3.915862       21418.046650
HLA A*2602      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.434148       0.518215        -3.915933       27173.639049
HLA A*0212      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.319848       0.403811        -3.916036       20885.636082
HLA B*5301      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.572617       0.656423        -3.916194       37378.085267
HLA A*3001      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.248771       0.332159        -3.916612       17732.545634
HLA A*3002      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.499797       0.583145        -3.916652       31608.006956
HLA B*1801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.477919       0.561253        -3.916666       30055.136720
HLA A*0212      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.418940       0.502118        -3.916822       26238.535174
HLA A*0219      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.452366       0.535432        -3.916934       28337.772476
HLA B*1509      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.513664       0.596633        -3.917031       32633.508837
HLA B*0801      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.309853       0.392663        -3.917190       20410.469612
HLA B*4402      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.332175       0.414917        -3.917258       21486.983694
HLA A*2301      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.519777       0.602482        -3.917295       33096.123822
HLA A*0212      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.278212       0.360868        -3.917345       18976.341297
HLA A*2601      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.368534       0.451113        -3.917421       23363.275739
HLA A*6901      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.129953       0.212403        -3.917550       13488.166883
HLA A*3301      1:219-227       9       PQPTGTILA       1.103044        -0.390422       -4.630262       0.712622        -3.917640       42683.661287
HLA B*1501      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.228439       0.310721        -3.917717       16921.491610
HLA A*3301      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.574224       0.656423        -3.917801       37516.654014
HLA A*0216      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.334443       0.416603        -3.917839       21599.450731
HLA A*0203      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.291849       0.373896        -3.917953       19581.632411
HLA A*0301      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.366323       0.448362        -3.917960       23244.642399
HLA A*3002      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.534163       0.615847        -3.918316       34210.784194
HLA B*4402      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.418479       0.500136        -3.918343       26210.728196
HLA A*2601      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.301066       0.382667        -3.918399       20001.654599
HLA A*0301      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.363560       0.445146        -3.918414       23097.228717
HLA A*3201      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.578883       0.660357        -3.918526       37921.292116
HLA A*6801      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.579057       0.660357        -3.918700       37936.476254
HLA A*6802      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.420822       0.502118        -3.918704       26352.481880
HLA B*5701      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.421002       0.502118        -3.918884       26363.461595
HLA A*0101      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.370063       0.451113        -3.918950       23445.702469
HLA B*1801      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.535056       0.615847        -3.919209       34281.185622
HLA A*2402      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.579757       0.660357        -3.919400       37997.684754
HLA A*3101      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.421665       0.502118        -3.919547       26403.712090
HLA A*8001      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.408120       0.488141        -3.919979       25592.941706
HLA B*7301      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.485228       0.565014        -3.920214       30565.250240
HLA B*1501      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.408022       0.487485        -3.920537       25587.127257
HLA A*0212      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.416341       0.495365        -3.920976       26082.009904
HLA A*3101      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.408543       0.487485        -3.921058       25617.875740
HLA A*2402      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.559129       0.637921        -3.921207       36235.032652
HLA B*1502      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.588723       0.667402        -3.921321       38790.267104
HLA B*0802      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.456912       0.535432        -3.921480       28635.974203
HLA A*0219      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.409650       0.488141        -3.921509       25683.234801
HLA A*0216      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.822697       -0.098967       -3.921664       6648.086783
HLA A*0250      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.547553       0.625647        -3.921905       35281.963342
HLA A*3002      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.580448       0.658536        -3.921912       38058.168441
HLA B*4501      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.612467       0.690533        -3.921934       40970.066184
HLA A*3201      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.456769       0.534755        -3.922014       28626.525798
HLA B*3801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.483463       0.561253        -3.922211       30441.320847
HLA A*2501      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.474204       0.551693        -3.922511       29799.170297
HLA B*5101      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.483898       0.561253        -3.922645       30471.802669
HLA A*3001      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.157343       0.234317        -3.923026       14366.243618
HLA B*4801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.351028       0.427495        -3.923532       22440.251600
HLA A*0250      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.570138       0.646348        -3.923790       37165.359983
HLA A*2902      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.459332       0.535432        -3.923900       28795.984562
HLA B*5301      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.570277       0.646348        -3.923929       37177.224444
HLA A*3101      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.327749       0.403811        -3.923938       21269.095658
HLA A*2602      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.580485       0.656423        -3.924062       38061.462831
HLA A*2301      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.524892       0.600711        -3.924181       33488.212094
HLA B*5701      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.419776       0.495365        -3.924411       26289.117200
HLA A*0203      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.421454       0.496962        -3.924492       26390.859516
HLA B*3801      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.521192       0.596633        -3.924558       33204.085438
HLA B*1502      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.584931       0.660357        -3.924574       38453.041911
HLA B*0803      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.485874       0.561253        -3.924621       30610.756602
HLA B*7301      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.571015       0.646348        -3.924667       37240.431258
HLA A*2602      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.525399       0.600711        -3.924689       33527.367149
HLA B*1501      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.328656       0.403811        -3.924845       21313.556556
HLA B*4801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.424982       0.500136        -3.924847       26606.176105
HLA B*5401      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.550572       0.625647        -3.924924       35528.087734
HLA B*0801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.352449       0.427495        -3.924954       22513.818486
HLA B*4501      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.550769       0.625647        -3.925122       35544.236457
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HLA A*2403      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.427459       0.502118        -3.925341       26758.318484
HLA B*4601      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.413017       0.487485        -3.925532       25883.114540
HLA A*2501      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.427858       0.502118        -3.925740       26782.938925
HLA A*8001      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.415039       0.489218        -3.925821       26003.957094
HLA A*6901      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.371184       0.445146        -3.926038       23506.282636
HLA B*0803      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.491456       0.565014        -3.926442       31006.763767
HLA A*0301      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.353953       0.427495        -3.926457       22591.903834
HLA A*2403      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.422607       0.495365        -3.927242       26461.053569
HLA A*2403      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.375726       0.448362        -3.927363       23753.385017
HLA B*0803      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.480524       0.553011        -3.927513       30235.996526
HLA B*3801      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.528348       0.600711        -3.927638       33755.772713
HLA A*2301      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.531745       0.603848        -3.927897       34020.869520
HLA B*4601      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.279528       0.351592        -3.927936       19033.918014
HLA B*2705      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.428429       0.500136        -3.928294       26818.171012
HLA A*0216      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.480193       0.551693        -3.928500       30212.941473
HLA B*5801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.356119       0.427495        -3.928624       22704.871897
HLA B*4501      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.625774       0.697019        -3.928755       42244.886593
HLA A*3301      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.529645       0.600711        -3.928934       33856.726849
HLA A*2603      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.619595       0.690533        -3.929062       41648.081730
HLA A*2301      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.544989       0.615847        -3.929143       35074.335855
HLA B*4601      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.417502       0.488141        -3.929361       26151.806914
HLA B*5101      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.464825       0.535432        -3.929393       29162.518546
HLA A*2403      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.417821       0.488141        -3.929680       26171.055054
HLA A*0219      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.431986       0.502118        -3.929868       27038.729193
HLA A*0203      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.290890       0.360868        -3.930022       19538.458816
HLA B*1501      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.357799       0.427495        -3.930304       22792.866021
HLA A*2603      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.483402       0.553011        -3.930391       30437.039359
HLA B*5401      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.527068       0.596633        -3.930434       33656.394119
HLA B*0702      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.347052       0.416603        -3.930449       22235.781269
HLA A*2902      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.433276       0.502118        -3.931158       27119.154380
HLA A*3001      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.293327       0.362044        -3.931283       19648.378685
HLA B*5401      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.554965       0.623682        -3.931283       35889.331554
HLA A*2301      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.527998       0.596633        -3.931365       33728.574043
HLA B*4403      1:208-216       9       LAFTVEPGT       0.857007        -0.166474       -4.621912       0.690533        -3.931378       41870.832439
HLA A*3101      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.382840       0.451113        -3.931727       24145.697133
HLA B*5101      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.431878       0.500136        -3.931743       27032.001309
HLA B*5401      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.535620       0.603848        -3.931771       34325.724309
HLA B*4801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.434192       0.502118        -3.932074       27176.432314
HLA A*3201      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.590873       0.658536        -3.932337       38982.756833
HLA A*2902      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.359841       0.427495        -3.932345       22900.271969
HLA B*7301      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.529095       0.596633        -3.932462       33813.894259
HLA B*5701      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.421912       0.489218        -3.932694       26418.714672
HLA A*8001      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.435029       0.502118        -3.932911       27228.822396
HLA B*4403      1:190-198       9       AVTPSTTAT       0.839277        -0.132742       -4.639535       0.706535        -3.933000       43604.878653
HLA A*0101      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.349623       0.416603        -3.933020       22367.772137
HLA A*3301      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.571062       0.637921        -3.933140       37244.460808
HLA A*6901      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.141019       0.207531        -3.933488       13836.269260
HLA B*3901      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.485352       0.551693        -3.933659       30574.015292
HLA A*3001      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.153208       0.219167        -3.934041       14230.105935
HLA A*2602      1:5-13  9       TDFELLELA       1.003059        -0.335657       -4.601737       0.667402        -3.934335       39970.222656
HLA B*1501      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.064919       0.130576        -3.934343       11612.325097
HLA B*1503      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.434606       0.500136        -3.934470       27202.320418
HLA B*4801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.382847       0.448362        -3.934484       24146.089013
HLA A*1101      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.469282       0.534755        -3.934527       29463.341601
HLA B*1503      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.429909       0.495365        -3.934544       26909.729449
HLA A*6802      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.286208       0.351592        -3.934616       19328.928528
HLA B*4402      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.422974       0.488141        -3.934833       26483.394608
HLA B*4501      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.535606       0.600711        -3.934895       34324.610137
HLA B*3801      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.558605       0.623682        -3.934923       36191.344875
HLA B*3501      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.432038       0.496962        -3.935076       27041.947468
HLA B*5801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.350276       0.414917        -3.935358       22401.437439
HLA A*0212      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.424950       0.489218        -3.935732       26604.161070
HLA A*0101      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.380930       0.445146        -3.935784       24039.731766
HLA A*0101      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.384311       0.448362        -3.935948       24227.607344
HLA B*5401      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.538505       0.602482        -3.936023       34554.521045
HLA B*4001      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.424231       0.488141        -3.936090       26560.156282
HLA A*0203      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.384496       0.448362        -3.936134       24237.963982
HLA A*3101      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.425598       0.489218        -3.936380       26643.914196
HLA A*8001      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.436565       0.500136        -3.936430       27325.330433
HLA A*0212      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.423965       0.487485        -3.936480       26543.924556
HLA B*0802      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.454718       0.518215        -3.936503       28491.646248
HLA B*1509      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.471300       0.534755        -3.936546       29600.579172
HLA A*1101      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.472068       0.535432        -3.936637       29652.989940
HLA A*6901      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.196852       0.259962        -3.936891       15734.471734
HLA B*0803      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.439364       0.502462        -3.936902       27501.960820
HLA B*4402      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.432484       0.495365        -3.937119       27069.757606
HLA A*1101      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.465786       0.528496        -3.937290       29227.116276
HLA B*4801      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.432698       0.495365        -3.937333       27083.087326
HLA A*2603      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.385882       0.448362        -3.937520       24315.451151
HLA A*2601      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.382859       0.445146        -3.937713       24146.742160
HLA A*2603      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.561932       0.623682        -3.938250       36469.649766
HLA B*4002      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.649300       0.710864        -3.938435       44596.373278
HLA A*2602      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.541106       0.602482        -3.938624       34762.080228
HLA A*0201      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.390769       0.451113        -3.939656       24590.607658
HLA A*3201      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.577741       0.637921        -3.939820       37821.720177
HLA A*0206      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.367697       0.427495        -3.940202       23318.323228
HLA A*2403      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.356836       0.416603        -3.940232       22742.366228
HLA B*3901      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.429611       0.489218        -3.940393       26891.247309
HLA B*2705      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.475964       0.535432        -3.940532       29920.161706
HLA B*7301      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.578495       0.637921        -3.940574       37887.457471
HLA B*4801      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.437930       0.496962        -3.940969       27411.353045
HLA A*1101      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.443198       0.502118        -3.941080       27745.849009
HLA B*4501      1:162-170       9       PPSRGTVYQ       1.033521        -0.322657       -4.651971       0.710864        -3.941107       44871.532922
HLA A*3201      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.591157       0.649819        -3.941338       39008.283167
HLA B*0702      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.428876       0.487485        -3.941391       26845.751017
HLA B*4001      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.368952       0.427495        -3.941457       23385.784481
HLA A*3001      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.279011       0.337522        -3.941489       19011.277785
HLA B*5101      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.436859       0.495365        -3.941494       27343.815058
HLA A*2501      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.438725       0.496962        -3.941763       27461.521724
HLA A*0203      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.369558       0.427495        -3.942063       23418.448012
HLA A*6802      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.429616       0.487485        -3.942131       26891.538268
HLA A*3001      1:73-81 9       AILDATKPE       0.570602        -0.547669       -3.965249       0.022933        -3.942316       9231.012371
HLA B*1801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.369941       0.427495        -3.942446       23439.107787
HLA B*5701      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.430071       0.487485        -3.942587       26919.776251
HLA B*1502      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.303479       0.360868        -3.942611       20113.092199
HLA B*4001      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.394120       0.451113        -3.943007       24781.045571
HLA A*0206      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.431157       0.488141        -3.943016       26987.142851
HLA A*0216      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.478504       0.535432        -3.943072       30095.650146
HLA B*0802      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.443315       0.500136        -3.943180       27753.355122
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HLA B*4801	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.432416	0.489218	-3.943198	27065.511052
HLA B*3901	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.478736	0.535432	-3.943305	30111.773062
HLA A*2601	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.391768	0.448362	-3.943405	24647.211501
HLA B*4402	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.430999	0.487485	-3.943515	26977.362794
HLA B*5301	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.581639	0.637921	-3.943718	38162.698197
HLA B*1503	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.201730	0.257963	-3.943767	15912.180532
HLA B*4002	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.540634	0.596633	-3.944000	34724.300913
HLA A*2501	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.431538	0.487485	-3.944053	27010.804805
HLA A*2402	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.546566	0.602482	-3.944084	35201.888314
HLA A*0202	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.232900	0.288570	-3.944331	17096.228547
HLA B*0802	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.496040	0.551693	-3.944347	31335.763855
HLA B*3501	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.372319	0.427495	-3.944823	23567.784316
HLA A*6901	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.393307	0.448362	-3.944944	24734.703259
HLA B*0702	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.393678	0.448362	-3.945316	24755.854594
HLA B*0801	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.390494	0.445146	-3.945349	24575.047785
HLA B*1503	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.498479	0.553011	-3.945468	31512.223726
HLA B*7301	1:69-77	9	HLRTAILDA	0.775000	-0.174289	-4.546221	0.600711	-3.945510	35173.905010
HLA A*6901	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.319429	0.373896	-3.945534	20865.533725
HLA B*1509	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.506982	0.561253	-3.945729	32135.261431
HLA B*3501	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.434136	0.488141	-3.945995	27172.904027
HLA B*5301	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.571903	0.625647	-3.946255	37316.663553
HLA B*5801	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.297896	0.351592	-3.946304	19856.215065
HLA B*1502	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.562218	0.615847	-3.946372	36493.727916
HLA B*3501	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.284370	0.337522	-3.946848	19247.329577
HLA B*5101	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.500114	0.553011	-3.947103	31631.099822
HLA A*2402	1:61-69	9	ATTAEPPAH	0.752441	-0.126794	-4.573223	0.625647	-3.947576	37430.292207
HLA B*5801	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.351469	0.403811	-3.947658	22463.086273
HLA B*4801	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.435179	0.487485	-3.947694	27238.251543
HLA B*3801	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.530855	0.583145	-3.947710	33951.186361
HLA B*0803	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.483283	0.535432	-3.947851	30428.642806
HLA A*0301	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.362796	0.414917	-3.947879	23056.654526
HLA A*2602	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.551742	0.603848	-3.947893	35623.933889
HLA B*5101	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.466223	0.518215	-3.948008	29256.540553
HLA B*1517	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.476582	0.528496	-3.948086	29962.762437
HLA A*3201	1:201-209	9	DLGASTALA	1.029007	-0.426525	-4.550579	0.602482	-3.948097	35528.664348
HLA A*6802	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.135474	0.187363	-3.948111	13660.739835
HLA B*0702	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.330787	0.382667	-3.948120	21418.394261
HLA B*0702	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.448534	0.500136	-3.948398	28088.833190
HLA A*2301	1:70-78	9	LRTAILDAT	0.824289	-0.241144	-4.531607	0.583145	-3.948462	34010.012354
HLA B*5401	1:177-185	9	AKGPRSAGT	0.922438	-0.306591	-4.564483	0.615847	-3.948637	36684.544701
HLA A*0301	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.260049	0.311316	-3.948733	18199.045642
HLA A*0101	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.376541	0.427495	-3.949045	23798.017500
HLA B*4002	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.484638	0.535432	-3.949207	30523.774398
HLA A*2402	1:150-158	9	RNTGLLVMN	1.201693	-0.605060	-4.545889	0.596633	-3.949256	35147.084784
HLA A*0201	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.394446	0.445146	-3.949300	24799.687296
HLA A*2603	1:154-162	9	LLVMNNVAP	0.581178	0.075245	-4.605846	0.656423	-3.949423	40350.211623
HLA B*4002	1:159-167	9	NVAPPSRGT	0.858730	-0.161711	-4.646515	0.697019	-3.949496	44311.392917
HLA B*2705	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.364577	0.414917	-3.949660	23151.396979
HLA A*0201	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.398055	0.448362	-3.949693	25006.621099
HLA B*4501	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.398255	0.448362	-3.949892	25018.122802
HLA A*3001	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.016421	0.066377	-3.950044	10385.349496
HLA B*4403	1:162-170	9	PPSRGTVYQ	1.033521	-0.322657	-4.660988	0.710864	-3.950124	45812.947036
HLA A*2902	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.366920	0.416603	-3.950316	23276.605092
HLA A*3101	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.395666	0.445146	-3.950520	24869.416027
HLA A*6901	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.378106	0.427495	-3.950610	23883.916081
HLA A*1101	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.446297	0.495365	-3.950932	27944.541560
HLA B*4402	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.448000	0.496962	-3.951038	28054.360015
HLA B*0702	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.185471	0.234317	-3.951154	15327.497757
HLA A*0202	1:46-54	9	DEVRAVRET	1.031728	-0.408046	-4.574866	0.623682	-3.951184	37572.103287
HLA A*6901	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.170684	0.219167	-3.951516	14814.384168
HLA B*5701	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.403048	0.451113	-3.951935	25295.756343
HLA B*3801	1:124-132	9	VLTAPDVRT	0.912054	-0.308206	-4.555990	0.603848	-3.952141	35974.084053
HLA A*0206	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.513426	0.561253	-3.952174	32615.682797
HLA B*0802	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.441469	0.489218	-3.952251	27635.593607
HLA B*2705	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.368860	0.416603	-3.952257	23380.850936
HLA A*2902	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.403569	0.451113	-3.952456	25326.154680
HLA B*0702	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.440691	0.488141	-3.952550	27586.151568
HLA A*0212	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.449589	0.496962	-3.952627	28157.145028
HLA B*1509	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.504494	0.551693	-3.952801	31951.682555
HLA B*5801	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.336202	0.382667	-3.953536	21687.149413
HLA B*4002	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.488301	0.534755	-3.953547	30782.301112
HLA A*2501	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.489008	0.535432	-3.953577	30832.467126
HLA A*2902	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.449001	0.495365	-3.953636	28119.089011
HLA B*0801	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.441925	0.488141	-3.953784	27664.612900
HLA A*2403	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.404937	0.451113	-3.953824	25406.021149
HLA A*3201	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.506874	0.553011	-3.953863	32127.265408
HLA B*4601	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.405068	0.451113	-3.953955	25413.719166
HLA A*2501	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.515323	0.561253	-3.954070	32758.386991
HLA A*3101	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.402735	0.448362	-3.954373	25277.562207
HLA A*6901	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.358184	0.403811	-3.954373	22813.097323
HLA B*1801	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.449887	0.495365	-3.954522	28176.497209
HLA B*5401	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.519594	0.565014	-3.954580	33082.161152
HLA B*0702	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.452143	0.496962	-3.955181	28323.212318
HLA A*0219	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.444554	0.489218	-3.955336	27832.593160
HLA A*2402	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.520350	0.565014	-3.955336	33139.839980
HLA B*0702	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.450822	0.495365	-3.955457	28237.230396
HLA A*6801	1:219-227	9	PQPTGTILA	1.103044	-0.390422	-4.668208	0.712622	-3.955586	46580.934518
HLA A*0101	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.370669	0.414917	-3.955752	23478.449689
HLA A*2602	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.593781	0.637921	-3.955860	39244.717871
HLA A*8001	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.443729	0.487485	-3.956244	27779.792800
HLA A*0216	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.459085	0.502118	-3.956967	28779.631983
HLA A*1101	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.446217	0.489218	-3.956999	27939.402019
HLA A*3301	1:106-114	9	FGLGVLTRP	0.696435	-0.037899	-4.615678	0.658536	-3.957142	41274.175979
HLA B*3501	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.217133	0.259962	-3.957171	16486.669089
HLA A*0301	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.361004	0.403811	-3.957192	22961.678679
HLA B*5801	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.350219	0.392663	-3.957556	22398.529084
HLA A*0201	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.385316	0.427495	-3.957821	24283.769730
HLA A*2902	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.445409	0.487485	-3.957924	27887.455092
HLA A*0203	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.445442	0.487485	-3.957957	27889.567324
HLA B*4002	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.595889	0.637921	-3.957967	39435.622382
HLA B*1801	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.409130	0.451113	-3.958018	25652.546647
HLA A*3002	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.024475	0.066377	-3.958098	10579.743801
HLA A*3301	1:58-66	9	VSAATTAEP	0.530485	0.115863	-4.604629	0.646348	-3.958281	40237.295602
HLA A*2403	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.373259	0.414917	-3.958341	23618.839176
HLA A*3002	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.510132	0.551693	-3.958439	32369.239559
HLA B*0803	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.510631	0.551693	-3.958938	32406.385024
HLA B*3901	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.459137	0.500136	-3.959001	28783.057468
HLA A*8001	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.407366	0.448362	-3.959004	25548.536226
HLA A*0202	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.454790	0.495365	-3.959425	28496.424885
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HLA B*1509      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.563275       0.603848        -3.959427       36582.678305
HLA A*6801      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.618035       0.658536        -3.959499       41498.743275
HLA A*0202      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.325778       0.366173        -3.959605       21172.776182
HLA B*1517      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.455084       0.495365        -3.959719       28515.701714
HLA A*0212      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.448033       0.488141        -3.959892       28056.484889
HLA B*5701      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.408388       0.448362        -3.960026       25608.730441
HLA B*5801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.354907       0.394780        -3.960127       22641.579565
HLA A*2603      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.525291       0.565014        -3.960277       33519.024738
HLA A*2501      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.408651       0.448362        -3.960289       25624.251667
HLA A*3301      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.564215       0.603848        -3.960367       36661.927313
HLA A*2402      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.561257       0.600711        -3.960547       36413.069531
HLA A*0206      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.195156       0.234317        -3.960838       15673.133702
HLA A*0212      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.388406       0.427495        -3.960910       24457.140519
HLA B*1501      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.353603       0.392663        -3.960939       22573.700437
HLA B*4402      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.450312       0.489218        -3.961094       28204.100863
HLA A*3002      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.353878       0.392663        -3.961214       22587.993143
HLA A*2402      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.585628       0.623682        -3.961947       38514.875501
HLA A*3002      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.523341       0.561253        -3.962089       33368.854745
HLA A*2301      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.527211       0.565014        -3.962197       33667.502671
HLA B*3801      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.515306       0.553011        -3.962295       32757.146480
HLA B*3501      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.410820       0.448362        -3.962457       25752.521933
HLA A*0101      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.366309       0.403811        -3.962497       23243.887905
HLA B*4403      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.622877       0.660357        -3.962520       41964.034323
HLA B*5801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.336428       0.373896        -3.962532       21698.415546
HLA A*8001      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.458209       0.495365        -3.962844       28721.616444
HLA A*3301      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.623239       0.660357        -3.962882       41999.010089
HLA A*0212      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.411280       0.448362        -3.962918       25779.842800
HLA B*4501      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.600905       0.637921        -3.962983       39893.748903
HLA A*0301      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.314705       0.351592        -3.963113       20639.761938
HLA B*5101      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.491710       0.528496        -3.963214       31024.885321
HLA A*2603      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.613110       0.649819        -3.963292       41030.841541
HLA A*6801      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.567347       0.603848        -3.963499       36927.266064
HLA A*0250      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.547003       0.583145        -3.963858       35237.327667
HLA A*0101      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.346707       0.382667        -3.964040       22218.105211
HLA A*8001      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.367864       0.403811        -3.964053       23327.281566
HLA B*1502      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.588009       0.623682        -3.964327       38726.524816
HLA A*3301      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.614473       0.649819        -3.964655       41159.787671
HLA A*0206      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.493169       0.528496        -3.964673       31129.289978
HLA A*2403      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.409894       0.445146        -3.964748       25697.688986
HLA B*1501      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.415930       0.451113        -3.964817       26057.328952
HLA B*1501      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.359622       0.394780        -3.964843       22888.753289
HLA B*1517      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.454081       0.489218        -3.964863       28449.905821
HLA A*0211      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.368935       0.403811        -3.965124       23384.898896
HLA B*3801      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.567747       0.602482        -3.965265       36961.242996
HLA B*1517      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.467503       0.502118        -3.965385       29342.927521
HLA A*2602      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.623923       0.658536        -3.965387       42065.180268
HLA A*0203      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.270490       0.305034        -3.965456       18641.880750
HLA B*4002      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.624259       0.658536        -3.965723       42097.735077
HLA B*5801      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.331903       0.366173        -3.965730       21473.503829
HLA A*0206      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.414205       0.448362        -3.965843       25954.064143
HLA B*7301      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.615685       0.649819        -3.965867       41274.845851
HLA A*0219      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.461261       0.495365        -3.965896       28924.166925
HLA A*2603      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.612551       0.646348        -3.966203       40978.046128
HLA A*2501      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.466411       0.500136        -3.966275       29269.205265
HLA B*4001      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.383056       0.416603        -3.966453       24157.717674
HLA A*0250      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.590238       0.623682        -3.966556       38925.857453
HLA A*0201      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.370423       0.403811        -3.966611       23465.116816
HLA A*0301      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.200945       0.234317        -3.966627       15883.454726
HLA A*0211      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.468749       0.502118        -3.966631       29427.181504
HLA A*2501      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.495270       0.528496        -3.966773       31280.209612
HLA B*7301      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.518494       0.551693        -3.966801       32998.508747
HLA B*5101      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.469266       0.502462        -3.966804       29462.225868
HLA A*2402      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.582746       0.615847        -3.966899       38260.062950
HLA B*4403      1:159-167       9       NVAPPSRGT       0.858730        -0.161711       -4.663953       0.697019        -3.966934       46126.795003
HLA B*4501      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.563623       0.596633        -3.966990       36611.980453
HLA A*0216      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.456212       0.489218        -3.966994       28589.845997
HLA A*0203      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.349696       0.382667        -3.967029       22371.523674
HLA B*4601      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.394573       0.427495        -3.967078       24806.933186
HLA B*7301      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.592825       0.625647        -3.967178       39158.402935
HLA B*5301      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.550501       0.583145        -3.967356       35522.322112
HLA A*2601      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.395285       0.427495        -3.967790       24847.629968
HLA B*4002      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.624374       0.656423        -3.967951       42108.896016
HLA B*1509      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.416339       0.448362        -3.967976       26081.868803
HLA A*0216      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.371825       0.403811        -3.968014       23541.024708
HLA B*1501      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.273084       0.305034        -3.968050       18753.552861
HLA A*6901      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.383002       0.414917        -3.968084       24154.711978
HLA A*0206      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.457391       0.489218        -3.968173       28667.594807
HLA A*0203      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.228143       0.259962        -3.968181       16909.961073
HLA B*0803      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.497041       0.528496        -3.968545       31408.063937
HLA B*4801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.385389       0.416603        -3.968786       24287.842619
HLA B*0803      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.503617       0.534755        -3.968863       31887.272626
HLA A*2301      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.530528       0.561253        -3.969276       33925.665528
HLA A*0211      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.457525       0.488141        -3.969384       28676.436215
HLA A*0211      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.530686       0.561253        -3.969433       33937.964541
HLA B*1801      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.352155       0.382667        -3.969489       22498.598975
HLA A*2902      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.352268       0.382667        -3.969601       22504.442050
HLA A*3301      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.595259       0.625647        -3.969612       39378.488062
HLA B*5301      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.593556       0.623682        -3.969874       39224.341444
HLA B*5401      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.472374       0.502462        -3.969912       29673.851796
HLA B*2705      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.373806       0.403811        -3.969995       23648.629593
HLA A*0219      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.467351       0.496962        -3.970389       29332.611106
HLA A*0206      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.258991       0.288570        -3.970422       18154.794858
HLA B*5301      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.574318       0.603848        -3.970470       37524.773330
HLA B*1502      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.460103       0.489218        -3.970885       28847.126774
HLA B*5401      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.523992       0.553011        -3.970981       33418.896770
HLA B*4402      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.422170       0.451113        -3.971057       26434.440806
HLA B*3501      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.218942       0.247860        -3.971082       16555.489439
HLA B*4501      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.617652       0.646348        -3.971304       41462.165318
HLA A*0301      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.366370       0.394780        -3.971590       23247.157553
HLA A*2402      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.575594       0.603848        -3.971745       37635.167036
HLA B*7301      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.574299       0.602482        -3.971817       37523.149326
HLA B*3901      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.467304       0.495365        -3.971939       29329.437554
HLA A*0211      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.467381       0.495365        -3.972016       29334.674099
HLA B*3901      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.420523       0.448362        -3.972161       26334.382470
HLA A*0201      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.323992       0.351592        -3.972400       21085.902692
HLA A*0216      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.459910       0.487485        -3.972425       28834.332712
HLA B*1801      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.490660       0.518215        -3.972445       30949.950950
HLA B*4403      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.598100       0.625647        -3.972452       39636.889390
HLA A*0206      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.508046       0.535432        -3.972615       32214.111244
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HLA B*4001      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.387879       0.414917        -3.972962       24427.520936
HLA A*0301      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.365771       0.392663        -3.973107       23215.109705
HLA B*5301      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.160548       0.187363        -3.973185       14472.645497
HLA A*0219      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.424435       0.451113        -3.973322       26572.660037
HLA B*1503      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.461700       0.488141        -3.973559       28953.442844
HLA B*4501      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.491863       0.518215        -3.973648       31035.796917
HLA B*2705      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.469815       0.495365        -3.974450       29499.546131
HLA B*1801      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.462262       0.487485        -3.974777       28990.902801
HLA A*6901      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.341054       0.366173        -3.974881       21930.784030
HLA B*5701      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.402651       0.427495        -3.975155       25272.639729
HLA B*4402      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.420462       0.445146        -3.975316       26330.678612
HLA A*0216      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.470746       0.495365        -3.975381       29562.811226
HLA B*1501      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.420617       0.445146        -3.975471       26340.081730
HLA A*8001      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.426705       0.451113        -3.975592       26711.890997
HLA A*0212      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.426733       0.451113        -3.975620       26713.625154
HLA B*4601      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.420885       0.445146        -3.975739       26356.331389
HLA B*5401      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.537208       0.561253        -3.975955       34451.486223
HLA A*0206      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.478156       0.502118        -3.976038       30071.563298
HLA A*3101      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.368771       0.392663        -3.976108       23376.044893
HLA A*2602      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.559319       0.583145        -3.976174       36250.914360
HLA A*0202      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.504773       0.528496        -3.976277       31972.258930
HLA A*2301      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.528172       0.551693        -3.976479       33742.079367
HLA A*0203      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.308678       0.332159        -3.976519       20355.335025
HLA A*2601      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.391634       0.414917        -3.976716       24639.612368
HLA B*3901      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.404276       0.427495        -3.976781       25367.428795
HLA B*3801      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.541801       0.565014        -3.976787       34817.790286
HLA B*7301      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.580892       0.603848        -3.977044       38097.101640
HLA B*0801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.425671       0.448362        -3.977308       26648.382930
HLA A*2601      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -3.788516       -0.189096       -3.977612       6144.921966
HLA B*5701      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.422788       0.445146        -3.977642       26472.078520
HLA B*2705      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.465901       0.488141        -3.977760       29234.864961
HLA A*0202      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.480306       0.502118        -3.978188       30220.788027
HLA B*4002      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.582156       0.603848        -3.978308       38208.145550
HLA A*8001      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.361177       0.382667        -3.978511       22970.872810
HLA A*2602      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.575272       0.596633        -3.978639       37607.283885
HLA A*2902      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.427003       0.448362        -3.978641       26730.249866
HLA B*4801      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.423824       0.445146        -3.978678       26535.309973
HLA A*0201      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.393687       0.414917        -3.978770       24756.390305
HLA B*0803      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.497098       0.518215        -3.978883       31412.142141
HLA A*2501      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.474580       0.495365        -3.979215       29824.975097
HLA A*0202      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.213562       0.234317        -3.979244       16351.654565
HLA A*0206      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.353436       0.373896        -3.979540       22565.031496
HLA B*0802      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.475102       0.495365        -3.979737       29860.816273
HLA B*3901      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.396410       0.416603        -3.979807       24912.102047
HLA B*5701      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.396481       0.416603        -3.979878       24916.145526
HLA A*0211      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.291276       0.311316        -3.979960       19555.801455
HLA B*1509      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.515449       0.535432        -3.980018       32767.958228
HLA A*6802      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.425217       0.445146        -3.980072       26620.573645
HLA B*5301      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.480315       0.500136        -3.980180       30221.441999
HLA B*0802      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.477195       0.496962        -3.980233       30005.099172
HLA A*0203      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.291602       0.311316        -3.980286       19570.512451
HLA A*3002      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.533341       0.553011        -3.980329       34146.068689
HLA B*5301      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.581338       0.600711        -3.980628       38136.280981
HLA A*3101      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.318422       0.337522        -3.980899       20817.164259
HLA A*2603      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.596760       0.615847        -3.980914       39514.851875
HLA B*5801      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.228805       0.247860        -3.980946       16935.778407
HLA B*5701      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.396063       0.414917        -3.981145       24892.163816
HLA A*2601      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.347334       0.366173        -3.981161       22250.221129
HLA A*0203      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.239152       0.257963        -3.981189       17344.120995
HLA A*0301      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.355182       0.373896        -3.981286       22655.915248
HLA A*3002      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.292056       0.310721        -3.981334       19590.956863
HLA A*6801      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.470656       0.489218        -3.981438       29556.734453
HLA A*3101      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.396610       0.414917        -3.981693       24923.560276
HLA B*1503      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.483837       0.502118        -3.981719       30467.516895
HLA B*0802      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.483858       0.502118        -3.981740       30469.000364
HLA B*1801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.398360       0.416603        -3.981757       25024.214081
HLA B*5301      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.597712       0.615847        -3.981865       39601.524032
HLA B*0801      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.386073       0.403811        -3.982261       24326.108541
HLA B*4601      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.319850       0.337522        -3.982328       20885.749071
HLA B*1801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.484753       0.502118        -3.982635       30531.866852
HLA A*0216      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.431112       0.448362        -3.982750       26984.369042
HLA A*0212      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.427952       0.445146        -3.982806       26788.735262
HLA B*5301      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.471110       0.488141        -3.982969       29587.611010
HLA B*3901      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.485165       0.502118        -3.983047       30560.785992
HLA B*5801      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.345333       0.362044        -3.983288       22147.900831
HLA B*5401      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.501578       0.518215        -3.983363       31737.887902
HLA A*3001      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.294755       0.311316        -3.983439       19713.112784
HLA A*0216      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.480541       0.496962        -3.983579       30237.141562
HLA A*0211      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.512160       0.528496        -3.983664       32520.716266
HLA B*3901      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.480703       0.496962        -3.983741       30248.430660
HLA A*0250      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.580436       0.596633        -3.983803       38057.139002
HLA A*2603      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.642437       0.658536        -3.983901       43897.187540
HLA A*0203      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.429111       0.445146        -3.983965       26860.278200
HLA B*1517      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.435412       0.451113        -3.984299       27252.843686
HLA A*2902      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.295709       0.311316        -3.984393       19756.458545
HLA B*5301      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.549411       0.565014        -3.984397       35433.266205
HLA B*0802      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.472296       0.487485        -3.984811       29668.554705
HLA A*2501      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.473036       0.488141        -3.984896       29719.156439
HLA A*2602      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.485129       0.500136        -3.984994       30558.306136
HLA B*4801      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.436126       0.451113        -3.985013       27297.700761
HLA B*4002      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.631436       0.646348        -3.985088       42799.274518
HLA B*1517      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.412986       0.427495        -3.985491       25881.294282
HLA B*1509      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.436685       0.451113        -3.985572       27332.870651
HLA A*3002      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.609386       0.623682        -3.985705       40680.519533
HLA A*6901      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.346970       0.360868        -3.986102       22231.571409
HLA A*0211      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.538084       0.551693        -3.986391       34521.075675
HLA B*4002      1:61-69 9       ATTAEPPAH       0.752441        -0.126794       -4.612126       0.625647        -3.986479       40937.940476
HLA B*5801      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.347558       0.360868        -3.986690       22261.659335
HLA B*2705      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.483856       0.496962        -3.986894       30468.835530
HLA A*3201      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.602860       0.615847        -3.987013       40073.716490
HLA B*7301      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.247077       0.259962        -3.987116       17663.514024
HLA B*1517      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.298061       0.310721        -3.987340       19863.735883
HLA B*4001      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.370247       0.382667        -3.987580       23455.597972
HLA A*6802      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.276201       0.288570        -3.987632       18888.667580
HLA B*3801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.523139       0.535432        -3.987708       33353.333480
HLA A*2402      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.380495       0.392663        -3.987832       24015.684130
HLA B*2705      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.490122       0.502118        -3.988004       30911.631892
HLA A*3201      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.611795       0.623682        -3.988113       40906.725153
HLA A*3002      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.485301       0.496962        -3.988339       30570.376663
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HLA B*4501      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.644864       0.656423        -3.988440       44143.190005
HLA A*0301      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.354684       0.366173        -3.988510       22629.946153
HLA B*1509      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.506904       0.518215        -3.988689       32129.524952
HLA A*6802      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.437127       0.448362        -3.988765       27360.683939
HLA A*0301      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.293815       0.305034        -3.988781       19670.500604
HLA B*1517      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.248773       0.259962        -3.988812       17732.641565
HLA B*5101      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.477073       0.488141        -3.988932       29996.659498
HLA B*1801      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.518078       0.528496        -3.989582       32966.926136
HLA B*3801      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.524450       0.534755        -3.989696       33454.169915
HLA A*3301      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.613425       0.623682        -3.989743       41060.596613
HLA B*4403      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.605634       0.615847        -3.989788       40330.570290
HLA B*4501      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.648863       0.658536        -3.990326       44551.521220
HLA B*3801      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.519131       0.528496        -3.990635       33046.922680
HLA B*1801      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.480073       0.489218        -3.990855       30204.606741
HLA A*2603      1:60-68 9       AATTAEPPA       0.798576        -0.138219       -4.651228       0.660357        -3.990872       44794.889446
HLA A*2403      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.357266       0.366173        -3.991093       22764.892540
HLA B*5301      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.587738       0.596633        -3.991105       38702.439095
HLA B*3501      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.373973       0.382667        -3.991306       23657.714827
HLA B*1501      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.210667       0.219167        -3.991500       16243.033440
HLA A*0301      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.323969       0.332159        -3.991810       21084.761999
HLA B*4501      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.574959       0.583145        -3.991814       37580.234603
HLA B*4002      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.641678       0.649819        -3.991859       43820.548828
HLA A*8001      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.437021       0.445146        -3.991875       27354.023927
HLA A*0216      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.366060       0.373896        -3.992164       23230.562559
HLA A*0250      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.303495       0.311316        -3.992180       20113.853881
HLA A*2501      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.408896       0.416603        -3.992292       25638.672657
HLA A*0216      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.443445       0.451113        -3.992332       27761.614193
HLA B*0802      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.480487       0.488141        -3.992346       30233.379465
HLA A*2902      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.407270       0.414917        -3.992352       25542.870050
HLA B*1502      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.575653       0.583145        -3.992508       37640.257432
HLA B*0702      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.180035       0.187363        -3.992672       15136.816738
HLA B*1509      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.480162       0.487485        -3.992678       30210.816715
HLA A*0101      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.385372       0.392663        -3.992709       24286.922874
HLA B*5301      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.595416       0.602482        -3.992934       39392.763877
HLA A*6801      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.546253       0.553011        -3.993242       35176.569128
HLA A*2403      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.330829       0.337522        -3.993307       21420.480043
HLA A*3301      1:184-192       9       GTMGTAAVT       0.864297        -0.299283       -4.558405       0.565014        -3.993391       36174.706452
HLA B*4501      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.643402       0.649819        -3.993584       43994.899966
HLA A*2301      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.490660       0.496962        -3.993698       30949.950950
HLA A*2601      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.331412       0.337522        -3.993889       21449.238171
HLA B*4403      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.408898       0.414917        -3.993980       25638.811360
HLA B*5401      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.494222       0.500136        -3.994086       31204.827370
HLA B*5101      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.491233       0.496962        -3.994271       30990.832262
HLA A*2902      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.346028       0.351592        -3.994436       22183.395279
HLA B*1801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.494718       0.500136        -3.994582       31240.467600
HLA B*2705      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.483933       0.489218        -3.994715       30474.275506
HLA A*2301      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.547933       0.553011        -3.994922       35312.898081
HLA A*3002      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.443520       0.448362        -3.995157       27766.420601
HLA A*0101      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.389985       0.394780        -3.995205       24546.214935
HLA A*0101      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.327674       0.332159        -3.995515       21265.413947
HLA B*2705      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.446675       0.451113        -3.995562       27968.891640
HLA A*2902      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.390741       0.394780        -3.995961       24589.011321
HLA A*0211      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.531536       0.535432        -3.996105       34004.493090
HLA B*7301      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.514716       0.518215        -3.996501       32712.696320
HLA B*0803      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.496980       0.500136        -3.996844       31403.646480
HLA A*6901      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.307581       0.310721        -3.996860       20303.973842
HLA A*0219      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.445421       0.448362        -3.997058       27888.209442
HLA A*2402      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.499588       0.502462        -3.997126       31592.791992
HLA A*0206      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.494295       0.496962        -3.997333       31210.061063
HLA B*3801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.549103       0.551693        -3.997410       35408.163706
HLA B*0803      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.486797       0.489218        -3.997579       30675.906949
HLA B*4601      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.412735       0.414917        -3.997817       25866.317019
HLA B*1517      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.485583       0.487485        -3.998098       30590.228989
HLA A*6801      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.594763       0.596633        -3.998130       39333.563690
HLA B*4001      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.390938       0.392663        -3.998275       24600.187861
HLA A*2603      1:9-17  9       LLELATPYA       0.993939        -0.356018       -4.636251       0.637921        -3.998329       43276.337812
HLA A*0219      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.359345       0.360868        -3.998477       22874.146529
HLA A*0212      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.350071       0.351592        -3.998479       22390.896451
HLA A*3001      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.301954       0.303280        -3.998674       20042.598594
HLA A*2403      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.372777       0.373896        -3.998881       23592.659759
HLA B*0702      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.444027       0.445146        -3.998882       27798.885629
HLA A*6802      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.426498       0.427495        -3.999003       26699.177287
HLA A*0101      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.365512       0.366173        -3.999339       23201.298786
HLA A*3002      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.351004       0.351592        -3.999412       22439.037640
HLA B*1501      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.414332       0.414917        -3.999415       25961.647316
HLA A*6901      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.394498       0.394780        -3.999718       24802.639069
HLA B*0801      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.351343       0.351592        -3.999750       22456.525000
HLA A*0212      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.900963       -0.098967       -3.999930       7960.910188
HLA B*1503      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.451048       0.451113        -3.999935       28251.899192
HLA A*3301      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.311267       0.311316        -3.999952       20477.049834
HLA A*3101      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.366128       0.366173        -3.999955       23234.207414
HLA A*0101      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.373914       0.373896        -4.000018       23654.515403
HLA A*6901      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.337664       0.337522        -4.000141       21760.248528
HLA A*3201      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.383108       0.382667        -4.000441       24160.593038
HLA B*1503      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.383401       0.382667        -4.000735       24176.936830
HLA A*2402      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.562000       0.561253        -4.000747       36475.371821
HLA A*0201      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.395724       0.394780        -4.000945       24872.779774
HLA B*7301      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.415932       0.414917        -4.001015       26057.469920
HLA B*4403      1:106-114       9       FGLGVLTRP       0.696435        -0.037899       -4.659710       0.658536        -4.001174       45678.318665
HLA B*2705      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.488797       0.487485        -4.001312       30817.458759
HLA B*4403      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.598175       0.596633        -4.001542       39643.751782
HLA A*2902      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.394644       0.392663        -4.001980       24810.959596
HLA B*7301      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.489513       0.487485        -4.002028       30868.350039
HLA B*4402      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.429641       0.427495        -4.002146       26893.138599
HLA A*1101      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.490322       0.488141        -4.002181       30925.849583
HLA B*3501      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.368397       0.366173        -4.002224       23355.946111
HLA B*5701      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.406060       0.403811        -4.002248       25471.804284
HLA B*0803      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.497692       0.495365        -4.002327       31455.165437
HLA B*5101      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.491581       0.489218        -4.002363       31015.655429
HLA A*0201      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.385286       0.382667        -4.002619       24282.061947
HLA A*2601      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.397418       0.394780        -4.002639       24969.986254
HLA A*1101      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.453787       0.451113        -4.002674       28430.673470
HLA A*2402      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.586009       0.583145        -4.002864       38548.644812
HLA B*4601      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.406816       0.403811        -4.003005       25516.214437
HLA A*6901      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.395790       0.392663        -4.003127       24876.547711
HLA A*8001      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.335486       0.332159        -4.003327       21651.394772
HLA A*2403      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.386202       0.382667        -4.003535       24333.347704
HLA A*0203      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.237884       0.234317        -4.003566       17293.526855
HLA A*8001      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.418665       0.414917        -4.003747       26221.932563
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HLA A*2601      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.407589       0.403811        -4.003778       25561.670002
HLA B*7301      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.500981       0.496962        -4.004019       31694.306444
HLA A*0202      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.555985       0.551693        -4.004292       35973.694823
HLA A*3001      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.124089       0.119790        -4.004298       13307.259196
HLA A*6801      1:46-54 9       DEVRAVRET       1.031728        -0.408046       -4.628161       0.623682        -4.004479       42477.722688
HLA B*4501      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.539264       0.534755        -4.004509       34614.954199
HLA A*8001      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.432209       0.427495        -4.004714       27052.629034
HLA A*0301      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.366767       0.362044        -4.004723       23268.421481
HLA B*4002      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.620727       0.615847        -4.004881       41756.823590
HLA B*1502      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.601713       0.596633        -4.005080       39968.060369
HLA A*2603      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.523355       0.518215        -4.005141       33369.937893
HLA A*2902      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.337429       0.332159        -4.005270       21748.479659
HLA A*3002      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.500744       0.495365        -4.005379       31676.993443
HLA B*4002      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.523595       0.518215        -4.005380       33388.356796
HLA A*0201      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.398088       0.392663        -4.005425       25008.515133
HLA B*5801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.316159       0.310721        -4.005438       20708.994606
HLA A*2301      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.540213       0.534755        -4.005458       34690.691213
HLA B*4601      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.400249       0.394780        -4.005470       25133.295228
HLA A*2601      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.398224       0.392663        -4.005561       25016.363376
HLA A*3002      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.493815       0.488141        -4.005674       31175.636097
HLA A*0219      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.409567       0.403811        -4.005756       25678.372241
HLA B*4403      1:58-66 9       VSAATTAEP       0.530485        0.115863        -4.652375       0.646348        -4.006027       44913.305357
HLA A*3101      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.294924       0.288570        -4.006355       19720.792774
HLA A*2301      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.541912       0.535432        -4.006480       34826.644349
HLA A*2602      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.622483       0.615847        -4.006636       41925.912159
HLA B*5101      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.508899       0.502118        -4.006781       32277.435143
HLA B*2705      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.455178       0.448362        -4.006816       28521.873053
HLA A*0206      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.457979       0.451113        -4.006866       28706.393165
HLA A*0219      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.434423       0.427495        -4.006927       27190.844239
HLA A*2602      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.509190       0.502118        -4.007072       32299.094958
HLA B*1801      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.504383       0.496962        -4.007421       31943.559400
HLA A*6901      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.369657       0.362044        -4.007613       23423.769648
HLA A*3201      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.590873       0.583145        -4.007727       38982.756833
HLA A*2402      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.199766       0.191859        -4.007907       15840.377526
HLA A*2301      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.510438       0.502462        -4.007976       32392.012386
HLA B*4601      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.400827       0.392663        -4.008164       25166.765707
HLA B*4402      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.403064       0.394780        -4.008285       25296.714292
HLA A*0219      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.423277       0.414917        -4.008359       26501.883176
HLA A*0201      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.382624       0.373896        -4.008728       24133.682573
HLA B*0803      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.510870       0.502118        -4.008752       32424.272083
HLA A*8001      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.268758       0.259962        -4.008797       18567.701903
HLA A*3101      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.403593       0.394780        -4.008813       25327.524834
HLA B*4403      1:115-123       9       SPPPTVAEQ       0.875652        -0.225833       -4.658667       0.649819        -4.008848       45568.731431
HLA A*0101      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.371027       0.362044        -4.008982       23497.764032
HLA A*3002      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.511559       0.502118        -4.009441       32475.708471
HLA B*5701      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.392233       0.382667        -4.009566       24673.626705
HLA B*4501      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.512160       0.502462        -4.009698       32520.716266
HLA A*0219      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.454863       0.445146        -4.009717       28501.204323
HLA A*0212      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.424658       0.414917        -4.009741       26586.320285
HLA B*4801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.425163       0.414917        -4.010246       26617.261521
HLA B*1502      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.563327       0.553011        -4.010316       36587.032545
HLA B*1517      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.458730       0.448362        -4.010368       28756.131695
HLA B*7301      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.512895       0.502462        -4.010434       32575.830091
HLA A*1101      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.498035       0.487485        -4.010550       31480.019920
HLA B*0801      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.270765       0.259962        -4.010803       18653.683995
HLA B*5701      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.405714       0.394780        -4.010935       25451.555790
HLA B*1503      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.508300       0.496962        -4.011338       32232.938419
HLA B*5701      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.404453       0.392663        -4.011789       25377.723506
HLA B*4403      1:154-162       9       LLVMNNVAP       0.581178        0.075245        -4.668709       0.656423        -4.012285       46634.640963
HLA A*0201      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.373214       0.360868        -4.012346       23616.411570
HLA A*6801      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.613061       0.600711        -4.012351       41026.180387
HLA B*4001      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.416170       0.403811        -4.012358       26071.711580
HLA A*2301      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.540892       0.528496        -4.012396       34744.971071
HLA A*0203      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.349996       0.337522        -4.012474       22387.020554
HLA A*0250      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.573799       0.561253        -4.012546       37479.936064
HLA B*1501      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.386453       0.373896        -4.012558       24347.437338
HLA B*3901      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.500706       0.488141        -4.012565       31674.251657
HLA B*3801      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.501818       0.489218        -4.012600       31755.405977
HLA A*3101      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.373486       0.360868        -4.012619       23631.236633
HLA A*3201      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.573975       0.561253        -4.012722       37495.146322
HLA A*6801      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.192181       0.179262        -4.012920       15566.156426
HLA A*6801      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.501216       0.488141        -4.013075       31711.457351
HLA B*4601      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.395955       0.382667        -4.013288       24885.970050
HLA B*0801      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.379480       0.366173        -4.013307       23959.623279
HLA A*3002      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.271549       0.257963        -4.013586       18687.419861
HLA B*4402      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.430365       0.416603        -4.013762       26937.986533
HLA A*0216      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.396894       0.382667        -4.014228       24939.880495
HLA B*5701      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.388218       0.373896        -4.014322       24446.557976
HLA B*5301      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.274517       0.259962        -4.014555       18815.542420
HLA B*5101      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.431220       0.416603        -4.014617       26991.085070
HLA B*0802      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.465849       0.451113        -4.014736       29231.385705
HLA B*0803      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.418859       0.403811        -4.014748       26215.549742
HLA A*0201      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.381259       0.366173        -4.015086       24057.945983
HLA A*8001      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.431742       0.416603        -4.015139       27023.520712
HLA A*6801      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.249647       0.234317        -4.015330       17768.364063
HLA B*1502      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.533609       0.518215        -4.015394       34167.133998
HLA A*0202      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.576806       0.561253        -4.015553       37740.372482
HLA B*1509      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.517719       0.502118        -4.015601       32939.650271
HLA A*6802      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.376527       0.360868        -4.015659       23797.245045
HLA A*0211      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.505015       0.489218        -4.015797       31990.079431
HLA B*1509      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.505741       0.489218        -4.016523       32043.600553
HLA B*0802      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.444232       0.427495        -4.016736       27811.972542
HLA B*0803      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.513765       0.496962        -4.016803       32641.101097
HLA B*0702      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.420655       0.403811        -4.016843       26342.361779
HLA A*0211      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.224492       0.207531        -4.016961       16768.395478
HLA A*2301      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.535263       0.518215        -4.017048       34297.509760
HLA A*2603      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.621078       0.603848        -4.017229       41790.496227
HLA A*0101      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.230034       0.212403        -4.017631       16983.763877
HLA B*0702      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.432555       0.414917        -4.017637       27074.151294
HLA B*4501      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.620657       0.602482        -4.018175       41750.047146
HLA A*3301      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.634143       0.615847        -4.018296       43066.840723
HLA B*0801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.433220       0.414917        -4.018302       27115.633529
HLA A*3301      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.615089       0.596633        -4.018456       41218.168546
HLA B*5801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.350701       0.332159        -4.018542       22423.383444
HLA A*0216      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.463852       0.445146        -4.018706       29097.276513
HLA B*0801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.413491       0.394780        -4.018712       25911.415006
HLA A*3101      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.392816       0.373896        -4.018920       24706.752355
HLA B*3801      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.537293       0.518215        -4.019078       34458.196511
HLA B*5101      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.370709       0.351592        -4.019117       23480.609057
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HLA B*1509	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.507285	0.488141	-4.019144	32157.695676
HLA A*0216	1:109-117	9	GVLTRPSPP	0.250080	0.054954	-4.324260	0.305034	-4.019226	21098.910956
HLA B*0802	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.467640	0.448362	-4.019277	29352.136001
HLA B*4002	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.584623	0.565014	-4.019609	38425.800068
HLA B*2705	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.464870	0.445146	-4.019724	29165.516254
HLA B*1501	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.331055	0.311316	-4.019739	21431.607645
HLA B*4601	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.393793	0.373896	-4.019897	24762.417859
HLA B*0802	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.465072	0.445146	-4.019926	29179.088681
HLA B*7301	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.554726	0.534755	-4.019971	35869.532972
HLA A*2501	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.471101	0.451113	-4.019988	29586.970754
HLA A*0202	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.554763	0.534755	-4.020009	35872.637909
HLA B*1509	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.517367	0.496962	-4.020405	32912.931135
HLA A*0202	1:151-159	9	NTGLLVMNN	0.907671	-0.575512	-4.352658	0.332159	-4.020499	22524.661052
HLA B*4001	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.415382	0.394780	-4.020603	26024.504272
HLA B*5301	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.581952	0.561253	-4.020699	38190.166722
HLA B*0803	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.472052	0.451113	-4.020939	29651.867026
HLA A*3002	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.555804	0.534755	-4.021050	35958.712689
HLA B*4403	1:9-17	9	LLELATPYA	0.993939	-0.356018	-4.659332	0.637921	-4.021410	45638.550529
HLA B*5301	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.573115	0.551693	-4.021422	37420.978654
HLA A*0202	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.510663	0.489218	-4.021445	32408.839526
HLA B*0803	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.448968	0.427495	-4.021473	28116.959395
HLA B*1503	1:109-117	9	GVLTRPSPP	0.250080	0.054954	-4.326555	0.305034	-4.021522	21210.723672
HLA B*0801	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.382508	0.360868	-4.021641	24127.285954
HLA B*3501	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.279617	0.257963	-4.021654	19037.831329
HLA A*2602	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.583014	0.561253	-4.021761	38283.666256
HLA A*3201	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.509914	0.488141	-4.021773	32352.958053
HLA A*0250	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.511042	0.489218	-4.021824	32437.079667
HLA A*3101	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.333336	0.311316	-4.022020	21544.484141
HLA B*4601	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.382983	0.360868	-4.022115	24153.666606
HLA A*3002	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.557679	0.535432	-4.022247	36114.285312
HLA B*0801	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.209840	0.187363	-4.022477	16212.131572
HLA A*0250	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.510680	0.488141	-4.022539	32410.066847
HLA A*6802	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.437468	0.414917	-4.022550	27382.155008
HLA B*1503	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.510121	0.487485	-4.022636	32368.364001
HLA A*3101	1:151-159	9	NTGLLVMNN	0.907671	-0.575512	-4.354890	0.332159	-4.022731	22640.722162
HLA A*2602	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.525350	0.502462	-4.022888	33523.558400
HLA A*0250	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.525223	0.502118	-4.023105	33513.766458
HLA B*5701	1:96-104	9	AAAIAVGLG	0.855432	-0.489259	-4.389310	0.366173	-4.023137	24508.133116
HLA A*2601	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.397242	0.373896	-4.023346	24959.856945
HLA B*3501	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.418293	0.394780	-4.023514	26199.528616
HLA A*2601	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.384663	0.360868	-4.023795	24247.275624
HLA A*1101	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.451492	0.427495	-4.023996	28280.800657
HLA A*0101	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.384865	0.360868	-4.023997	24258.559304
HLA A*2402	1:187-195	9	GTAAVTPST	0.889490	-0.371275	-4.542299	0.518215	-4.024084	34857.745595
HLA A*0212	1:109-117	9	GVLTRPSPP	0.250080	0.054954	-4.329163	0.305034	-4.024129	21338.476772
HLA B*5401	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.375791	0.351592	-4.024199	23756.983379
HLA B*4403	1:184-192	9	GTMGTAAVT	0.864297	-0.299283	-4.589226	0.565014	-4.024211	38835.201233
HLA A*3201	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.526652	0.502118	-4.024534	33624.181851
HLA B*4601	1:96-104	9	AAAIAVGLG	0.855432	-0.489259	-4.390720	0.366173	-4.024547	24587.814135
HLA A*0203	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.439629	0.414917	-4.024712	27518.778389
HLA A*2601	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.386766	0.362044	-4.024722	24364.961994
HLA A*3002	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.553403	0.528496	-4.024907	35760.448917
HLA A*2402	1:28-36	9	DIDRRVAAA	0.875321	-0.322310	-4.577986	0.553011	-4.024974	37843.005741
HLA A*0301	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.362519	0.337522	-4.024997	23041.940618
HLA B*1503	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.514340	0.489218	-4.025122	32684.393042
HLA B*5401	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.553708	0.528496	-4.025212	35785.607572
HLA A*2301	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.513584	0.488141	-4.025443	32627.506904
HLA A*3001	1:195-203	9	TTATLTDLG	0.805893	-0.593490	-4.238245	0.212403	-4.025842	17307.940492
HLA B*3501	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.418517	0.392663	-4.025853	26212.997048
HLA B*4001	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.399829	0.373896	-4.025933	25108.968676
HLA A*0250	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.554578	0.528496	-4.026081	35857.309892
HLA A*3002	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.387353	0.360868	-4.026485	24397.937224
HLA A*0212	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.419433	0.392663	-4.026770	26268.361102
HLA B*5801	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.364514	0.337522	-4.026991	23148.015571
HLA B*4001	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.389261	0.362044	-4.027217	24505.348962
HLA B*4001	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.388178	0.360868	-4.027310	24444.309775
HLA A*0201	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.234874	0.207531	-4.027343	17174.095849
HLA A*2501	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.472599	0.445146	-4.027454	29689.266894
HLA B*1501	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.316112	0.288570	-4.027542	20706.754060
HLA A*6802	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.431498	0.403811	-4.027686	27008.320787
HLA B*0803	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.515851	0.488141	-4.027710	32798.285598
HLA A*0211	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.476333	0.448362	-4.027970	29945.585269
HLA A*3101	1:109-117	9	GVLTRPSPP	0.250080	0.054954	-4.333122	0.305034	-4.028088	21533.880404
HLA A*3101	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.390184	0.362044	-4.028140	24557.504876
HLA A*6802	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.390391	0.362044	-4.028347	24569.198757
HLA B*5801	1:195-203	9	TTATLTDLG	0.805893	-0.593490	-4.241262	0.212403	-4.028859	17428.585131
HLA B*5801	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.288999	0.259962	-4.029037	19453.554606
HLA A*2603	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.557726	0.528496	-4.029230	36118.193009
HLA A*0250	1:135-143	9	RPLGAGTAT	0.836354	-0.301599	-4.564159	0.534755	-4.029404	36657.167535
HLA A*0216	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.340295	0.310721	-4.029574	21892.495768
HLA A*0212	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.340652	0.310721	-4.029931	21910.505440
HLA B*1517	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.403830	0.373896	-4.029934	25341.367545
HLA B*5801	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.318563	0.288570	-4.029993	20823.922469
HLA A*0212	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.425029	0.394780	-4.030250	26609.054990
HLA A*0101	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.382081	0.351592	-4.030489	24103.541924
HLA A*0211	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.527624	0.496962	-4.030662	33699.574130
HLA A*0219	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.382398	0.351592	-4.030806	24121.152015
HLA A*0201	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.392863	0.362044	-4.030818	24709.425716
HLA B*1501	1:151-159	9	NTGLLVMNN	0.907671	-0.575512	-4.363224	0.332159	-4.031065	23079.367284
HLA B*1501	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.368682	0.337522	-4.031159	23371.239838
HLA B*5801	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-4.357876	0.326268	-4.031608	22796.935512
HLA A*0211	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.291699	0.259962	-4.031737	19574.853779
HLA B*5101	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.480583	0.448362	-4.032221	30240.086138
HLA B*1517	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.436060	0.403811	-4.032249	27293.566103
HLA B*3501	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.436258	0.403811	-4.032446	27305.971955
HLA B*0801	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.370122	0.337522	-4.032600	23448.873650
HLA A*0202	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.240400	0.207531	-4.032869	17394.016235
HLA A*1101	1:109-117	9	GVLTRPSPP	0.250080	0.054954	-4.337941	0.305034	-4.032907	21774.143986
HLA A*2902	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.393805	0.360868	-4.032937	24763.087678
HLA B*4402	1:168-176	9	VYQMWLLGG	0.877304	-0.473493	-4.436791	0.403811	-4.032980	27339.525512
HLA A*8001	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.384611	0.351592	-4.033019	24244.389944
HLA B*4501	1:51-59	9	VRETMAVVS	1.416891	-0.855638	-4.594465	0.561253	-4.033212	39306.548614
HLA A*0203	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.428065	0.394780	-4.033285	26795.692521
HLA A*2402	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.521469	0.488141	-4.033328	33225.288594
HLA A*2402	1:108-116	9	LGVLTRPSP	0.601016	-0.049323	-4.585029	0.551693	-4.033336	38461.780025
HLA A*2601	1:111-119	9	LTRPSPPPT	0.624592	-0.273000	-4.385232	0.351592	-4.033639	24279.040780
HLA B*1509	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.450312	0.416603	-4.033709	28204.100863
HLA A*0216	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.241314	0.207531	-4.033783	17430.659562
HLA A*0202	1:29-37	9	IDRRVAAAP	0.654385	-0.118953	-4.569297	0.535432	-4.033866	37093.449990
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HLA A*0250      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.585896       0.551693        -4.034203       38538.636005
HLA A*8001      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.395198       0.360868        -4.034330       24842.656817
HLA B*4402      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.427283       0.392663        -4.034619       26747.463721
HLA B*1503      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.323219       0.288570        -4.034650       21048.406253
HLA A*1101      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.483720       0.448362        -4.035357       30459.276715
HLA B*3801      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.522855       0.487485        -4.035370       33331.507647
HLA A*0216      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.347109       0.311316        -4.035793       22238.668491
HLA B*1801      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.523992       0.488141        -4.035851       33418.896770
HLA B*4501      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.640115       0.603848        -4.036267       43663.184296
HLA B*1502      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.564840       0.528496        -4.036344       36714.722923
HLA A*0203      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.429202       0.392663        -4.036539       26865.945932
HLA A*3301      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.619811       0.583145        -4.036666       41668.815548
HLA B*0803      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.524340       0.487485        -4.036855       33445.664779
HLA B*1502      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.453562       0.416603        -4.036958       28415.911852
HLA A*0202      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.420190       0.382667        -4.037523       26314.160053
HLA A*6801      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.621016       0.583145        -4.037871       41784.618510
HLA B*5401      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.526304       0.488141        -4.038163       33597.270968
HLA A*0201      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.370458       0.332159        -4.038299       23467.021049
HLA A*2403      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.370484       0.332159        -4.038325       23468.417584
HLA A*2902      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.343657       0.305034        -4.038623       22062.635371
HLA A*3201      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.272985       0.234317        -4.038667       18749.292250
HLA B*4801      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.443010       0.403811        -4.039199       27733.843450
HLA B*5301      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.557498       0.518215        -4.039283       36099.244626
HLA A*6802      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.432437       0.392663        -4.039774       27066.828877
HLA B*4801      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.422562       0.382667        -4.039896       26458.333832
HLA A*2301      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.540150       0.500136        -4.040014       34685.624417
HLA B*4402      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.422776       0.382667        -4.040110       26471.362474
HLA A*2602      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.574976       0.534755        -4.040221       37581.657764
HLA A*0301      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.351063       0.310721        -4.040342       22442.072663
HLA A*0212      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.372657       0.332159        -4.040498       23586.151339
HLA B*0801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.414445       0.373896        -4.040549       25968.389773
HLA B*5301      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.535984       0.495365        -4.040619       34354.519626
HLA B*5301      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.569184       0.528496        -4.040688       37083.819011
HLA B*4002      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.643487       0.602482        -4.041005       44003.469071
HLA A*2402      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.576491       0.535432        -4.041060       37713.023452
HLA A*0101      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.378686       0.337522        -4.041163       23915.852120
HLA B*5801      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.352564       0.311316        -4.041249       22519.787343
HLA A*2301      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.434270       0.392663        -4.041607       27181.284456
HLA A*0301      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.368012       0.326268        -4.041744       23335.233395
HLA B*0801      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.368080       0.326268        -4.041812       23338.894672
HLA A*8001      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.415718       0.373896        -4.041823       26044.644987
HLA B*0702      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.437035       0.394780        -4.042256       27354.911835
HLA B*3801      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.537713       0.495365        -4.042348       34491.580961
HLA A*2301      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.537852       0.495365        -4.042487       34502.591861
HLA A*3101      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.300481       0.257963        -4.042518       19974.729261
HLA B*0802      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.459130       0.416603        -4.042527       28782.590333
HLA A*0211      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.353257       0.310721        -4.042536       22555.755755
HLA B*4801      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.394129       0.351592        -4.042537       24781.581827
HLA B*1517      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.457772       0.414917        -4.042854       28692.730158
HLA B*0803      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.491355       0.448362        -4.042993       30999.551650
HLA B*1501      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.405040       0.362044        -4.042996       25412.069395
HLA B*4002      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.604643       0.561253        -4.043390       40238.601699
HLA B*5801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.348481       0.305034        -4.043447       22309.039897
HLA B*1509      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.539008       0.495365        -4.043643       34594.548542
HLA A*2403      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.406149       0.362044        -4.044105       25477.041209
HLA A*2601      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.376503       0.332159        -4.044344       23795.957675
HLA A*3101      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.370949       0.326268        -4.044681       23493.569437
HLA A*2402      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.579720       0.534755        -4.044965       37994.395884
HLA A*3301      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.542177       0.496962        -4.045215       34847.940994
HLA A*2301      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.547348       0.502118        -4.045230       35265.361428
HLA B*3801      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.548150       0.502462        -4.045688       35330.478031
HLA A*3201      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.541096       0.495365        -4.045731       34761.328001
HLA B*4403      1:69-77 9       HLRTAILDA       0.775000        -0.174289       -4.646537       0.600711        -4.045826       44313.550447
HLA B*7301      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.598943       0.553011        -4.045932       39713.944985
HLA B*4001      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.412206       0.366173        -4.046033       25834.851044
HLA A*2301      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.535361       0.489218        -4.046143       34305.303566
HLA B*5301      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.599347       0.553011        -4.046336       39750.916046
HLA B*5101      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.233885       0.187363        -4.046522       17135.025268
HLA A*0216      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.461538       0.414917        -4.046621       28942.637051
HLA A*6802      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.441560       0.394780        -4.046781       27641.424937
HLA A*0212      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.429465       0.382667        -4.046799       26882.229145
HLA A*1101      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.281119       0.234317        -4.046801       19103.757458
HLA B*1517      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.491973       0.445146        -4.046827       31043.689231
HLA A*6801      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.498007       0.451113        -4.046894       31477.976345
HLA B*3501      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.461959       0.414917        -4.047041       28970.677812
HLA A*0201      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.853235       -0.194071       -4.047307       7132.393344
HLA B*4402      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.413484       0.366173        -4.047311       25910.994476
HLA B*4801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.442343       0.394780        -4.047563       27691.265653
HLA B*0802      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.430281       0.382667        -4.047614       26932.740709
HLA A*3201      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.537166       0.489218        -4.047948       34448.131570
HLA B*1502      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.609351       0.561253        -4.048099       40677.218511
HLA B*5401      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.545276       0.496962        -4.048314       35097.492785
HLA A*0216      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.476063       0.427495        -4.048567       29926.960799
HLA A*0206      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.071643       0.022933        -4.048711       11793.519022
HLA A*2603      1:150-158       9       RNTGLLVMN       1.201693        -0.605060       -4.645451       0.596633        -4.048818       44202.932837
HLA A*0101      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.375305       0.326268        -4.049037       23730.394081
HLA A*2603      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.632278       0.583145        -4.049132       42882.245919
HLA B*2705      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.410148       0.360868        -4.049280       25712.707711
HLA B*3801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.551547       0.502118        -4.049429       35607.941593
HLA B*0803      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.494577       0.445146        -4.049431       31230.328798
HLA A*1101      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.464952       0.414917        -4.050034       29171.039154
HLA A*0216      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.310067       0.259962        -4.050105       20420.520158
HLA A*2601      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.310121       0.259962        -4.050159       20423.061189
HLA A*2403      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.411066       0.360868        -4.050199       25767.154509
HLA B*1502      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.585765       0.535432        -4.050333       38526.962347
HLA A*0101      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.361713       0.311316        -4.050397       22999.223822
HLA A*0202      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.424426       0.373896        -4.050530       26572.085022
HLA B*3501      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.411501       0.360868        -4.050633       25792.955947
HLA A*6801      1:177-185       9       AKGPRSAGT       0.922438        -0.306591       -4.666566       0.615847        -4.050719       46405.120761
HLA A*2501      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.402533       0.351592        -4.050941       25265.804544
HLA A*8001      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.445893       0.394780        -4.051113       27918.551232
HLA A*2403      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.377391       0.326268        -4.051123       23844.668724
HLA A*2403      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.402848       0.351592        -4.051256       25284.127002
HLA B*0702      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.356314       0.305034        -4.051280       22715.069146
HLA B*5701      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.413437       0.362044        -4.051393       25908.191115
HLA B*3901      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.496642       0.445146        -4.051496       31379.191811
HLA A*2402      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.551822       0.500136        -4.051686       35630.487024
HLA A*3301      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.455965       0.403811        -4.052154       28573.610479
HLA A*1101      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.456188       0.403811        -4.052377       28588.299359
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HLA A*6901      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.310473       0.257963        -4.052510       20439.640890
HLA A*0219      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.426599       0.373896        -4.052703       26705.388912
HLA A*2902      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.426625       0.373896        -4.052729       26706.978164
HLA A*2902      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.363854       0.310721        -4.053132       23112.853180
HLA A*2602      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.404730       0.351592        -4.053138       25393.928977
HLA B*4403      1:70-78 9       LRTAILDAT       0.824289        -0.241144       -4.636575       0.583145        -4.053430       43308.658461
HLA A*0202      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.550628       0.496962        -4.053666       35532.700906
HLA A*1101      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.498881       0.445146        -4.053735       31541.388891
HLA B*5401      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.542985       0.489218        -4.053767       34912.853460
HLA B*4601      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.415817       0.362044        -4.053773       26050.563402
HLA B*0702      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.446835       0.392663        -4.054172       27979.182517
HLA A*2603      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.406020       0.351592        -4.054428       25469.461798
HLA A*0250      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.549982       0.495365        -4.054617       35479.877517
HLA A*2902      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.416766       0.362044        -4.054722       26107.561653
HLA A*2402      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.471460       0.416603        -4.054857       29611.470413
HLA A*2402      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.583371       0.528496        -4.054874       38315.159982
HLA B*1801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.387085       0.332159        -4.054926       24382.894987
HLA A*1101      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.416083       0.360868        -4.055215       26066.493435
HLA B*4403      1:201-209       9       DLGASTALA       1.029007        -0.426525       -4.657936       0.602482        -4.055454       45492.127616
HLA B*5401      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.557613       0.502118        -4.055495       36108.815247
HLA A*0211      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.543079       0.487485        -4.055594       34920.409264
HLA A*8001      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.448329       0.392663        -4.055666       28075.616000
HLA A*6801      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.303575       0.247860        -4.055716       20117.553888
HLA A*0201      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.393318       0.337522        -4.055796       24735.372328
HLA A*0212      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.429712       0.373896        -4.055816       26897.503620
HLA B*4801      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.448520       0.392663        -4.055856       28087.921460
HLA A*2902      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.422161       0.366173        -4.055988       26433.868783
HLA B*1503      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.449264       0.392663        -4.056601       28136.131742
HLA A*2603      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.545859       0.489218        -4.056641       35144.613027
HLA A*2301      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.544155       0.487485        -4.056670       35007.039862
HLA B*1509      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.431044       0.373896        -4.057148       26980.135883
HLA B*4601      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.362294       0.305034        -4.057260       23029.976908
HLA A*2602      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.368665       0.311316        -4.057350       23370.354804
HLA A*6901      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.362559       0.305034        -4.057525       23044.059839
HLA B*5701      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.395128       0.337522        -4.057605       24838.625264
HLA A*3301      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.389797       0.332159        -4.057638       24535.593850
HLA B*5801      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.361403       0.303280        -4.058123       22982.805816
HLA A*0206      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.424299       0.366173        -4.058126       26564.323546
HLA A*3101      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.368928       0.310721        -4.058207       23384.519370
HLA B*4801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.432113       0.373896        -4.058217       27046.629279
HLA A*0206      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.545784       0.487485        -4.058299       35138.529443
HLA B*5101      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.473321       0.414917        -4.058403       29738.616866
HLA B*5701      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.419280       0.360868        -4.058412       26259.125646
HLA A*2501      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.432318       0.373896        -4.058422       27059.362051
HLA A*0250      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.593932       0.535432        -4.058500       39258.308036
HLA A*1101      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.451318       0.392663        -4.058655       28269.481219
HLA B*2705      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.425048       0.366173        -4.058875       26610.206631
HLA B*4501      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.559096       0.500136        -4.058960       36232.288371
HLA B*1502      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.611066       0.551693        -4.059373       40838.179384
HLA A*6901      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.386075       0.326268        -4.059807       24326.240143
HLA A*0301      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.348436       0.288570        -4.059867       22306.746915
HLA B*1509      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.442749       0.382667        -4.060083       27717.194340
HLA B*1509      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.560386       0.500136        -4.060250       36340.059285
HLA A*2602      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.596074       0.535432        -4.060643       39452.480029
HLA A*0101      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.320649       0.259962        -4.060687       20924.200883
HLA A*0219      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.372617       0.311316        -4.061301       23583.982265
HLA A*2501      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.399547       0.337522        -4.062024       25092.673557
HLA B*0702      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.435978       0.373896        -4.062082       27288.398661
HLA B*5301      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.551617       0.489218        -4.062399       35613.721112
HLA B*3801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.511072       0.448362        -4.062710       32439.361001
HLA A*2402      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.457934       0.394780        -4.063154       28703.442647
HLA B*2705      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.414851       0.351592        -4.063259       25992.705247
HLA A*0206      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.368592       0.305034        -4.063559       23366.435771
HLA A*0219      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.446492       0.382667        -4.063825       27957.092058
HLA B*5101      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.508995       0.445146        -4.063849       32284.595248
HLA B*0803      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.478983       0.414917        -4.064066       30128.882563
HLA B*4402      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.396629       0.332159        -4.064470       24924.638969
HLA A*3201      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.491983       0.427495        -4.064487       31044.361010
HLA B*1501      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.390997       0.326268        -4.064729       24603.515194
HLA B*5401      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.430950       0.366173        -4.064777       26974.298133
HLA A*3301      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.564962       0.500136        -4.064827       36725.052751
HLA B*0803      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.481485       0.416603        -4.064882       30302.972112
HLA A*0219      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.459682       0.394780        -4.064902       28819.205599
HLA A*0203      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.353765       0.288570        -4.065195       22582.128374
HLA A*3201      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.370385       0.305034        -4.065351       23463.085805
HLA A*0301      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.368632       0.303280        -4.065353       23368.584837
HLA B*4501      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.600804       0.535432        -4.065372       39884.469690
HLA B*0801      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.376696       0.311316        -4.065380       23806.516163
HLA A*3201      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.600844       0.535432        -4.065412       39888.137958
HLA B*4002      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.617133       0.551693        -4.065440       41412.623376
HLA B*4001      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.417142       0.351592        -4.065550       26130.169679
HLA B*4801      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.426648       0.360868        -4.065780       26708.423021
HLA B*4403      1:124-132       9       VLTAPDVRT       0.912054        -0.308206       -4.669735       0.603848        -4.065887       46745.021348
HLA A*2301      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.493590       0.427495        -4.066094       31159.449254
HLA A*3301      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.584602       0.518215        -4.066387       38423.929200
HLA B*5301      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.602094       0.535432        -4.066662       40003.103813
HLA A*0101      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.355391       0.288570        -4.066821       22666.826248
HLA A*2603      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.601821       0.534755        -4.067067       39978.007855
HLA A*0203      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.274632       0.207531        -4.067101       18820.530791
HLA A*2602      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.554754       0.487485        -4.067269       35871.861650
HLA B*5301      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.569800       0.502462        -4.067338       37136.418549
HLA B*0802      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.482472       0.414917        -4.067555       30371.903396
HLA A*0201      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.372664       0.305034        -4.067630       23586.534138
HLA B*4801      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.429865       0.362044        -4.067820       26906.963596
HLA A*3201      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.564836       0.496962        -4.067874       36714.325680
HLA B*1517      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.400076       0.332159        -4.067917       25123.235585
HLA B*0802      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.460676       0.392663        -4.068013       28885.230498
HLA A*2601      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.373118       0.305034        -4.068084       23611.173902
HLA B*3801      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.568339       0.500136        -4.068203       37011.666329
HLA B*1509      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.513394       0.445146        -4.068248       32613.212629
HLA A*1101      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.400764       0.332159        -4.068605       25163.089941
HLA A*0216      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.463462       0.394780        -4.068683       29071.157678
HLA B*4001      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.380065       0.311316        -4.068749       23991.920134
HLA A*6901      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.316927       0.247860        -4.069068       20745.661940
HLA A*1101      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.443222       0.373896        -4.069326       27747.350069
HLA B*0801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.401805       0.332159        -4.069646       25223.467643
HLA A*2403      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.327636       0.257963        -4.069673       21263.573330
HLA A*0201      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.396072       0.326268        -4.069804       24892.702478
HLA A*2403      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.380876       0.310721        -4.070154       24036.740750
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HLA A*2602      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.622179       0.551693        -4.070486       41896.663291
HLA B*0702      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.431387       0.360868        -4.070519       27001.454395
HLA A*0219      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.463199       0.392663        -4.070536       29053.548579
HLA B*4801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.375629       0.305034        -4.070595       23748.116971
HLA A*3201      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.622407       0.551693        -4.070714       41918.654722
HLA A*0216      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.463399       0.392663        -4.070736       29066.911651
HLA A*0202      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.515973       0.445146        -4.070827       32807.513521
HLA B*5701      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.403045       0.332159        -4.070886       25295.619496
HLA B*4402      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.444843       0.373896        -4.070947       27851.119586
HLA A*3002      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.487721       0.416603        -4.071118       30741.195959
HLA B*4801      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.437409       0.366173        -4.071236       27378.451897
HLA B*4402      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.433664       0.362044        -4.071620       27143.372604
HLA A*1101      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.437808       0.366173        -4.071635       27403.642926
HLA A*0101      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.374936       0.303280        -4.071657       23710.247167
HLA A*3002      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.437947       0.366173        -4.071774       27412.391111
HLA B*1801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.486732       0.414917        -4.071814       30671.260610
HLA A*0216      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.360463       0.288570        -4.071894       22933.125815
HLA A*3101      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.319761       0.247860        -4.071901       20881.455908
HLA A*2902      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.306286       0.234317        -4.071969       20243.540879
HLA B*1517      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.360600       0.288570        -4.072030       22940.322753
HLA B*0802      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.475933       0.403811        -4.072122       29918.057539
HLA B*2705      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.467022       0.394780        -4.072242       29310.403453
HLA B*4001      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.409892       0.337522        -4.072369       25697.549965
HLA A*2501      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.476218       0.403811        -4.072406       29937.648208
HLA B*3801      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.560947       0.488141        -4.072806       36387.076045
HLA A*0219      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.405153       0.332159        -4.072994       25418.669122
HLA B*5701      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.331163       0.257963        -4.073200       21436.941669
HLA B*0802      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.424874       0.351592        -4.073282       26599.555851
HLA A*1101      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.285813       0.212403        -4.073410       19311.369192
HLA A*0212      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.439758       0.366173        -4.073585       27526.967652
HLA A*3301      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.609079       0.535432        -4.073647       40651.699647
HLA A*0203      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.293599       0.219167        -4.074432       19660.712839
HLA A*0202      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.502053       0.427495        -4.074557       31772.589947
HLA B*7301      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.576881       0.502118        -4.074763       37746.906527
HLA A*0206      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.412302       0.337522        -4.074780       25840.581991
HLA B*1517      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.435651       0.360868        -4.074784       27267.886192
HLA A*2301      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.491823       0.416603        -4.075220       31032.942744
HLA A*2501      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.503192       0.427495        -4.075697       31856.064211
HLA B*4601      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.407937       0.332159        -4.075778       25582.144496
HLA A*2601      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.402070       0.326268        -4.075802       25238.891903
HLA A*2602      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.604337       0.528496        -4.075841       40210.312419
HLA B*3901      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.458669       0.382667        -4.076003       28752.087225
HLA A*3301      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.637329       0.561253        -4.076076       43383.932510
HLA A*3201      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.604751       0.528496        -4.076255       40248.616518
HLA B*3501      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.196744       0.120389        -4.076355       15730.556621
HLA B*2705      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.365103       0.288570        -4.076534       23179.469199
HLA B*1509      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.469277       0.392663        -4.076614       29463.022815
HLA A*1101      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.438816       0.362044        -4.076772       27467.316323
HLA A*0203      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.324659       0.247860        -4.076800       21118.324152
HLA A*3301      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.564993       0.488141        -4.076852       36727.635661
HLA A*8001      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.439065       0.362044        -4.077021       27483.071924
HLA A*0216      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.443494       0.366173        -4.077321       27764.768304
HLA A*0211      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.528630       0.451113        -4.077517       33777.693626
HLA B*1502      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.574706       0.496962        -4.077744       37558.284086
HLA B*0802      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.451755       0.373896        -4.077859       28297.941401
HLA A*0201      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.388650       0.310721        -4.077929       24470.904674
HLA A*2402      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.573461       0.495365        -4.078096       37450.749662
HLA B*7301      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.566485       0.488141        -4.078344       36854.022322
HLA A*2603      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.566605       0.488141        -4.078464       36864.191909
HLA B*3801      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.575488       0.496962        -4.078526       37626.006057
HLA A*0201      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.338496       0.259962        -4.078534       21801.961526
HLA A*0101      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.383587       0.305034        -4.078553       24187.271807
HLA A*1101      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.367209       0.288570        -4.078639       23292.098880
HLA B*4402      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.381919       0.303280        -4.078639       24094.546176
HLA A*2402      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.575657       0.496962        -4.078695       37640.664694
HLA A*3001      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.293618       0.214819        -4.078799       19661.563755
HLA B*5101      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.506460       0.427495        -4.078965       32096.690296
HLA A*0250      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.576106       0.496962        -4.079144       37679.578473
HLA A*3002      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.313840       0.234317        -4.079523       20598.712366
HLA A*0202      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.339706       0.259962        -4.079744       21862.788512
HLA A*6802      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.314613       0.234317        -4.080296       20635.407704
HLA A*0211      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.507966       0.427495        -4.080471       32208.186447
HLA B*4403      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.641791       0.561253        -4.080538       43831.929393
HLA A*0206      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.338613       0.257963        -4.080650       21807.859633
HLA A*2501      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.495587       0.414917        -4.080669       31303.062989
HLA B*3801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.508246       0.427495        -4.080751       32228.928006
HLA A*0203      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.443435       0.362044        -4.081391       27761.013450
HLA A*0203      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.148039       0.066377        -4.081662       14061.746559
HLA B*1509      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.433377       0.351592        -4.081785       27125.463713
HLA A*3301      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.498472       0.416603        -4.081869       31511.712298
HLA B*5401      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.530371       0.448362        -4.082009       33913.370972
HLA B*2705      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.444168       0.362044        -4.082124       27807.910427
HLA A*0212      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.444568       0.362044        -4.082524       27833.496602
HLA A*2603      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.618098       0.535432        -4.082667       41504.805315
HLA A*1101      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.477519       0.394780        -4.082740       30027.508284
HLA A*0301      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.340810       0.257963        -4.082847       21918.448617
HLA B*2705      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.465553       0.382667        -4.082887       29211.467037
HLA B*4402      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.393889       0.310721        -4.083168       24767.910907
HLA B*4601      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.409443       0.326268        -4.083175       25671.010688
HLA A*2403      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.372046       0.288570        -4.083477       23552.999060
HLA B*4001      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.388603       0.305034        -4.083569       24468.257120
HLA B*0702      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.449979       0.366173        -4.083806       28182.442673
HLA B*4001      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.416019       0.332159        -4.083860       26062.686259
HLA B*0803      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.476568       0.392663        -4.083904       29961.789881
HLA B*3501      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.446377       0.362044        -4.084333       27949.682047
HLA B*4501      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.637428       0.553011        -4.084416       43393.791125
HLA A*3301      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.636246       0.551693        -4.084553       43275.869574
HLA A*3201      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.297262       0.212403        -4.084859       19827.232858
HLA B*0702      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.422527       0.337522        -4.085005       26456.186870
HLA A*6901      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.373606       0.288570        -4.085037       23637.757493
HLA B*0801      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.447148       0.362044        -4.085103       27999.321210
HLA B*2705      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.477827       0.392663        -4.085164       30048.796186
HLA B*5701      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.411471       0.326268        -4.085202       25791.142029
HLA B*3801      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.536480       0.451113        -4.085367       34393.757241
HLA A*2601      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.396253       0.310721        -4.085532       24903.073978
HLA A*2902      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.298026       0.212403        -4.085622       19862.124040
HLA B*5301      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.582602       0.496962        -4.085640       38247.439089
HLA B*4403      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.621094       0.535432        -4.085662       41792.078831
HLA A*0201      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.374264       0.288570        -4.085695       23673.590367
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HLA A*2602      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.574924       0.489218        -4.085706       37577.185153
HLA B*5301      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.502346       0.416603        -4.085743       31794.082987
HLA B*4501      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.500871       0.414917        -4.085953       31686.248722
HLA B*5101      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.459901       0.373896        -4.086005       28833.708757
HLA A*2601      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.389294       0.303280        -4.086014       24507.205029
HLA A*3001      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.265337       0.179262        -4.086076       18422.022352
HLA B*4402      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.437867       0.351592        -4.086275       27407.349443
HLA A*3101      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.320973       0.234317        -4.086656       20939.827986
HLA B*2705      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.392287       0.305034        -4.087253       24676.696973
HLA B*3901      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.345431       0.257963        -4.087468       22152.933746
HLA A*3002      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.482698       0.394780        -4.087918       30387.681121
HLA B*4402      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.449011       0.360868        -4.088143       28119.697502
HLA A*6801      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.649412       0.561253        -4.088160       44607.955330
HLA A*0250      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.536581       0.448362        -4.088218       34401.759027
HLA B*2705      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.348514       0.259962        -4.088552       22310.729613
HLA B*1509      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.415023       0.326268        -4.088755       26002.972363
HLA A*0216      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.420955       0.332159        -4.088797       26360.609281
HLA A*2603      1:51-59 9       VRETMAVVS       1.416891        -0.855638       -4.650307       0.561253        -4.089055       44699.994631
HLA B*1801      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.492951       0.403811        -4.089139       31113.632158
HLA A*1101      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.426688       0.337522        -4.089166       26710.879458
HLA B*0803      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.472038       0.382667        -4.089371       29650.904562
HLA A*0250      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -3.990492       -0.098967       -4.089459       9783.453831
HLA B*3901      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.493446       0.403811        -4.089635       31149.168231
HLA B*4501      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.618470       0.528496        -4.089973       41540.297232
HLA A*0219      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.456285       0.366173        -4.090112       28594.641103
HLA A*6901      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.393394       0.303280        -4.090114       24739.654799
HLA B*5101      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.494003       0.403811        -4.090192       31189.131556
HLA A*2402      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.535533       0.445146        -4.090387       34318.854157
HLA A*3301      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.625297       0.534755        -4.090543       42198.518407
HLA A*0202      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.442291       0.351592        -4.090699       27687.970102
HLA A*6801      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.642502       0.551693        -4.090809       43903.837454
HLA B*0702      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.417145       0.326268        -4.090876       26130.311041
HLA A*2402      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.580276       0.489218        -4.091058       38043.141404
HLA A*2402      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.578824       0.487485        -4.091339       37916.163713
HLA A*2301      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.539741       0.448362        -4.091378       34652.989483
HLA A*3101      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.270680       0.179262        -4.091418       18650.051431
HLA A*2301      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.536686       0.445146        -4.091541       34410.134983
HLA B*2705      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.465683       0.373896        -4.091787       29220.160024
HLA A*2602      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.350060       0.257963        -4.092097       22390.290798
HLA A*3001      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.283999       0.191859        -4.092140       19230.884711
HLA A*2301      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.543310       0.451113        -4.092197       34938.927896
HLA B*1801      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.279561       0.187363        -4.092198       19035.359668
HLA B*1801      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.443821       0.351592        -4.092229       27785.654556
HLA A*3301      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.587750       0.495365        -4.092385       38703.485989
HLA B*0802      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.487368       0.394780        -4.092589       30716.260109
HLA A*1101      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.444267       0.351592        -4.092675       27814.229529
HLA B*4402      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.430203       0.337522        -4.092681       26927.932934
HLA B*1503      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.496656       0.403811        -4.092845       31380.210375
HLA A*8001      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.459083       0.366173        -4.092910       28779.476289
HLA B*5401      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.353011       0.259962        -4.093049       22542.946858
HLA B*5101      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.485733       0.392663        -4.093070       30600.822166
HLA B*4002      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.646139       0.553011        -4.093128       44273.054356
HLA A*0202      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.544449       0.451113        -4.093336       35030.720894
HLA A*0201      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.396836       0.303280        -4.093556       24936.507673
HLA B*1517      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.327982       0.234317        -4.093664       21280.489991
HLA A*0250      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.497537       0.403811        -4.093726       31443.936291
HLA A*0211      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.538979       0.445146        -4.093834       34592.302783
HLA B*1517      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.486544       0.392663        -4.093880       30657.989232
HLA B*1502      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.595999       0.502118        -4.093881       39445.650747
HLA A*2602      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.542508       0.448362        -4.094146       34874.532948
HLA B*0801      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.382889       0.288570        -4.094319       24148.440425
HLA B*5301      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.596556       0.502118        -4.094438       39496.258177
HLA A*0101      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.405261       0.310721        -4.094539       25424.995470
HLA A*6802      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.240334       0.145735        -4.094599       17391.381643
HLA B*5101      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.460894       0.366173        -4.094721       28899.766883
HLA B*4001      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.405632       0.310721        -4.094911       25446.737093
HLA A*2402      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.543514       0.448362        -4.095152       34955.376135
HLA B*3901      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.400299       0.305034        -4.095265       25136.150725
HLA B*5801      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.329833       0.234317        -4.095516       21371.402205
HLA A*2402      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.597705       0.502118        -4.095587       39600.881318
HLA B*7301      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.591014       0.495365        -4.095649       38995.412431
HLA A*0206      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.540934       0.445146        -4.095788       34748.354632
HLA B*3901      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.469740       0.373896        -4.095844       29494.439716
HLA A*0211      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.469846       0.373896        -4.095950       29501.620864
HLA B*5701      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.406694       0.310721        -4.095973       25509.037372
HLA B*0802      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.462236       0.366173        -4.096063       28989.177639
HLA A*0201      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.407472       0.311316        -4.096156       25554.756647
HLA B*7301      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.513130       0.416603        -4.096527       32593.458022
HLA B*4601      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.408125       0.311316        -4.096809       25593.218617
HLA A*2402      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.511796       0.414917        -4.096878       32493.458008
HLA B*0801      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.355283       0.257963        -4.097320       22661.186199
HLA B*7301      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.546164       0.448362        -4.097802       35169.338420
HLA B*1509      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.492598       0.394780        -4.097819       31088.394205
HLA B*1503      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.409163       0.311316        -4.097848       25654.489605
HLA A*6801      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.593257       0.495365        -4.097892       39197.401384
HLA A*2501      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.458902       0.360868        -4.098034       28767.490364
HLA B*3501      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.409408       0.311316        -4.098092       25668.927612
HLA B*5701      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.386707       0.288570        -4.098137       24361.666923
HLA B*4801      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.435715       0.337522        -4.098192       27271.869422
HLA A*2601      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.387106       0.288570        -4.098537       24384.082195
HLA A*2603      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.650296       0.551693        -4.098603       44698.785538
HLA B*3801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.513701       0.414917        -4.098784       32636.333658
HLA B*1502      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.586834       0.487485        -4.099349       38621.913261
HLA B*4501      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.651325       0.551693        -4.099632       44804.826299
HLA B*1502      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.600012       0.500136        -4.099876       39811.821255
HLA A*3002      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.587384       0.487485        -4.099899       38670.836244
HLA A*2501      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.432087       0.332159        -4.099928       27045.019815
HLA A*0202      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.503789       0.403811        -4.099978       31899.868095
HLA A*3001      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.287716       0.187363        -4.100353       19396.177488
HLA A*3101      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.312820       0.212403        -4.100417       20550.405548
HLA A*0211      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.515339       0.414917        -4.100422       32759.627549
HLA B*2705      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.432794       0.332159        -4.100636       27089.095169
HLA B*4403      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.635492       0.534755        -4.100737       43200.783022
HLA B*3901      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.493820       0.392663        -4.101157       31175.973412
HLA A*6901      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.335533       0.234317        -4.101215       21653.737532
HLA A*2301      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.496167       0.394780        -4.101388       31344.919435
HLA A*0212      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.438997       0.337522        -4.101475       27478.760532
HLA B*5701      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.361506       0.259962        -4.101545       22988.277182
HLA B*4002      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.630447       0.528496        -4.101951       42701.907382
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HLA A*2602      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.597620       0.495365        -4.102255       39593.169559
HLA B*1501      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.314761       0.212403        -4.102358       20642.441924
HLA A*3001      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.224957       0.122444        -4.102513       16786.366703
HLA B*4801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.434860       0.332159        -4.102701       27218.218508
HLA A*2601      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.315301       0.212403        -4.102898       20668.142774
HLA B*4801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.413780       0.310721        -4.103059       25928.662623
HLA A*2601      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.322279       0.219167        -4.103112       21002.907681
HLA B*4403      1:187-195       9       GTAAVTPST       0.889490        -0.371275       -4.621374       0.518215        -4.103159       41818.992264
HLA B*4801      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.429613       0.326268        -4.103345       26891.392789
HLA B*1502      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.598734       0.495365        -4.103369       39694.828112
HLA B*1517      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.498467       0.394780        -4.103688       31511.371350
HLA B*4601      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.414887       0.310721        -4.104165       25994.814598
HLA B*5401      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.519378       0.414917        -4.104460       33065.699933
HLA A*2402      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.364436       0.259962        -4.104475       23143.883409
HLA A*0301      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.323652       0.219167        -4.104484       21069.368680
HLA B*1503      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.549825       0.445146        -4.104679       35467.019719
HLA A*0101      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.362705       0.257963        -4.104742       23051.790416
HLA B*4402      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.431046       0.326268        -4.104778       26980.281843
HLA B*4001      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.431072       0.326268        -4.104804       26981.887455
HLA B*1501      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.408536       0.303280        -4.105257       25617.459974
HLA B*4601      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.408804       0.303280        -4.105524       25633.263835
HLA A*0301      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.353553       0.247860        -4.105694       22571.136037
HLA B*0801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.416468       0.310721        -4.105747       26089.630459
HLA B*5401      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.488435       0.382667        -4.105768       30791.794720
HLA A*3301      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.457365       0.351592        -4.105773       28665.888884
HLA B*4001      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.394477       0.288570        -4.105907       24801.431483
HLA B*5101      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.488684       0.382667        -4.106017       30809.457284
HLA B*4601      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.394820       0.288570        -4.106250       24821.028479
HLA B*1517      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.411438       0.305034        -4.106404       25789.188722
HLA B*7301      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.606678       0.500136        -4.106542       40427.560386
HLA B*1509      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.534295       0.427495        -4.106799       34221.150050
HLA B*5701      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.418145       0.311316        -4.106830       26190.600735
HLA A*0250      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.594383       0.487485        -4.106898       39299.106776
HLA A*2501      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.499846       0.392663        -4.107183       31611.598072
HLA B*1801      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.500074       0.392663        -4.107411       31628.190904
HLA A*6802      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.418629       0.310721        -4.107908       26219.804784
HLA A*6802      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.434385       0.326268        -4.108117       27188.490750
HLA A*3301      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.597399       0.489218        -4.108181       39573.040380
HLA B*1503      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.482094       0.373896        -4.108198       30345.461223
HLA A*0216      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.470591       0.362044        -4.108546       29552.257629
HLA A*0212      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.435395       0.326268        -4.109127       27251.811662
HLA A*2501      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.420619       0.311316        -4.109304       26340.224227
HLA A*2902      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.357345       0.247860        -4.109486       22769.080213
HLA A*2501      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.504294       0.394780        -4.109514       31936.993253
HLA B*5101      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.504327       0.394780        -4.109547       31939.412203
HLA A*0203      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.435865       0.326268        -4.109597       27281.313475
HLA A*0202      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.558015       0.448362        -4.109653       36142.234644
HLA B*4801      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.421355       0.311316        -4.110039       26384.863789
HLA A*8001      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.436460       0.326268        -4.110192       27318.679027
HLA A*2603      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.612918       0.502462        -4.110456       41012.643848
HLA B*4402      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.399039       0.288570        -4.110470       25063.368988
HLA A*6802      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.011605       -0.098967       -4.110571       10270.809452
HLA A*0202      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.598057       0.487485        -4.110572       39633.029817
HLA B*3901      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.505375       0.394780        -4.110595       32016.568998
HLA A*8001      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.344971       0.234317        -4.110653       22129.456592
HLA B*5401      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.555844       0.445146        -4.110698       35962.019896
HLA B*4601      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.358758       0.247860        -4.110898       22843.230791
HLA A*2902      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.448442       0.337522        -4.110920       28082.907474
HLA A*1101      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.422342       0.311316        -4.111026       26444.882407
HLA A*0219      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.421853       0.310721        -4.111132       26415.141856
HLA A*3201      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.611367       0.500136        -4.111232       40866.468220
HLA B*0702      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.422734       0.311316        -4.111418       26468.784872
HLA B*5701      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.416538       0.305034        -4.111504       26093.865063
HLA B*0702      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.473605       0.362044        -4.111561       29758.090036
HLA B*4601      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.369570       0.257963        -4.111607       23419.081477
HLA A*1101      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.369814       0.257963        -4.111851       23432.261426
HLA A*3301      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.640418       0.528496        -4.111922       43693.666407
HLA A*0212      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.400576       0.288570        -4.112006       25152.201935
HLA A*3201      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.422823       0.310721        -4.112102       26474.226772
HLA A*2402      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.494905       0.382667        -4.112239       31253.991124
HLA A*2403      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.423824       0.311316        -4.112508       26535.309973
HLA B*4601      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.372805       0.259962        -4.112844       23594.191413
HLA A*0211      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.479039       0.366173        -4.112866       30132.794671
HLA A*0219      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.475073       0.362044        -4.113029       29858.877811
HLA A*0201      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.371614       0.257963        -4.113651       23529.565608
HLA A*2403      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.418792       0.305034        -4.113758       26229.594001
HLA B*1509      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.301242       0.187363        -4.113879       20009.771751
HLA A*0211      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.418937       0.305034        -4.113903       26238.393227
HLA B*1509      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.154425       0.040386        -4.114039       14270.039209
HLA A*2603      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.446238       0.332159        -4.114079       27940.762394
HLA A*3201      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.475341       0.360868        -4.114473       29877.298278
HLA A*3301      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.616614       0.502118        -4.114496       41363.140631
HLA B*3901      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.452037       0.337522        -4.114514       28316.318013
HLA B*5101      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.475445       0.360868        -4.114577       29884.410971
HLA B*1517      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.476871       0.362044        -4.114827       29982.706784
HLA B*5101      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.452558       0.337522        -4.115036       28350.346210
HLA A*0216      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.452695       0.337522        -4.115172       28359.243195
HLA A*3002      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.566365       0.451113        -4.115252       36843.855539
HLA B*0802      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.476164       0.360868        -4.115296       29933.923375
HLA A*8001      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.420396       0.305034        -4.115362       26326.690425
HLA A*2601      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.373674       0.257963        -4.115711       23641.466236
HLA A*0211      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.363586       0.247860        -4.115726       23098.603246
HLA A*0203      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.328329       0.212403        -4.115926       21297.535327
HLA B*0801      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.350283       0.234317        -4.115965       22401.801009
HLA A*3301      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.498683       0.382667        -4.116017       31527.058772
HLA A*0206      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.531095       0.414917        -4.116177       33969.926090
HLA B*5401      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.544021       0.427495        -4.116526       34996.246627
HLA B*3901      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.478008       0.360868        -4.117140       30061.315964
HLA A*0219      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.422525       0.305034        -4.117491       26456.043745
HLA A*0301      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.325061       0.207531        -4.117530       21137.869564
HLA B*0801      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.420932       0.303280        -4.117652       26359.183240
HLA B*1502      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.568804       0.451113        -4.117691       37051.332914
HLA A*0219      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.455249       0.337522        -4.117726       28526.502434
HLA B*4002      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.617913       0.500136        -4.117777       41487.070730
HLA A*2402      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.568989       0.451113        -4.117877       37067.171343
HLA B*3901      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.484072       0.366173        -4.117899       30484.003943
HLA B*5701      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.421599       0.303280        -4.118320       26399.712841
HLA B*4403      1:28-36 9       DIDRRVAAA       0.875321        -0.322310       -4.671413       0.553011        -4.118402       46925.930682
HLA A*3201      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.141696       0.023284        -4.118412       13857.843635
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HLA B*4001      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.378383       0.259962        -4.118421       23899.167650
HLA A*6901      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.184865       0.066377        -4.118488       15306.119303
HLA B*1503      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.484692       0.366173        -4.118519       30527.572630
HLA B*4403      1:108-116       9       LGVLTRPSP       0.601016        -0.049323       -4.670259       0.551693        -4.118566       46801.448819
HLA B*4002      1:54-62 9       TMAVVSAAT       0.831597        -0.329135       -4.621117       0.502462        -4.118655       41794.339797
HLA A*2301      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.533733       0.414917        -4.118816       34176.931945
HLA A*0203      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.430203       0.310721        -4.119482       26927.932934
HLA B*4001      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.377791       0.257963        -4.119828       23866.608303
HLA A*2902      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.446370       0.326268        -4.120102       27949.228436
HLA A*8001      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.457633       0.337522        -4.120111       28683.573375
HLA A*2501      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.486335       0.366173        -4.120162       30643.231573
HLA A*0101      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.368148       0.247860        -4.120289       23342.556524
HLA B*5101      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.380540       0.259962        -4.120578       24018.152778
HLA B*0803      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.515445       0.394780        -4.120665       32767.603688
HLA B*7301      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.609906       0.489218        -4.120688       40729.185659
HLA A*0212      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.378942       0.257963        -4.120979       23929.958928
HLA A*1101      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.447472       0.326268        -4.121204       28020.232320
HLA B*1503      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.516401       0.394780        -4.121621       32839.831701
HLA B*1801      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.459409       0.337522        -4.121887       28801.125862
HLA A*0101      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.356267       0.234317        -4.121950       22712.611559
HLA B*1517      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.460098       0.337522        -4.122575       28846.814657
HLA B*3501      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.454779       0.332159        -4.122620       28495.654083
HLA A*6801      1:29-37 9       IDRRVAAAP       0.654385        -0.118953       -4.658474       0.535432        -4.123043       45548.521128
HLA A*8001      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.434406       0.311316        -4.123090       27189.814563
HLA A*0219      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.411870       0.288570        -4.123300       25814.872567
HLA A*2902      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.330928       0.207531        -4.123397       21425.347658
HLA B*4501      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.625769       0.502118        -4.123651       42244.429515
HLA B*3501      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.428713       0.305034        -4.123679       26835.731842
HLA B*7301      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.551326       0.427495        -4.123831       35589.838504
HLA A*0203      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.427398       0.303280        -4.124118       26754.555001
HLA B*1502      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.612347       0.488141        -4.124206       40958.763924
HLA A*3001      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.299365       0.174997        -4.124368       19923.466146
HLA B*3801      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.569690       0.445146        -4.124544       37126.977265
HLA A*2603      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.621700       0.496962        -4.124738       41850.450910
HLA B*1501      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.332276       0.207531        -4.124746       21491.982690
HLA A*3201      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.457039       0.332159        -4.124880       28644.340967
HLA B*0803      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.476481       0.351592        -4.124889       29955.793153
HLA B*1502      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.476518       0.351592        -4.124926       29958.386185
HLA B*3501      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.413557       0.288570        -4.124987       25915.340284
HLA B*4403      1:203-211       9       GASTALAFT       0.843184        -0.343048       -4.625135       0.500136        -4.124999       42182.769385
HLA A*0250      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.576221       0.451113        -4.125108       37689.568072
HLA A*0216      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.359883       0.234317        -4.125565       22902.502060
HLA B*2705      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.437352       0.311316        -4.126037       27374.897383
HLA B*4402      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.437360       0.311316        -4.126044       27375.341672
HLA B*1502      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.437580       0.311316        -4.126265       27389.266383
HLA B*5401      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.487718       0.360868        -4.126851       30741.029653
HLA A*0211      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.415422       0.288570        -4.126853       26026.897807
HLA B*0702      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.459066       0.332159        -4.126908       28778.386453
HLA B*1517      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.438231       0.311316        -4.126915       27430.341043
HLA A*6802      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.432092       0.305034        -4.127058       27045.312438
HLA B*1509      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.531085       0.403811        -4.127274       33969.191004
HLA B*1503      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.465065       0.337522        -4.127542       29178.615118
HLA B*0801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.346733       0.219167        -4.127566       22219.427423
HLA B*0802      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.489718       0.362044        -4.127674       30882.881967
HLA B*0803      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.488543       0.360868        -4.127675       30799.458362
HLA A*2601      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.362176       0.234317        -4.127859       23023.748269
HLA A*3101      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.431272       0.303280        -4.127992       26994.297674
HLA B*5101      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.490148       0.362044        -4.128104       30913.471460
HLA A*0212      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.440212       0.311316        -4.128896       27555.723805
HLA B*1517      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.455420       0.326268        -4.129152       28537.770400
HLA A*2601      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.377105       0.247860        -4.129245       23828.936280
HLA B*5801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.336903       0.207531        -4.129372       21722.140483
HLA B*1509      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.440792       0.311316        -4.129476       27592.569550
HLA B*3801      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.546122       0.416603        -4.129519       35165.913867
HLA A*6802      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.432886       0.303280        -4.129607       27094.811183
HLA B*0802      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.462053       0.332159        -4.129894       28976.947617
HLA A*0212      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.377873       0.247860        -4.130013       23871.127781
HLA B*5801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.349468       0.219167        -4.130300       22359.787089
HLA A*6801      1:20-28 9       AVSDDERAD       1.108502        -0.606384       -4.632621       0.502118        -4.130503       42916.129576
HLA A*3201      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.534337       0.403811        -4.130526       34224.482600
HLA A*0211      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.525468       0.394780        -4.130688       33532.627563
HLA B*4601      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.365578       0.234317        -4.131261       23204.813513
HLA A*0201      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.379616       0.247860        -4.131757       23967.142355
HLA B*4001      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.366081       0.234317        -4.131763       23231.693660
HLA B*4501      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.559394       0.427495        -4.131899       36257.190533
HLA A*0211      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.514662       0.382667        -4.131996       32708.626216
HLA B*0802      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.469538       0.337522        -4.132016       29480.720606
HLA A*0211      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.469752       0.337522        -4.132229       29495.237535
HLA A*3001      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.224101       0.091860        -4.132242       16753.343521
HLA A*3002      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.577401       0.445146        -4.132255       37792.063170
HLA B*7301      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.583451       0.451113        -4.132338       38322.208176
HLA B*4403      1:180-188       9       PRSAGTMGT       0.969384        -0.440888       -4.660974       0.528496        -4.132478       45811.460003
HLA A*2403      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.436220       0.303280        -4.132940       27303.608501
HLA B*1517      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.199333       0.066377        -4.132956       15824.617549
HLA B*1801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.527787       0.394780        -4.133007       33712.155934
HLA B*3901      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.444347       0.311316        -4.133031       27819.346044
HLA B*2705      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.391002       0.257963        -4.133039       24603.781400
HLA B*4501      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.628629       0.495365        -4.133264       42523.477467
HLA B*1801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.507167       0.373896        -4.133272       32148.998374
HLA A*2601      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.340803       0.207531        -4.133272       21918.092891
HLA A*0206      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.525945       0.392663        -4.133281       33569.473574
HLA A*0216      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.459647       0.326268        -4.133379       28816.867063
HLA B*4501      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.621014       0.487485        -4.133529       41784.392460
HLA B*4001      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.381865       0.247860        -4.134005       24091.548340
HLA B*0801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.341580       0.207531        -4.134050       21957.376196
HLA A*3201      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.349214       0.214819        -4.134395       22346.726796
HLA A*3201      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.582819       0.448362        -4.134456       38266.479952
HLA A*0301      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.347236       0.212403        -4.134832       22245.166112
HLA A*6801      1:135-143       9       RPLGAGTAT       0.836354        -0.301599       -4.669806       0.534755        -4.135051       46752.608525
HLA B*5401      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.538893       0.403811        -4.135081       34585.379277
HLA B*3901      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.486969       0.351592        -4.135377       30688.023929
HLA A*3201      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.623209       0.487485        -4.135724       41996.056463
HLA B*7301      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.487526       0.351592        -4.135934       30727.395621
HLA B*2705      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.473478       0.337522        -4.135956       29749.397956
HLA B*3901      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.462779       0.326268        -4.136510       29025.427607
HLA B*4402      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.442120       0.305034        -4.137086       27677.037675
HLA A*2603      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.520374       0.382667        -4.137707       33141.632857
HLA B*3901      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.499776       0.362044        -4.137732       31606.468031
HLA A*0212      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.441076       0.303280        -4.137797       27610.637464
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HLA A*6801	1:180-188	9	PRSAGTMGT	0.969384	-0.440888	-4.666324	0.528496	-4.137828	46379.270169
HLA B*4002	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.633215	0.495365	-4.137850	42974.909183
HLA A*0219	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-4.464172	0.326268	-4.137904	29118.692564
HLA A*2602	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.565674	0.427495	-4.138179	36785.301692
HLA B*1801	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.500337	0.362044	-4.138293	31647.360471
HLA A*3001	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.259081	0.120389	-4.138691	18158.527428
HLA A*3101	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.326638	0.187363	-4.139275	21214.740221
HLA B*1801	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.500427	0.360868	-4.139559	31653.867071
HLA A*8001	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.428133	0.288570	-4.139564	26799.896741
HLA A*3101	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.358734	0.219167	-4.139567	22841.995031
HLA B*4801	1:128-136	9	PDVRTVSRP	0.500795	-0.197515	-4.442930	0.303280	-4.139651	27728.742660
HLA A*2501	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.502029	0.362044	-4.139985	31770.871132
HLA B*1801	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.374379	0.234317	-4.140062	23679.866702
HLA B*5401	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.532725	0.392663	-4.140062	34097.704643
HLA B*5801	1:114-122	9	PSPPPTVAE	1.033102	-0.818283	-4.355283	0.214819	-4.140463	22661.186199
HLA A*2603	1:203-211	9	GASTALAFT	0.843184	-0.343048	-4.641241	0.500136	-4.141105	43776.477043
HLA B*1801	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.452814	0.311316	-4.141499	28367.068713
HLA B*4501	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.638497	0.496962	-4.141535	43500.736492
HLA A*0250	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.586817	0.445146	-4.141671	38620.450707
HLA A*2603	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.644048	0.502118	-4.141930	44060.400748
HLA B*4402	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.400226	0.257963	-4.142263	25131.935581
HLA A*3201	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.165256	0.022933	-4.142323	14630.403107
HLA A*2403	1:195-203	9	TTATLTDLG	0.805893	-0.593490	-4.354733	0.212403	-4.142329	22632.517235
HLA A*0202	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.535103	0.392663	-4.142440	34284.894971
HLA A*8001	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.453435	0.310721	-4.142713	28407.611810
HLA A*0301	1:114-122	9	PSPPPTVAE	1.033102	-0.818283	-4.357637	0.214819	-4.142817	22784.359435
HLA B*4002	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.645174	0.502118	-4.143056	44174.724152
HLA B*4002	1:143-151	9	TVVFSRDRN	0.914767	-0.417805	-4.640146	0.496962	-4.143184	43666.255173
HLA A*2902	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.431876	0.288570	-4.143306	27031.855070
HLA A*6801	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.631655	0.487485	-4.144170	42820.813093
HLA B*3501	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.454927	0.310721	-4.144205	28505.367713
HLA A*3201	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.589352	0.445146	-4.144207	38846.547973
HLA A*2403	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.351845	0.207531	-4.144315	22482.538340
HLA B*3501	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-4.470628	0.326268	-4.144360	29554.815731
HLA A*2603	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.632743	0.487485	-4.145258	42928.204192
HLA A*3301	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.632855	0.487485	-4.145371	42939.353007
HLA B*0803	1:96-104	9	AAAIAVGLG	0.855432	-0.489259	-4.511566	0.366173	-4.145393	32476.235546
HLA B*1503	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.405407	0.259962	-4.145445	25433.524778
HLA B*0803	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.507705	0.362044	-4.145661	32188.851311
HLA A*0211	1:145-153	9	VFSRDRNTG	0.879698	-0.487035	-4.538599	0.392663	-4.145936	34561.999299
HLA B*5301	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.591591	0.445146	-4.146446	39047.343350
HLA B*1801	1:96-104	9	AAAIAVGLG	0.855432	-0.489259	-4.512792	0.366173	-4.146619	32568.076822
HLA A*0202	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.508796	0.362044	-4.146751	32269.752894
HLA A*1101	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.457523	0.310721	-4.146801	28676.281079
HLA B*4501	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.635017	0.488141	-4.146876	43153.599095
HLA B*4801	1:139-147	9	AGTATVVFS	1.346924	-1.058354	-4.435724	0.288570	-4.147155	27272.459579
HLA B*0803	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.458895	0.311316	-4.147579	28767.023481
HLA B*4002	1:118-126	9	PTVAEQVLT	1.042362	-0.554221	-4.635792	0.488141	-4.147651	43230.708447
HLA B*4002	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.575298	0.427495	-4.147802	37609.521915
HLA A*2902	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.267936	0.119790	-4.148145	18532.577943
HLA B*4501	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.530815	0.382667	-4.148148	33948.064078
HLA B*1502	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.575878	0.427495	-4.148383	37659.810953
HLA B*0801	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-4.396533	0.247860	-4.148673	24919.111161
HLA A*3002	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.564079	0.414917	-4.149162	36650.425574
HLA A*0201	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.383570	0.234317	-4.149253	24186.355871
HLA A*2603	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.594651	0.445146	-4.149505	39323.351085
HLA A*2602	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.600945	0.451113	-4.149832	39897.418025
HLA B*0702	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.460601	0.310721	-4.149879	28880.230423
HLA B*0803	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.523863	0.373896	-4.149967	33408.954661
HLA A*3301	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.578206	0.427495	-4.150711	37862.254923
HLA A*3001	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.210625	0.059757	-4.150867	16241.451802
HLA A*2603	1:155-163	9	LVMNNVAPP	0.261618	0.154985	-4.567648	0.416603	-4.151045	36952.845789
HLA A*2301	1:205-213	9	STALAFTVE	0.973168	-0.590501	-4.533761	0.382667	-4.151095	34179.150738
HLA A*2603	1:120-128	9	VAEQVLTAP	0.460145	0.035220	-4.646971	0.495365	-4.151606	44357.922956
HLA A*1101	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.370839	0.219167	-4.151671	23487.596609
HLA B*4403	1:54-62	9	TMAVVSAAT	0.831597	-0.329135	-4.654722	0.502462	-4.152260	45156.695490
HLA A*0250	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.526248	0.373896	-4.152352	33592.909071
HLA A*2501	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.386827	0.234317	-4.152509	24368.389340
HLA A*6901	1:114-122	9	PSPPPTVAE	1.033102	-0.818283	-4.367836	0.214819	-4.153017	23325.767239
HLA B*2705	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-4.400903	0.247860	-4.153043	25171.122865
HLA A*0250	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.490639	0.337522	-4.153116	30948.444064
HLA B*4403	1:20-28	9	AVSDDERAD	1.108502	-0.606384	-4.655298	0.502118	-4.153180	45216.586887
HLA A*3301	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.413251	0.259962	-4.153290	25897.120806
HLA B*5301	1:212-220	9	VEPGTGSPQ	0.529704	-0.081342	-4.601748	0.448362	-4.153386	39971.303843
HLA B*1502	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.598645	0.445146	-4.153499	39686.668655
HLA A*3002	1:11-19	9	ELATPYALN	0.932404	-0.621088	-4.464818	0.311316	-4.153502	29162.045252
HLA B*1503	1:215-223	9	GTGSPQPTG	1.137233	-0.826512	-4.464766	0.310721	-4.154045	29158.574663
HLA A*0219	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.412044	0.257963	-4.154081	25825.209150
HLA B*3501	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.373684	0.219167	-4.154517	23641.977832
HLA B*3901	1:151-159	9	NTGLLVMNN	0.907671	-0.575512	-4.486739	0.332159	-4.154580	30671.758398
HLA A*3301	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.492258	0.337522	-4.154735	31064.016976
HLA B*4001	1:128-136	9	PDVRTVSRP	0.500795	-0.197515	-4.458409	0.303280	-4.155129	28734.826846
HLA A*0206	1:222-230	9	TGTILAELP	0.521964	-0.159920	-4.518039	0.362044	-4.155994	32963.894370
HLA B*1503	1:128-136	9	PDVRTVSRP	0.500795	-0.197515	-4.459280	0.303280	-4.156001	28792.557538
HLA B*4002	1:213-221	9	EPGTGSPQP	0.714790	-0.227305	-4.643623	0.487485	-4.156138	44017.278363
HLA B*1503	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.390685	0.234317	-4.156367	24585.818956
HLA A*0250	1:87-95	9	RWRTAAFAS	1.146634	-0.719139	-4.583904	0.427495	-4.156409	38362.241620
HLA A*0206	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.551199	0.394780	-4.156420	35579.443021
HLA B*7301	1:110-118	9	VLTRPSPPP	0.309978	0.050890	-4.517317	0.360868	-4.156449	32909.192186
HLA A*0219	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-4.404333	0.247860	-4.156473	25370.722648
HLA B*4801	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.414544	0.257963	-4.156581	25974.290860
HLA A*0202	1:68-76	9	AHLRTAILD	1.193151	-0.778234	-4.571717	0.414917	-4.156800	37300.718519
HLA A*2403	1:99-107	9	IAVGLGAFG	0.719922	-0.472062	-4.404770	0.247860	-4.156910	25396.264517
HLA B*0801	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.336252	0.179262	-4.156990	21689.613380
HLA B*4002	1:211-219	9	TVEPGTGSP	0.502550	-0.013332	-4.646332	0.489218	-4.157114	44292.698723
HLA B*0702	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.415138	0.257963	-4.157175	26009.866264
HLA A*0216	1:94-102	9	ASAAAIAVG	0.821433	-0.563470	-4.415169	0.257963	-4.157206	26011.695564
HLA B*5401	1:126-134	9	TAPDVRTVS	1.285972	-0.948450	-4.494873	0.337522	-4.157350	31251.624084
HLA A*2602	1:6-14	9	DFELLELAT	0.874861	-0.429715	-4.602528	0.445146	-4.157382	40043.160140
HLA A*3101	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.365042	0.207531	-4.157512	23176.209071
HLA A*3002	1:216-224	9	TGSPQPTGT	0.820922	-0.447026	-4.531557	0.373896	-4.157662	34006.148775
HLA B*4801	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.417817	0.259962	-4.157855	26170.771890
HLA A*3201	1:192-200	9	TPSTTATLT	0.881040	-0.429927	-4.609020	0.451113	-4.157907	40646.201989
HLA A*3002	1:130-138	9	VRTVSRPLG	0.891121	-0.564853	-4.484530	0.326268	-4.158262	30516.179352
HLA B*4402	1:167-175	9	TVYQMWLLG	0.746394	-0.486432	-4.418364	0.259962	-4.158402	26203.781057
HLA A*3201	1:156-164	9	VMNNVAPPS	0.722767	-0.916838	-3.964488	-0.194071	-4.158559	9214.846387
HLA A*3001	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.304642	0.145735	-4.158907	20167.025132
HLA B*0702	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.135300	-0.023878	-4.159178	13655.272101
HLA A*0202	1:209-217	9	AFTVEPGTG	0.859209	-0.464429	-4.554028	0.394780	-4.159248	35811.946339
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HLA A*0201      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.372617       0.212403        -4.160214       23583.982265
HLA A*0101      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.379579       0.219167        -4.160411       23965.067891
HLA B*1501      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.375622       0.214819        -4.160803       23747.731550
HLA B*3501      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.373298       0.212403        -4.160895       23621.011456
HLA B*0702      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.449485       0.288570        -4.160916       28150.443436
HLA A*6801      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.527206       0.366173        -4.161033       33667.138398
HLA A*0219      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.464651       0.303280        -4.161372       29150.846199
HLA B*4501      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.650629       0.489218        -4.161411       44733.136528
HLA B*0802      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.487815       0.326268        -4.161547       30747.848937
HLA A*1101      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.369215       0.207531        -4.161684       23399.958399
HLA A*2403      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.421721       0.259962        -4.161760       26407.140501
HLA A*2301      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.513464       0.351592        -4.161872       32618.506075
HLA B*1503      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.377025       0.214819        -4.162205       23824.553679
HLA A*3201      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.577490       0.414917        -4.162572       37799.833102
HLA B*5701      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.396892       0.234317        -4.162575       24939.745573
HLA A*2902      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.466434       0.303280        -4.163155       29270.788739
HLA B*5401      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.558149       0.394780        -4.163369       36153.381315
HLA B*1502      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.537351       0.373896        -4.163456       34462.857201
HLA B*1801      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.423474       0.259962        -4.163513       26513.929182
HLA B*3801      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.567425       0.403811        -4.163613       36933.859142
HLA B*4403      1:118-126       9       PTVAEQVLT       1.042362        -0.554221       -4.651811       0.488141        -4.163670       44855.028956
HLA A*0206      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.475036       0.311316        -4.163720       29856.293392
HLA B*0803      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.490639       0.326268        -4.164371       30948.444064
HLA A*2301      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.538735       0.373896        -4.164839       34572.845643
HLA A*8001      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.468128       0.303280        -4.164849       29385.183286
HLA A*0216      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.413125       0.247860        -4.165265       25889.556481
HLA B*5101      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.491691       0.326268        -4.165423       31023.542621
HLA B*5101      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.497737       0.332159        -4.165578       31458.398814
HLA A*0211      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.498051       0.332159        -4.165893       31481.212066
HLA B*1517      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.378467       0.212403        -4.166064       23903.822610
HLA B*3901      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.454917       0.288570        -4.166348       28504.750876
HLA A*2501      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.492784       0.326268        -4.166516       31101.683641
HLA B*4501      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.617643       0.451113        -4.166530       41461.268105
HLA B*4403      1:143-151       9       TVVFSRDRN       0.914767        -0.417805       -4.663554       0.496962        -4.166592       46084.392560
HLA B*5801      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.345936       0.179262        -4.166675       22178.715394
HLA A*3301      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.559342       0.392663        -4.166679       36252.875547
HLA B*4403      1:120-128       9       VAEQVLTAP       0.460145        0.035220        -4.662128       0.495365        -4.166763       45933.308707
HLA A*2501      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.471819       0.305034        -4.166785       29635.990360
HLA B*3801      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.559500       0.392663        -4.166837       36266.018240
HLA B*1503      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.499073       0.332159        -4.166915       31555.384099
HLA A*0101      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.374466       0.207531        -4.166935       23684.607079
HLA A*3301      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.618129       0.451113        -4.167016       41507.724391
HLA B*4501      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.612187       0.445146        -4.167041       40943.699094
HLA B*5801      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.359049       0.191859        -4.167190       22858.559771
HLA A*0219      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.374924       0.207531        -4.167394       23709.605826
HLA A*0212      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.401835       0.234317        -4.167518       25225.241635
HLA B*5801      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.354996       0.187363        -4.167633       22646.234604
HLA B*5701      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.380053       0.212403        -4.167650       23991.271175
HLA B*1509      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.529873       0.362044        -4.167829       33874.498142
HLA A*0301      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.355210       0.187363        -4.167847       22657.386088
HLA B*0801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.298444       0.130576        -4.167868       19881.259688
HLA B*1501      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.355306       0.187363        -4.167943       22662.412177
HLA A*0301      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.360242       0.191859        -4.168384       22921.466607
HLA A*2301      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.428455       0.259962        -4.168493       26819.766976
HLA B*0803      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.473807       0.305034        -4.168773       29771.938223
HLA B*7301      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.572601       0.403811        -4.168789       37376.669815
HLA B*5101      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.480115       0.311316        -4.168800       30207.548148
HLA B*0802      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.480247       0.311316        -4.168931       30216.701026
HLA B*4601      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.388171       0.219167        -4.169004       24443.913055
HLA B*1503      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.416879       0.247860        -4.169019       26114.342006
HLA A*2403      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.384005       0.214819        -4.169186       24210.574407
HLA B*1509      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.530284       0.360868        -4.169416       33906.583351
HLA B*0702      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.472773       0.303280        -4.169494       29701.154831
HLA B*4501      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.427583       0.257963        -4.169620       26765.991840
HLA A*2301      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.532312       0.362044        -4.170267       34065.254289
HLA B*5301      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.585375       0.414917        -4.170457       38492.379063
HLA A*0250      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.585445       0.414917        -4.170528       38498.626755
HLA A*0250      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.378150       0.207531        -4.170619       23886.371184
HLA A*6802      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.385530       0.214819        -4.170711       24295.727571
HLA A*3201      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.522505       0.351592        -4.170913       33304.650828
HLA A*6801      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.616061       0.445146        -4.170916       41310.588092
HLA B*4801      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.418813       0.247860        -4.170953       26230.871125
HLA A*6802      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.378543       0.207531        -4.171012       23907.961113
HLA A*1101      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.474839       0.303280        -4.171559       29842.728858
HLA B*0702      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.431608       0.259962        -4.171646       27015.188925
HLA B*5101      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.419522       0.247860        -4.171663       26273.761796
HLA B*7301      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.564601       0.392663        -4.171937       36694.469009
HLA B*4801      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.406546       0.234317        -4.172229       25500.344787
HLA B*0802      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.477345       0.305034        -4.172311       30015.489724
HLA B*3801      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.523999       0.351592        -4.172407       33419.439152
HLA A*6901      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.351871       0.179262        -4.172609       22483.876288
HLA A*0301      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.351906       0.179262        -4.172645       22485.700891
HLA B*0802      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.483407       0.310721        -4.172686       30437.368683
HLA B*7301      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.617859       0.445146        -4.172713       41481.908921
HLA A*0202      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -3.978787       -0.194071       -4.172858       9523.291230
HLA B*7301      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.555755       0.382667        -4.173088       35954.627735
HLA B*1517      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.476500       0.303280        -4.173220       29957.089641
HLA A*2501      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.433542       0.259962        -4.173580       27135.737861
HLA B*0702      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.304264       0.130576        -4.173688       20149.467459
HLA A*2403      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.408014       0.234317        -4.173697       25586.711990
HLA B*1503      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.535770       0.362044        -4.173726       34337.611062
HLA B*3501      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.477031       0.303280        -4.173751       29993.738625
HLA A*2602      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.577906       0.403811        -4.174094       37836.045682
HLA A*2601      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.389026       0.214819        -4.174207       24492.095425
HLA B*1502      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.569260       0.394780        -4.174480       37090.239386
HLA B*3901      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.434639       0.259962        -4.174677       27204.380758
HLA B*4403      1:213-221       9       EPGTGSPQP       0.714790        -0.227305       -4.662520       0.487485        -4.175035       45974.825975
HLA A*6901      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.321243       0.145735        -4.175508       20952.859486
HLA B*4002      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.620659       0.445146        -4.175513       41750.273010
HLA A*0211      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.433525       0.257963        -4.175562       27134.710271
HLA A*3002      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.464677       0.288570        -4.176107       29152.580982
HLA A*2402      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.537140       0.360868        -4.176272       34446.081664
HLA A*0212      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.395579       0.219167        -4.176411       24864.438516
HLA B*1509      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.508601       0.332159        -4.176442       32255.266357
HLA A*3301      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.624809       0.448362        -4.176446       42151.060938
HLA B*3801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.571292       0.394780        -4.176512       37264.211907
HLA A*0201      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.395785       0.219167        -4.176618       24876.278553
HLA B*0803      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.508876       0.332159        -4.176717       32275.689017
HLA A*0212      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.384346       0.207531        -4.176815       24229.573454
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HLA A*0101      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.391859       0.214819        -4.177040       24652.412259
HLA A*2402      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.488510       0.311316        -4.177194       30797.125747
HLA A*2501      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.488012       0.310721        -4.177291       30761.824879
HLA B*3801      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.538251       0.360868        -4.177383       34534.337840
HLA B*1509      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.488177       0.310721        -4.177455       30773.476349
HLA B*0802      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.466301       0.288570        -4.177731       29261.764083
HLA B*5301      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.605688       0.427495        -4.178193       40335.588832
HLA B*4601      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.393161       0.214819        -4.178342       24726.408306
HLA A*0206      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.397592       0.219167        -4.178425       24979.984535
HLA A*3201      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.571120       0.392663        -4.178457       37249.498359
HLA B*4001      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.391206       0.212403        -4.178803       24615.364150
HLA A*2301      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.539872       0.360868        -4.179004       34663.489328
HLA B*5101      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.484056       0.305034        -4.179022       30482.849559
HLA B*2705      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.489842       0.310721        -4.179121       30891.738104
HLA A*0202      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.516805       0.337522        -4.179283       32870.403416
HLA B*1503      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.366701       0.187363        -4.179338       23264.897119
HLA A*2402      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.530951       0.351592        -4.179359       33958.717754
HLA B*4002      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.531362       0.351592        -4.179770       33990.882735
HLA A*0250      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.572648       0.392663        -4.179984       37380.714106
HLA A*2301      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.546237       0.366173        -4.180064       35175.237044
HLA A*0219      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.415049       0.234317        -4.180731       26004.519814
HLA B*0802      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.439110       0.257963        -4.181147       27485.896996
HLA B*4001      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.400679       0.219167        -4.181512       25158.189755
HLA B*5301      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.555503       0.373896        -4.181608       35933.821129
HLA B*3901      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.492657       0.310721        -4.181936       31092.599108
HLA B*0702      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.401112       0.219167        -4.181945       25183.245179
HLA B*5401      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.544158       0.362044        -4.182114       35007.229247
HLA A*0201      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.397056       0.214819        -4.182237       24949.191850
HLA A*0211      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.544350       0.362044        -4.182306       35022.762281
HLA A*8001      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.394745       0.212403        -4.182341       24816.731922
HLA B*5801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.357376       0.174997        -4.182379       22770.681586
HLA A*0101      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.369814       0.187363        -4.182451       23432.261426
HLA B*4402      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.430320       0.247860        -4.182461       26935.217776
HLA A*0219      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.442991       0.259962        -4.183030       27732.643180
HLA B*4601      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.395905       0.212403        -4.183502       24883.142974
HLA A*2501      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.441563       0.257963        -4.183600       27641.574474
HLA A*2602      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.396159       0.212403        -4.183756       24897.685646
HLA A*2603      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.612018       0.427495        -4.184523       40927.754137
HLA A*6801      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.536550       0.351592        -4.184958       34399.339686
HLA B*5101      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.495756       0.310721        -4.185035       31315.258283
HLA A*3101      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.399913       0.214819        -4.185094       25113.859274
HLA B*4002      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.636243       0.451113        -4.185131       43275.635457
HLA B*7301      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.495937       0.310721        -4.185215       31328.305730
HLA B*1801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.490263       0.305034        -4.185229       30921.667230
HLA B*3801      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.568050       0.382667        -4.185383       36987.046352
HLA A*8001      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.433466       0.247860        -4.185607       27131.040625
HLA B*3801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.559514       0.373896        -4.185618       36267.195429
HLA A*0250      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.568710       0.382667        -4.186043       37043.316037
HLA B*3501      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.400865       0.214819        -4.186046       25168.944192
HLA A*3201      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.581031       0.394780        -4.186251       38109.263546
HLA B*0803      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.523870       0.337522        -4.186347       33409.496881
HLA B*5101      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.489690       0.303280        -4.186410       30880.877157
HLA B*0802      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.489859       0.303280        -4.186579       30892.907972
HLA B*5301      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.552959       0.366173        -4.186786       35723.903652
HLA A*0203      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.374212       0.187363        -4.186849       23670.772962
HLA A*3002      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.524676       0.337522        -4.187153       33471.548829
HLA A*3101      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.317961       0.130576        -4.187385       20795.102722
HLA B*4402      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.421775       0.234317        -4.187458       26410.426478
HLA B*5401      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.561598       0.373896        -4.187702       36441.644384
HLA B*4403      1:211-219       9       TVEPGTGSP       0.502550        -0.013332       -4.677019       0.489218        -4.187801       47535.576573
HLA A*0206      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.520419       0.332159        -4.188260       33145.039591
HLA A*2402      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.554634       0.366173        -4.188461       35861.965812
HLA B*1509      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.554893       0.366173        -4.188719       35883.313182
HLA B*1509      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.527110       0.337522        -4.189587       33659.671672
HLA A*2601      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.369335       0.179262        -4.190073       23406.415440
HLA B*5301      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.594204       0.403811        -4.190393       39282.952207
HLA A*2902      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.405263       0.214819        -4.190444       25425.133017
HLA B*5301      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.583476       0.392663        -4.190813       38324.488752
HLA A*0250      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.586145       0.394780        -4.191366       38560.742256
HLA B*5301      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.167690       -0.023878       -4.191568       14712.631540
HLA B*4002      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.607014       0.414917        -4.192096       40458.847819
HLA A*6801      1:212-220       9       VEPGTGSPQ       0.529704        -0.081342       -4.640489       0.448362        -4.192127       43700.758319
HLA A*2902      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.450235       0.257963        -4.192272       28199.066138
HLA B*1502      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.585126       0.392663        -4.192462       38470.312004
HLA A*0301      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.367547       0.174997        -4.192550       23310.251055
HLA A*2602      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.525392       0.332159        -4.193233       33526.823016
HLA B*1501      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.216771       0.022933        -4.193838       16472.939387
HLA A*0206      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.520144       0.326268        -4.193875       33124.066844
HLA A*0212      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.453874       0.259962        -4.193913       28436.364891
HLA A*2403      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.413125       0.219167        -4.193957       25889.556481
HLA B*2705      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.497636       0.303280        -4.194356       31451.081648
HLA A*0212      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.406772       0.212403        -4.194368       25513.591814
HLA B*4801      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.409215       0.214819        -4.194396       25657.543121
HLA A*0216      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.497913       0.303280        -4.194633       31471.165387
HLA A*0101      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.373949       0.179262        -4.194688       23656.435005
HLA B*1502      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.609734       0.414917        -4.194817       40713.103987
HLA B*1502      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.382342       0.187363        -4.194979       24118.020392
HLA B*4601      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.402564       0.207531        -4.195033       25267.581515
HLA A*2902      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.414269       0.219167        -4.195102       25957.855452
HLA A*2603      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.646396       0.451113        -4.195283       44299.168897
HLA B*5301      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.590351       0.394780        -4.195571       38935.966825
HLA B*0803      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.455939       0.259962        -4.195978       28571.910149
HLA B*5701      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.415171       0.219167        -4.196004       26011.836285
HLA B*5701      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.403536       0.207531        -4.196006       25324.236589
HLA A*2301      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.534276       0.337522        -4.196753       34219.669021
HLA B*5401      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.376278       0.179262        -4.197016       23783.602468
HLA B*7301      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -3.683255       -0.513782       -4.197037       4822.305778
HLA A*0202      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.502212       0.305034        -4.197178       31784.280358
HLA A*8001      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.455296       0.257963        -4.197332       28529.589106
HLA A*2301      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.523912       0.326268        -4.197644       33412.750390
HLA A*6801      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.559812       0.362044        -4.197768       36292.121583
HLA B*4501      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.486605       0.288570        -4.198035       30662.301800
HLA A*6901      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.389973       0.191859        -4.198114       24545.550983
HLA A*2403      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.377525       0.179262        -4.198263       23852.022687
HLA B*4001      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.413233       0.214819        -4.198413       25896.000026
HLA B*1502      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.503624       0.305034        -4.198590       31887.790150
HLA B*0802      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.458942       0.259962        -4.198980       28770.136178
HLA B*4403      1:192-200       9       TPSTTATLT       0.881040        -0.429927       -4.650098       0.451113        -4.198985       44678.477652
HLA B*3901      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.502384       0.303280        -4.199104       31796.835146
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HLA A*2602      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.560386       0.360868        -4.199518       36340.059285
HLA B*4601      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.387008       0.187363        -4.199645       24378.542387
HLA A*3201      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.460192       0.259962        -4.200230       28853.057655
HLA B*0801      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.412638       0.212403        -4.200235       25860.580365
HLA A*0203      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.223575       0.023284        -4.200292       16733.053862
HLA A*0201      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.387663       0.187363        -4.200300       24415.366144
HLA B*3801      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.563626       0.362044        -4.201581       36612.178520
HLA B*1801      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.490237       0.288570        -4.201667       30919.827174
HLA B*1502      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.605646       0.403811        -4.201835       40331.661224
HLA B*5101      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.490601       0.288570        -4.202032       30945.765338
HLA B*4501      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.568235       0.366173        -4.202062       37002.857300
HLA A*2402      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.534238       0.332159        -4.202079       34216.707156
HLA A*2603      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.513476       0.311316        -4.202160       32619.388399
HLA B*3501      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.381454       0.179262        -4.202192       24068.750927
HLA B*5701      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.381653       0.179262        -4.202392       24079.821260
HLA A*0212      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.389855       0.187363        -4.202492       24538.912445
HLA B*4402      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.377582       0.174997        -4.202584       23855.119772
HLA B*4001      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.410221       0.207531        -4.202690       25717.020263
HLA A*3301      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.450705       0.247860        -4.202845       28229.593414
HLA B*3901      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.437230       0.234317        -4.202913       27367.197518
HLA B*1509      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.461040       0.257963        -4.203077       28909.461870
HLA B*4402      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.418232       0.214819        -4.203413       26195.843725
HLA B*4501      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.607272       0.403811        -4.203461       40482.931551
HLA B*4801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.411010       0.207531        -4.203479       25763.809188
HLA A*2301      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.535742       0.332159        -4.203583       34335.381982
HLA A*2601      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.391211       0.187363        -4.203848       24615.630484
HLA A*6901      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.378895       0.174997        -4.203898       23927.369900
HLA A*2602      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.596605       0.392663        -4.203942       39500.745510
HLA B*1517      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.391324       0.187363        -4.203961       24622.023370
HLA B*4002      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.620605       0.416603        -4.204002       41745.078453
HLA B*1501      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.349799       0.145735        -4.204064       22376.849516
HLA B*1502      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.587048       0.382667        -4.204381       38640.931506
HLA B*7301      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.536562       0.332159        -4.204403       34400.270182
HLA B*0801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.379710       0.174997        -4.204713       23972.329299
HLA B*4601      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.384693       0.179262        -4.205432       24248.980959
HLA B*5701      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.420260       0.214819        -4.205441       26318.431101
HLA B*1502      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.465464       0.259962        -4.205503       29205.462484
HLA B*7301      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.600630       0.394780        -4.205850       39868.505864
HLA A*0250      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.572032       0.366173        -4.205859       37327.768551
HLA A*0201      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.397790       0.191859        -4.205931       24991.338786
HLA B*5801      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.351688       0.145735        -4.205953       22474.390738
HLA B*1509      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.511432       0.305034        -4.206398       32466.222598
HLA A*2501      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.425734       0.219167        -4.206567       26652.275664
HLA B*7301      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.544308       0.337522        -4.206786       35019.352000
HLA A*2501      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.510194       0.303280        -4.206914       32373.792843
HLA B*5301      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.569102       0.362044        -4.207058       37076.797998
HLA B*0802      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.454992       0.247860        -4.207133       28509.685944
HLA A*2602      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.622454       0.414917        -4.207537       41923.190473
HLA B*4403      1:6-14  9       DFELLELAT       0.874861        -0.429715       -4.653204       0.445146        -4.208059       44999.157835
HLA B*5401      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.513095       0.305034        -4.208061       32590.813224
HLA A*0250      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.468305       0.259962        -4.208343       29397.108498
HLA B*0803      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.519624       0.310721        -4.208903       33084.487854
HLA A*0211      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.275598       0.066377        -4.209221       18862.424129
HLA A*2402      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.571294       0.362044        -4.209250       37264.413503
HLA B*3801      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.535725       0.326268        -4.209457       34334.081752
HLA B*0702      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.457861       0.247860        -4.210002       28698.629295
HLA B*5401      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.542172       0.332159        -4.210013       34847.563950
HLA A*2601      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.401899       0.191859        -4.210040       25228.926480
HLA B*5401      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.536423       0.326268        -4.210155       34389.291937
HLA A*2902      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.402279       0.191859        -4.210421       25251.046854
HLA B*1801      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.536726       0.326268        -4.210458       34413.299764
HLA A*1101      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.458552       0.247860        -4.210692       28744.310997
HLA B*5701      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.398144       0.187363        -4.210781       25011.762383
HLA A*0206      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.521633       0.310721        -4.210912       33237.873136
HLA A*0206      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.423467       0.212403        -4.211064       26513.498873
HLA A*2602      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.606081       0.394780        -4.211301       40372.046546
HLA A*2402      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.585213       0.373896        -4.211317       38478.013219
HLA A*2501      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.499971       0.288570        -4.211401       31620.663179
HLA B*4801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.342147       0.130576        -4.211571       21986.022526
HLA A*2403      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.333254       0.120389        -4.212865       21540.405163
HLA B*1801      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.460866       0.247860        -4.213006       28897.890810
HLA A*2501      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.427922       0.214819        -4.213102       26786.851315
HLA A*2601      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.388131       0.174997        -4.213134       24441.665098
HLA A*3001      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.019184       -0.194071       -4.213255       10451.632020
HLA A*0203      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.428342       0.214819        -4.213523       26812.803466
HLA A*0250      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.524290       0.310721        -4.213569       33441.865311
HLA A*2501      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.426009       0.212403        -4.213606       26669.150750
HLA A*3002      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.575911       0.362044        -4.213867       37662.663357
HLA A*3101      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.333907       0.119790        -4.214117       21572.825210
HLA B*4402      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.426580       0.212403        -4.214177       26704.233151
HLA B*4001      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.402033       0.187363        -4.214670       25236.707364
HLA B*1501      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.394432       0.179262        -4.215170       24798.882327
HLA B*0803      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.503928       0.288570        -4.215358       31910.051630
HLA B*4801      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.403736       0.187363        -4.216373       25335.884379
HLA B*7301      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.582739       0.366173        -4.216566       38259.442007
HLA B*5301      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.599871       0.382667        -4.217204       39798.900700
HLA A*0206      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.337013       0.119790        -4.217223       21727.664361
HLA B*4403      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.644779       0.427495        -4.217284       44134.593690
HLA A*6801      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.405348       0.187363        -4.217985       25430.085196
HLA A*6901      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.348669       0.130576        -4.218093       22318.697141
HLA A*0201      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.397522       0.179262        -4.218260       24975.930696
HLA A*8001      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.437764       0.219167        -4.218596       27400.826308
HLA B*4002      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.601692       0.382667        -4.219025       39966.114412
HLA A*2501      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.467165       0.247860        -4.219305       29320.077577
HLA B*3801      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.585539       0.366173        -4.219366       38505.958589
HLA A*0211      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.545856       0.326268        -4.219588       35144.422899
HLA B*0803      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.522890       0.303280        -4.219611       33334.212553
HLA B*1517      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.399117       0.179262        -4.219855       25067.843859
HLA A*3301      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.634857       0.414917        -4.219940       43137.726994
HLA B*4801      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.432350       0.212403        -4.219947       27061.411563
HLA B*3801      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.557557       0.337522        -4.220034       36104.127278
HLA A*0201      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.395189       0.174997        -4.220191       24842.119239
HLA B*0802      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.454725       0.234317        -4.220407       28492.108662
HLA B*5401      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.531891       0.311316        -4.220575       34032.282480
HLA B*1801      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.478628       0.257963        -4.220665       30104.280532
HLA B*0702      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.435499       0.214819        -4.220679       27258.299322
HLA B*4501      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.637378       0.416603        -4.220775       43388.861537
HLA B*1801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.531705       0.310721        -4.220984       34017.740829
HLA B*5701      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.412962       0.191859        -4.221104       25879.894170
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HLA A*3002      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.469195       0.247860        -4.221335       29457.444634
HLA A*0212      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.436314       0.214819        -4.221495       27309.517520
HLA B*5401      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.532218       0.310721        -4.221496       34057.883517
HLA B*4402      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.440773       0.219167        -4.221606       27591.375393
HLA B*4801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.440832       0.219167        -4.221665       27595.107303
HLA A*2402      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.527082       0.305034        -4.222048       33657.486601
HLA A*2301      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.533397       0.311316        -4.222081       34150.502411
HLA B*4501      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.616947       0.394780        -4.222168       41394.928179
HLA A*0301      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.368031       0.145735        -4.222296       23336.243346
HLA A*6801      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.596586       0.373896        -4.222691       39499.035989
HLA A*2301      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.528118       0.305034        -4.223084       33737.881187
HLA A*6901      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.342913       0.119790        -4.223122       22024.831813
HLA B*0801      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.437977       0.214819        -4.223158       27414.319053
HLA A*8001      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.430748       0.207531        -4.223217       26961.751247
HLA A*2301      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.526804       0.303280        -4.223525       33636.007632
HLA A*3301      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.618387       0.394780        -4.223608       41532.432483
HLA B*5301      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.575281       0.351592        -4.223689       37608.097699
HLA B*4402      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.415963       0.191859        -4.224104       26059.302568
HLA B*4002      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.627917       0.403811        -4.224106       42453.830234
HLA A*0101      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.416040       0.191859        -4.224182       26063.955256
HLA A*3002      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.437040       0.212403        -4.224637       27355.207811
HLA B*4601      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.416846       0.191859        -4.224987       26112.364222
HLA B*1501      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.417051       0.191859        -4.225192       26124.657169
HLA A*0219      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.437646       0.212403        -4.225243       27393.415538
HLA A*0101      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.400724       0.174997        -4.225727       25160.775846
HLA B*0801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.346571       0.120389        -4.226182       22211.134851
HLA A*3101      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.418246       0.191859        -4.226388       26196.694038
HLA B*1801      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.530258       0.303280        -4.226979       33904.565672
HLA B*2705      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.347271       0.119790        -4.227480       22246.971343
HLA A*2602      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.593920       0.366173        -4.227747       39257.246135
HLA B*0801      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.373548       0.145735        -4.227812       23634.560768
HLA A*3002      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.560139       0.332159        -4.227980       36319.422599
HLA A*2402      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.565710       0.337522        -4.228187       36788.286879
HLA A*3301      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.407754       0.179262        -4.228492       25571.351841
HLA B*1501      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.294934       0.066377        -4.228557       19721.219527
HLA B*5801      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.348540       0.119790        -4.228749       22312.057337
HLA B*3501      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.436528       0.207531        -4.228997       27322.965303
HLA B*5301      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.476923       0.247860        -4.229063       29986.275465
HLA A*2301      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.539999       0.310721        -4.229278       34673.617192
HLA B*5101      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.487350       0.257963        -4.229386       30714.930765
HLA A*0202      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.540222       0.310721        -4.229501       34691.441912
HLA B*7301      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.603445       0.373896        -4.229549       40127.734661
HLA B*1501      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.350158       0.120389        -4.229769       22395.378793
HLA A*0301      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.360487       0.130576        -4.229911       22934.366506
HLA B*4402      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.417354       0.187363        -4.229991       26142.895296
HLA B*4001      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.421949       0.191859        -4.230090       26421.001528
HLA B*1509      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.490087       0.259962        -4.230125       30909.123566
HLA B*1517      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.449311       0.219167        -4.230144       28139.176174
HLA A*3002      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.535848       0.305034        -4.230814       34343.741777
HLA A*0216      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.443419       0.212403        -4.231015       27759.962182
HLA B*0802      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.418453       0.187363        -4.231090       26209.168474
HLA A*8001      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.446457       0.214819        -4.231637       27954.823479
HLA A*2403      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.419043       0.187363        -4.231680       26244.781610
HLA B*4001      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.411066       0.179262        -4.231805       25767.154509
HLA B*2705      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.439432       0.207531        -4.231901       27506.275852
HLA A*3201      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.605867       0.373896        -4.231971       40352.176282
HLA B*4402      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.411572       0.179262        -4.232310       25797.142397
HLA B*5801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.353001       0.120389        -4.232612       22542.459044
HLA A*2603      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.492753       0.259962        -4.232792       31099.496381
HLA B*1517      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.440557       0.207531        -4.233026       27577.646312
HLA A*6801      1:87-95 9       RWRTAAFAS       1.146634        -0.719139       -4.660833       0.427495        -4.233338       45796.592321
HLA A*3001      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.291027       0.057558        -4.233469       19544.590430
HLA B*1502      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.467922       0.234317        -4.233604       29371.197204
HLA B*4601      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.364185       0.130576        -4.233609       23130.490260
HLA B*5101      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.467976       0.234317        -4.233658       29374.852014
HLA A*3201      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.571271       0.337522        -4.233748       37262.397594
HLA B*5301      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.571337       0.337522        -4.233814       37268.042414
HLA B*5801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.364664       0.130576        -4.234088       23156.031563
HLA A*0250      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.596199       0.362044        -4.234155       39463.793629
HLA B*1517      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.449206       0.214819        -4.234386       28132.326666
HLA B*3801      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.566776       0.332159        -4.234617       36878.753261
HLA A*8001      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.422104       0.187363        -4.234741       26430.436902
HLA B*4801      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.380507       0.145735        -4.234772       24016.333749
HLA A*0216      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.258096       0.023284        -4.234813       18117.413318
HLA A*3201      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.493035       0.257963        -4.235072       31119.692315
HLA A*0101      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.380824       0.145735        -4.235089       24033.880126
HLA B*5801      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.357651       0.122444        -4.235207       22785.099012
HLA B*0702      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.447960       0.212403        -4.235557       28051.780027
HLA B*1502      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.601929       0.366173        -4.235756       39987.957816
HLA A*2301      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.427948       0.191859        -4.236089       26788.445415
HLA B*1509      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.539419       0.303280        -4.236139       34627.315768
HLA B*3901      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.484004       0.247860        -4.236144       30479.221781
HLA A*0301      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.358647       0.122444        -4.236204       22837.423300
HLA A*2902      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.423730       0.187363        -4.236367       26529.568471
HLA B*0702      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.428368       0.191859        -4.236509       26814.399110
HLA B*5301      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.597404       0.360868        -4.236536       39573.468554
HLA A*3101      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.411886       0.174997        -4.236889       25815.850175
HLA A*2603      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.652004       0.414917        -4.237086       44874.931551
HLA B*5401      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.540455       0.303280        -4.237175       34710.026897
HLA B*4601      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.412422       0.174997        -4.237425       25847.712503
HLA A*2603      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.641248       0.403811        -4.237437       43777.187527
HLA A*2603      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.630205       0.392663        -4.237542       42678.119713
HLA A*6802      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.429573       0.191859        -4.237715       26888.919752
HLA A*2602      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.472054       0.234317        -4.237737       29652.027440
HLA B*4501      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.589395       0.351592        -4.237803       38850.330957
HLA B*3801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.548579       0.310721        -4.237858       35365.472867
HLA A*3001      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.261259       0.023284        -4.237975       18249.820573
HLA A*0211      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.541475       0.303280        -4.238195       34791.618034
HLA B*3901      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.450669       0.212403        -4.238266       28227.302723
HLA A*2501      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.426101       0.187363        -4.238738       26674.778152
HLA B*0801      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.430631       0.191859        -4.238772       26954.459229
HLA A*0202      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.049868       -0.189096       -4.238964       11216.784724
HLA B*7301      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.601196       0.362044        -4.239152       39920.519655
HLA B*3801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.544379       0.305034        -4.239345       35025.035986
HLA B*4801      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.431270       0.191859        -4.239411       26994.151639
HLA B*3501      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.359206       0.119790        -4.239416       22866.846645
HLA A*2601      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.385311       0.145735        -4.239576       24283.506986
HLA A*6901      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.360214       0.120389        -4.239825       22919.978625
HLA A*0211      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.474214       0.234317        -4.239896       29799.815145
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HLA B*3801      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.543206       0.303280        -4.239927       34930.612194
HLA A*0211      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.263432       0.023284        -4.240148       18341.374249
HLA A*0250      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.545394       0.305034        -4.240360       35106.987747
HLA A*2602      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.545438       0.305034        -4.240404       35110.596505
HLA A*3301      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.601281       0.360868        -4.240413       39928.295174
HLA B*4402      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.447949       0.207531        -4.240418       28051.021252
HLA B*0803      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.474874       0.234317        -4.240556       29845.150644
HLA B*1501      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.264348       0.023284        -4.241065       18380.112773
HLA A*0250      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.529687       0.288570        -4.241118       33860.023910
HLA A*0212      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.433135       0.191859        -4.241276       27110.353111
HLA B*0803      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.499543       0.257963        -4.241580       31589.544802
HLA A*6901      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.364070       0.122444        -4.241626       23124.359537
HLA B*0802      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.456698       0.214819        -4.241879       28621.880185
HLA A*0211      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.461698       0.219167        -4.242531       28953.286209
HLA A*3002      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.461926       0.219167        -4.242759       28968.483701
HLA B*5401      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.302741       0.059757        -4.242984       20078.954988
HLA A*6901      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.218110       -0.024958       -4.243068       16523.814349
HLA B*1503      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.144200       -0.098967       -4.243167       13937.991896
HLA A*6801      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.636251       0.392663        -4.243587       43276.337812
HLA B*5401      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.501768       0.257963        -4.243805       31751.798524
HLA A*0219      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.463035       0.219167        -4.243868       29042.548308
HLA A*2602      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.054779       -0.189096       -4.243874       11344.328879
HLA A*6802      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.418893       0.174997        -4.243895       26235.696376
HLA A*6802      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.310459       0.066377        -4.244082       20438.977444
HLA A*0206      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.547588       0.303280        -4.244308       35284.826531
HLA B*4403      1:155-163       9       LVMNNVAPP       0.261618        0.154985        -4.661179       0.416603        -4.244575       45833.026716
HLA A*0201      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.390450       0.145735        -4.244715       24572.521898
HLA A*1101      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.459550       0.214819        -4.244731       28810.476034
HLA B*3901      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.452427       0.207531        -4.244896       28341.758666
HLA A*0219      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.432414       0.187363        -4.245051       27065.364631
HLA A*3201      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.611330       0.366173        -4.245156       40862.931044
HLA B*2705      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.479780       0.234317        -4.245462       30184.188199
HLA A*2402      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.556589       0.310721        -4.245867       36023.745330
HLA A*0301      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.366360       0.120389        -4.245971       23246.654501
HLA B*5301      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.578221       0.332159        -4.246062       37863.483927
HLA B*0802      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.458510       0.212403        -4.246106       28741.512069
HLA A*0203      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.438436       0.191859        -4.246577       27443.254456
HLA B*4002      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.641621       0.394780        -4.246842       43814.859654
HLA A*2902      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.313246       0.066377        -4.246869       20570.538154
HLA A*2602      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.454452       0.207531        -4.246921       28474.234130
HLA B*5801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.338824       0.091860        -4.246965       21818.480248
HLA A*0301      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.367225       0.119790        -4.247435       23292.980951
HLA B*5401      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.536043       0.288570        -4.247473       34359.166294
HLA A*0101      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.367425       0.119790        -4.247634       23303.694472
HLA A*2602      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.558370       0.310721        -4.247648       36171.771054
HLA B*5301      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.222974       -0.024958       -4.247932       16709.895766
HLA A*1101      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.427231       0.179262        -4.247969       26744.280493
HLA A*2601      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.370496       0.122444        -4.248052       23469.052401
HLA B*4001      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.423166       0.174997        -4.248169       26495.145537
HLA A*0212      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.368322       0.119790        -4.248532       23351.903162
HLA B*5701      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.423568       0.174997        -4.248571       26519.667299
HLA B*1501      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.424010       0.174997        -4.249013       26546.653090
HLA B*4403      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.643933       0.394780        -4.249154       44048.722564
HLA A*0219      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.441253       0.191859        -4.249394       27621.842524
HLA A*0219      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.464574       0.214819        -4.249754       29145.642470
HLA B*4601      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.395680       0.145735        -4.249945       24870.223284
HLA A*2602      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.587485       0.337522        -4.249962       38679.833102
HLA A*2301      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.538542       0.288570        -4.249973       34557.512153
HLA B*1501      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.369868       0.119790        -4.250078       23435.177224
HLA A*2601      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.316462       0.066377        -4.250085       20723.451954
HLA A*2603      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.624790       0.373896        -4.250894       42149.236716
HLA B*4801      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.371191       0.119790        -4.251401       23506.664138
HLA A*0250      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.584144       0.332159        -4.251985       38383.416080
HLA A*8001      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.431256       0.179262        -4.251994       26993.275441
HLA B*4002      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.645329       0.392663        -4.252666       44190.499672
HLA A*0101      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.373200       0.120389        -4.252811       23615.645010
HLA B*4501      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.645688       0.392663        -4.253025       44227.091866
HLA A*1101      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.440412       0.187363        -4.253049       27568.397959
HLA A*3002      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.460584       0.207531        -4.253053       28879.136771
HLA A*3001      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.251995       -0.001650       -4.253644       17864.652779
HLA B*3801      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.564960       0.311316        -4.253644       36724.854073
HLA A*0201      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.154942       -0.098967       -4.253909       14287.033173
HLA B*1502      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.591566       0.337522        -4.254043       39045.019759
HLA A*0216      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.473511       0.219167        -4.254344       29751.651214
HLA B*4002      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.557644       0.303280        -4.254364       36111.354817
HLA A*2902      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.295072       0.040386        -4.254686       19727.515219
HLA B*1502      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.617022       0.362044        -4.254978       41402.094943
HLA B*0801      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.375267       0.119790        -4.255477       23728.340110
HLA A*6801      1:68-76 9       AHLRTAILD       1.193151        -0.778234       -4.670414       0.414917        -4.255497       46818.162385
HLA A*3201      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.617690       0.362044        -4.255645       41465.754365
HLA B*2705      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.468128       0.212403        -4.255725       29385.183286
HLA B*0802      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.475024       0.219167        -4.255857       29855.485806
HLA B*1801      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.375805       0.119790        -4.256015       23757.754527
HLA A*2402      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.582304       0.326268        -4.256036       38221.169984
HLA B*3801      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.544750       0.288570        -4.256180       35054.986871
HLA A*6901      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.279145       0.022933        -4.256212       19017.141077
HLA A*0203      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.401976       0.145735        -4.256241       25233.430910
HLA B*1503      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.376834       0.120389        -4.256445       23814.116022
HLA A*3301      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.622818       0.366173        -4.256645       41958.359187
HLA B*4403      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.660523       0.403811        -4.256712       45763.900402
HLA B*5101      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.475891       0.219167        -4.256724       29915.144320
HLA A*2603      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.471570       0.214819        -4.256751       29619.000525
HLA A*0212      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.436286       0.179262        -4.257024       27307.744680
HLA A*0206      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.316901       0.059757        -4.257144       20744.427428
HLA B*7301      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.568583       0.311316        -4.257267       37032.496005
HLA B*4402      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.403041       0.145735        -4.257305       25295.345805
HLA B*1501      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.317197       0.059757        -4.257440       20758.572605
HLA B*0702      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.465295       0.207531        -4.257764       29194.088820
HLA A*3301      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.562935       0.305034        -4.257901       36553.992863
HLA B*0803      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.505762       0.247860        -4.257903       32045.160762
HLA A*3101      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.403656       0.145735        -4.257921       25331.224620
HLA A*0203      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.388507       0.130576        -4.257931       24462.830529
HLA B*1509      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.546540       0.288570        -4.257971       35199.793555
HLA A*3301      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.631871       0.373896        -4.257975       42842.130736
HLA B*5401      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.477383       0.219167        -4.258216       30018.087924
HLA A*2601      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.388871       0.130576        -4.258295       24483.352018
HLA A*0212      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.324732       0.066377        -4.258355       21121.866131
HLA B*4501      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.632428       0.373896        -4.258532       42897.095734
HLA B*2705      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.445898       0.187363        -4.258535       27918.853306
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HLA A*0250      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.585184       0.326268        -4.258916       38475.515359
HLA A*6801      1:168-176       9       VYQMWLLGG       0.877304        -0.473493       -4.662997       0.403811        -4.259186       46025.343608
HLA A*2602      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.633196       0.373896        -4.259300       42973.049307
HLA A*2501      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.325891       0.066377        -4.259514       21178.274929
HLA A*0101      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.381963       0.122444        -4.259520       24097.022931
HLA B*3901      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.478776       0.219167        -4.259609       30114.542512
HLA A*3101      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.326017       0.066377        -4.259641       21184.462728
HLA B*4403      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.625838       0.366173        -4.259665       42251.057628
HLA A*3002      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.519629       0.259962        -4.259668       33084.845823
HLA B*4002      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.633800       0.373896        -4.259904       43032.838075
HLA B*4403      1:205-213       9       STALAFTVE       0.973168        -0.590501       -4.642629       0.382667        -4.259963       43916.665132
HLA A*6801      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.621125       0.360868        -4.260257       41795.018111
HLA A*0101      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.352353       0.091860        -4.260493       22508.825352
HLA A*6801      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.518952       0.257963        -4.260989       33033.338179
HLA A*0250      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.284375       0.023284        -4.261092       19247.537830
HLA B*2705      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.480393       0.219167        -4.261226       30226.837804
HLA A*0202      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.587569       0.326268        -4.261301       38687.366966
HLA A*0212      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.436373       0.174997        -4.261376       27313.211307
HLA A*8001      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.453630       0.191859        -4.261771       28420.370283
HLA A*0216      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.476873       0.214819        -4.262054       29982.868988
HLA A*2603      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.656905       0.394780        -4.262125       45384.214676
HLA B*4801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.437233       0.174997        -4.262235       27367.345571
HLA B*4001      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.393175       0.130576        -4.262599       24727.210922
HLA B*5101      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.441946       0.179262        -4.262684       27665.959895
HLA B*4001      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.382621       0.119790        -4.262831       24133.552013
HLA A*3101      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.384510       0.120389        -4.264121       24238.750743
HLA B*4801      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.443525       0.179262        -4.264263       27766.721029
HLA A*2501      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.471899       0.207531        -4.264369       29641.441994
HLA A*0206      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.451854       0.187363        -4.264491       28304.371858
HLA A*0203      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.439566       0.174997        -4.264569       27514.759097
HLA B*3501      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.456954       0.191859        -4.265095       28638.762852
HLA A*0101      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.396114       0.130576        -4.265539       24895.126597
HLA A*2902      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.444899       0.179262        -4.265637       27854.735936
HLA B*5101      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.478142       0.212403        -4.265738       30070.587211
HLA A*0250      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.500192       0.234317        -4.265874       31636.747311
HLA A*0201      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.385704       0.119790        -4.265913       24305.455870
HLA A*0203      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.445435       0.179262        -4.266173       27889.114690
HLA A*3001      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.306700       0.040386        -4.266314       20262.824753
HLA A*0301      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.358205       0.091860        -4.266346       22814.208097
HLA B*1517      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.397005       0.130576        -4.266429       24946.222634
HLA A*6801      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.555365       0.288570        -4.266795       35922.353478
HLA A*3002      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.290258       0.023284        -4.266975       19510.045954
HLA B*0702      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.442169       0.174997        -4.267172       27680.182178
HLA B*1501      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.390156       0.122444        -4.267712       24555.910688
HLA A*3001      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.169006       -0.098967       -4.267973       14757.271601
HLA A*2402      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.571398       0.303280        -4.268118       37273.284798
HLA B*7301      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.326828       0.057558        -4.269270       21224.038579
HLA A*0201      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.391805       0.122444        -4.269362       24649.345013
HLA B*5301      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.596173       0.326268        -4.269905       39461.445257
HLA B*0802      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.449173       0.179262        -4.269911       28130.196048
HLA B*5101      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.477475       0.207531        -4.269944       30024.421978
HLA A*2601      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.390577       0.120389        -4.270187       24579.701416
HLA A*2403      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.400842       0.130576        -4.270266       25167.582617
HLA A*0212      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.416195       0.145735        -4.270460       26073.263122
HLA B*1801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.489683       0.219167        -4.270515       30880.375974
HLA A*0201      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.401845       0.130576        -4.271269       25225.787504
HLA B*4002      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.637458       0.366173        -4.271285       43396.843055
HLA B*5101      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.486165       0.214819        -4.271346       30631.297990
HLA B*5701      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.417401       0.145735        -4.271666       26145.724052
HLA B*4001      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.392144       0.120389        -4.271755       24668.554926
HLA A*2403      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.394242       0.122444        -4.271798       24788.017812
HLA A*2403      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.446929       0.174997        -4.271932       27985.237744
HLA B*4601      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.338526       0.066377        -4.272149       21803.494881
HLA B*4601      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.391991       0.119790        -4.272201       24659.881932
HLA A*0301      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.295491       0.023284        -4.272207       19746.521182
HLA B*1502      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.083156       -0.189096       -4.272252       12110.327512
HLA B*4403      1:145-153       9       VFSRDRNTG       0.879698        -0.487035       -4.665558       0.392663        -4.272895       46297.546667
HLA B*7301      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.576625       0.303280        -4.273346       37724.654572
HLA A*6801      1:209-217       9       AFTVEPGTG       0.859209        -0.464429       -4.668131       0.394780        -4.273351       46572.619336
HLA B*4001      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.395955       0.122444        -4.273511       24885.970050
HLA B*5401      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.508542       0.234317        -4.274224       32250.904216
HLA B*7301      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.579510       0.305034        -4.274476       37976.106741
HLA A*0216      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.466338       0.191859        -4.274479       29264.297039
HLA A*2403      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.420248       0.145735        -4.274513       26317.719211
HLA B*4501      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.606673       0.332159        -4.274514       40427.122971
HLA B*4002      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.635853       0.360868        -4.274986       43236.789581
HLA A*1101      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.341501       0.066377        -4.275124       21953.337810
HLA A*2602      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.563818       0.288570        -4.275249       36628.423685
HLA A*3301      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.637296       0.362044        -4.275252       43380.646803
HLA A*2603      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.580420       0.305034        -4.275386       38055.697835
HLA B*0702      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.454835       0.179262        -4.275573       28499.354123
HLA A*6802      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.398081       0.122444        -4.275637       25008.109257
HLA A*0206      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.455700       0.179262        -4.276438       28556.148270
HLA A*2602      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.638696       0.362044        -4.276652       43520.744495
HLA A*0202      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.396453       0.119790        -4.276662       24914.528055
HLA A*2602      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.524612       0.247860        -4.276753       33466.660097
HLA A*2602      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.580142       0.303280        -4.276863       38031.412089
HLA B*4601      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.397630       0.120389        -4.277241       24982.146852
HLA B*1502      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.496552       0.219167        -4.277385       31372.741672
HLA A*0201      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.343857       0.066377        -4.277480       22072.782999
HLA A*0201      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.398177       0.120389        -4.277788       25013.656807
HLA A*0219      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.398337       0.119790        -4.278547       25022.860335
HLA B*4002      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.640759       0.362044        -4.278715       43727.954648
HLA A*2601      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.398762       0.119790        -4.278972       25047.374468
HLA B*1502      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.611151       0.332159        -4.278992       40846.133639
HLA A*0216      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.466418       0.187363        -4.279055       29269.680298
HLA B*5701      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.409817       0.130576        -4.279241       25693.101681
HLA A*2402      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.568047       0.288570        -4.279478       36986.846257
HLA B*1502      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.568118       0.288570        -4.279548       36992.849586
HLA A*6801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.498726       0.219167        -4.279559       31530.128963
HLA A*2501      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.471479       0.191859        -4.279620       29612.751999
HLA B*2705      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.494553       0.214819        -4.279734       31228.639317
HLA A*6901      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.339764       0.059757        -4.280007       21865.745593
HLA A*0301      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.346834       0.066377        -4.280457       22224.596824
HLA B*5401      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.495476       0.214819        -4.280657       31295.104734
HLA B*1801      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.472609       0.191859        -4.280750       29689.909364
HLA A*3101      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.403306       0.122444        -4.280863       25310.814019
HLA B*1502      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.591796       0.310721        -4.281074       39065.725712
HLA A*2301      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.539708       0.257963        -4.281745       34650.365019
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HLA A*6901      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.373627       0.091860        -4.281768       23638.908420
HLA A*0203      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.401629       0.119790        -4.281838       25213.235506
HLA A*3201      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.570507       0.288570        -4.281938       37196.939887
HLA A*0250      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.530026       0.247860        -4.282166       33886.411959
HLA B*2705      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.475633       0.191859        -4.283774       29897.347478
HLA B*1503      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.503232       0.219167        -4.284065       31858.994088
HLA B*5101      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.404589       0.120389        -4.284200       25385.687615
HLA B*0803      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.496618       0.212403        -4.284215       31377.494277
HLA B*5301      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.589287       0.305034        -4.284253       38840.664064
HLA A*0202      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.587550       0.303280        -4.284271       38685.692647
HLA B*5701      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.404081       0.119790        -4.284291       25356.040848
HLA A*3201      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.350701       0.066377        -4.284324       22423.383444
HLA A*0202      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.503556       0.219167        -4.284389       31882.787769
HLA B*7301      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.471794       0.187363        -4.284431       29634.226811
HLA A*2602      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.610700       0.326268        -4.284432       40803.728839
HLA A*0219      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.463721       0.179262        -4.284459       29088.462718
HLA A*6801      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.324883       0.040386        -4.284497       21129.180482
HLA A*3201      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.595861       0.311316        -4.284545       39433.062357
HLA B*0803      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.503862       0.219167        -4.284695       31905.218361
HLA B*0802      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.459980       0.174997        -4.284983       28839.012808
HLA B*4002      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.617161       0.332159        -4.285002       41415.311916
HLA B*5301      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.596615       0.311316        -4.285299       39501.600298
HLA B*5701      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.407756       0.122444        -4.285312       25571.490179
HLA B*3901      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.431058       0.145735        -4.285323       26981.011655
HLA B*3501      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.431171       0.145735        -4.285436       26988.018850
HLA A*0101      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.352057       0.066377        -4.285680       22493.487529
HLA B*4501      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.646795       0.360868        -4.285927       44339.928748
HLA A*2902      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.460972       0.174997        -4.285975       28904.926713
HLA B*4403      1:151-159       9       NTGLLVMNN       0.907671        -0.575512       -4.618317       0.332159        -4.286158       41525.692454
HLA B*1502      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.612561       0.326268        -4.286292       40978.932884
HLA B*1509      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.498770       0.212403        -4.286367       31533.370045
HLA B*5801      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.346218       0.059757        -4.286461       22193.118195
HLA B*1801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.494283       0.207531        -4.286752       31209.216860
HLA B*4501      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.648832       0.362044        -4.286788       44548.388086
HLA A*2603      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.647939       0.360868        -4.287071       44456.901456
HLA A*6802      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.417725       0.130576        -4.287149       26165.250815
HLA B*4402      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.417847       0.130576        -4.287271       26172.612508
HLA A*2402      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.535300       0.247860        -4.287441       34300.478620
HLA A*0211      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.310513       0.022933        -4.287580       20441.520772
HLA A*0211      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.500166       0.212403        -4.287763       31634.864703
HLA A*2603      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.522296       0.234317        -4.287978       33288.619160
HLA A*2403      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.354937       0.066377        -4.288560       22643.171970
HLA B*5301      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.577429       0.288570        -4.288859       37794.516661
HLA B*0802      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.496637       0.207531        -4.289106       31378.852297
HLA B*5301      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.592435       0.303280        -4.289155       39123.252846
HLA B*5701      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.409842       0.120389        -4.289453       25694.630692
HLA A*2403      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.349536       0.059757        -4.289778       22363.295320
HLA B*4002      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.578643       0.288570        -4.290074       37900.372590
HLA A*2301      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.538134       0.247860        -4.290274       34524.997756
HLA B*4403      1:216-224       9       TGSPQPTGT       0.820922        -0.447026       -4.664393       0.373896        -4.290497       46173.482753
HLA A*3301      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.524887       0.234317        -4.290570       33487.849761
HLA B*1503      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.498145       0.207531        -4.290615       31488.025198
HLA B*0801      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.357118       0.066377        -4.290741       22757.135063
HLA A*0250      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.594127       0.303280        -4.290847       39275.939791
HLA A*2602      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.550823       0.259962        -4.290862       35548.659411
HLA A*2402      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.548920       0.257963        -4.290957       35393.225627
HLA B*3501      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.466190       0.174997        -4.291193       29254.324792
HLA B*5301      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.602376       0.310721        -4.291654       40029.081727
HLA B*1509      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.526046       0.234317        -4.291728       33577.283589
HLA A*2603      1:96-104        9       AAAIAVGLG       0.855432        -0.489259       -4.658608       0.366173        -4.292435       45562.568803
HLA A*0203      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.415211       0.122444        -4.292767       26014.228655
HLA A*0216      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.472177       0.179262        -4.292915       29660.370151
HLA B*1801      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.505631       0.212403        -4.293227       32035.454030
HLA A*0101      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.352999       0.059757        -4.293242       22542.337092
HLA A*2603      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.630854       0.337522        -4.293331       42741.891267
HLA A*0212      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.424282       0.130576        -4.293707       26563.317595
HLA A*3101      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.385659       0.091860        -4.293799       24302.957692
HLA B*4002      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.631328       0.337522        -4.293806       42788.625034
HLA B*3901      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.485966       0.191859        -4.294107       30617.215714
HLA B*5801      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.360712       0.066377        -4.294335       22946.280548
HLA B*4601      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.417652       0.122444        -4.295208       26160.863098
HLA B*1509      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.487253       0.191859        -4.295394       30708.118781
HLA B*3901      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.510433       0.214819        -4.295614       32391.661913
HLA A*8001      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.470635       0.174997        -4.295638       29555.295400
HLA A*3301      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.621921       0.326268        -4.295653       41871.738515
HLA B*3901      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.470910       0.174997        -4.295913       29574.008553
HLA B*1517      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.418808       0.122444        -4.296364       26230.587314
HLA B*7301      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.554418       0.257963        -4.296455       35844.121401
HLA A*6802      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.354150       0.057558        -4.296592       22602.172622
HLA A*2301      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.530940       0.234317        -4.296622       33957.799202
HLA B*5801      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.354658       0.057558        -4.297100       22628.599513
HLA B*1503      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.363896       0.066377        -4.297519       23115.103973
HLA A*3001      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.276800       -0.020998       -4.297798       18914.742889
HLA B*0803      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.485280       0.187363        -4.297917       30568.888259
HLA B*4403      1:111-119       9       LTRPSPPPT       0.624592        -0.273000       -4.649661       0.351592        -4.298069       44633.543020
HLA A*2603      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.660178       0.362044        -4.298133       45727.520958
HLA A*2902      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.443908       0.145735        -4.298172       27791.216854
HLA B*1517      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.444333       0.145735        -4.298598       27818.443061
HLA B*4403      1:222-230       9       TGTILAELP       0.521964        -0.159920       -4.660669       0.362044        -4.298624       45779.252790
HLA A*6801      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.609638       0.310721        -4.298916       40704.074600
HLA B*2705      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.478219       0.179262        -4.298958       30075.956082
HLA B*1501      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.390823       0.091860        -4.298964       24593.667595
HLA A*0212      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.419449       0.120389        -4.299060       26269.355883
HLA A*1101      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.429811       0.130576        -4.299235       26903.615840
HLA B*0802      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.491221       0.191859        -4.299363       30989.993988
HLA A*8001      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.391326       0.091860        -4.299466       24622.156573
HLA B*5401      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.511899       0.212403        -4.299496       32501.193513
HLA A*0216      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.419294       0.119790        -4.299504       26259.978013
HLA A*2601      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.391453       0.091860        -4.299593       24629.350593
HLA B*1503      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.512000       0.212403        -4.299597       32508.754990
HLA A*0201      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.391540       0.091860        -4.299680       24634.281042
HLA B*1509      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.445599       0.145735        -4.299864       27899.678081
HLA A*0219      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.474925       0.174997        -4.299928       29848.702952
HLA B*0702      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.445836       0.145735        -4.300101       27914.926597
HLA B*1503      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.430682       0.130576        -4.300107       26957.667474
HLA A*3201      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.626401       0.326268        -4.300133       42305.950905
HLA A*3002      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.603640       0.303280        -4.300360       40145.756895
HLA A*2501      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.480123       0.179262        -4.300861       30208.038411
HLA A*0301      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.360792       0.059757        -4.301035       22950.501588
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HLA B*4001      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.446807       0.145735        -4.301072       27977.366205
HLA A*3301      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.611912       0.310721        -4.301191       40917.791692
HLA B*3501      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.393342       0.091860        -4.301482       24736.710521
HLA A*0250      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.559481       0.257963        -4.301518       36264.448712
HLA A*2603      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.513988       0.212403        -4.301585       32657.880959
HLA A*2301      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.509376       0.207531        -4.301845       32312.901936
HLA B*1517      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.393739       0.091860        -4.301879       24759.336926
HLA A*2602      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.517136       0.214819        -4.302317       32895.486340
HLA B*4501      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.613848       0.311316        -4.302532       41100.600077
HLA B*3901      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.481805       0.179262        -4.302543       30325.275573
HLA B*0702      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.369088       0.066377        -4.302711       23393.123474
HLA B*3801      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.562714       0.259962        -4.302752       36535.408802
HLA A*0203      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.326579       0.022933        -4.303646       21211.871180
HLA B*3901      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.279777       -0.023878       -4.303655       19044.836112
HLA A*0219      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.449401       0.145735        -4.303665       28144.961502
HLA A*3101      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.109752       -0.194071       -4.303823       12875.142919
HLA A*6802      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.423758       0.119790        -4.303968       26531.290791
HLA A*0203      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.424672       0.120389        -4.304283       26587.183274
HLA A*0206      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.519801       0.214819        -4.304981       33097.914334
HLA A*0211      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.492401       0.187363        -4.305038       31074.269894
HLA A*2402      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.517653       0.212403        -4.305250       32934.661053
HLA A*6802      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.365329       0.059757        -4.305572       23191.510568
HLA B*3801      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.563593       0.257963        -4.305630       36609.405675
HLA B*1517      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.497518       0.191859        -4.305659       31442.575455
HLA B*0803      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.520715       0.214819        -4.305895       33167.640478
HLA B*4002      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.632174       0.326268        -4.305906       42872.039653
HLA B*1502      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.452180       0.145735        -4.306445       28325.664031
HLA A*2603      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.617224       0.310721        -4.306503       41421.361769
HLA B*4001      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.373374       0.066377        -4.306997       23625.100996
HLA B*1509      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.554937       0.247860        -4.307078       35887.001742
HLA B*0702      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.426940       0.119790        -4.307149       26726.345744
HLA B*4501      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.618787       0.310721        -4.308065       41570.646648
HLA B*4501      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.634416       0.326268        -4.308147       43093.875677
HLA A*3201      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.527547       0.219167        -4.308380       33693.558405
HLA A*0219      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.331701       0.022933        -4.308768       21463.515595
HLA A*0301      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.366624       0.057558        -4.309066       23260.744093
HLA A*0301      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.332016       0.022933        -4.309083       21479.080678
HLA B*3501      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.439693       0.130576        -4.309117       27522.798268
HLA B*4501      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.646971       0.337522        -4.309449       44357.922956
HLA B*0702      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.401544       0.091860        -4.309684       25208.325555
HLA A*1101      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.484838       0.174997        -4.309841       30537.813696
HLA B*1801      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.285985       -0.023878       -4.309862       19318.997181
HLA A*1101      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.455737       0.145735        -4.310002       28558.620146
HLA B*4001      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.370120       0.059757        -4.310362       23448.746794
HLA B*0803      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.518194       0.207531        -4.310663       32975.666318
HLA B*2705      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.431324       0.120389        -4.310935       26997.510661
HLA A*6801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.122049       -0.189096       -4.311145       13244.917670
HLA B*1801      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.490453       0.179262        -4.311191       30935.220106
HLA B*4001      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.403156       0.091860        -4.311296       25302.052099
HLA B*4801      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.433751       0.122444        -4.311307       27148.806325
HLA B*0803      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.486339       0.174997        -4.311342       30643.563127
HLA B*5401      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.503375       0.191859        -4.311517       31869.509394
HLA B*1517      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.431373       0.119790        -4.311583       27000.577960
HLA B*4402      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.434122       0.122444        -4.311678       27172.022027
HLA B*1517      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.487016       0.174997        -4.312019       30691.344485
HLA A*3001      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.288202       -0.023878       -4.312080       19417.910407
HLA A*3002      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.499494       0.187363        -4.312131       31585.956191
HLA B*0803      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.504139       0.191859        -4.312280       31925.592099
HLA A*0211      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.527159       0.214819        -4.312340       33663.495886
HLA A*2402      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.519897       0.207531        -4.312366       33105.256446
HLA B*5801      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.352827       0.040386        -4.312441       22533.436387
HLA B*4801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.432846       0.120389        -4.312457       27092.319439
HLA B*4403      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.601130       0.288570        -4.312561       39914.473077
HLA A*0212      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.435193       0.122444        -4.312750       27239.135693
HLA A*2902      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.404878       0.091860        -4.313018       25402.585288
HLA B*4403      1:110-118       9       VLTRPSPPP       0.309978        0.050890        -4.674159       0.360868        -4.313292       47223.638178
HLA B*0801      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.289652       -0.023878       -4.313530       19482.833775
HLA B*1801      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.528954       0.214819        -4.314135       33802.920275
HLA A*0216      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.489659       0.174997        -4.314662       30878.705425
HLA A*3002      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.494358       0.179262        -4.315096       31214.620156
HLA A*0219      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.437597       0.122444        -4.315153       27390.303613
HLA B*1502      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.573188       0.257963        -4.315225       37427.254924
HLA B*7301      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.563111       0.247860        -4.315251       36568.827351
HLA B*3801      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.563127       0.247860        -4.315268       36570.212211
HLA B*1509      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.530152       0.214819        -4.315333       33896.312779
HLA B*1503      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.507440       0.191859        -4.315581       32169.179717
HLA B*5701      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.407488       0.091860        -4.315629       25555.724404
HLA B*3801      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.550006       0.234317        -4.315688       35481.796991
HLA B*1509      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.534948       0.219167        -4.315781       34272.655642
HLA B*3501      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.382358       0.066377        -4.315981       24118.933740
HLA B*3501      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.121951       -0.194071       -4.316022       13241.908563
HLA B*5101      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.508166       0.191859        -4.316307       32223.000484
HLA A*2902      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.438802       0.122444        -4.316359       27466.424766
HLA A*8001      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.462290       0.145735        -4.316555       28992.784912
HLA B*4402      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.436887       0.119790        -4.317097       27345.590240
HLA B*1502      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.620662       0.303280        -4.317382       41750.498875
HLA B*4601      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.340427       0.022933        -4.317494       21899.129187
HLA B*4402      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.438003       0.120389        -4.317614       27415.950494
HLA A*2301      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.533425       0.214819        -4.318606       34152.719488
HLA B*4402      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.410503       0.091860        -4.318643       25733.720831
HLA B*5401      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.449986       0.130576        -4.319410       28182.900069
HLA A*2402      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.534325       0.214819        -4.319506       34223.556859
HLA A*2603      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.567500       0.247860        -4.319640       36940.253554
HLA A*0219      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.220798       -0.098967       -4.319765       16626.395908
HLA A*8001      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.442862       0.122444        -4.320418       27724.392728
HLA A*3001      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.295733       -0.024958       -4.320690       19757.527377
HLA B*7301      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.440637       0.119790        -4.320847       27582.719307
HLA B*4002      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.580901       0.259962        -4.320940       38097.926054
HLA A*2301      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.500915       0.179262        -4.321654       31689.505852
HLA A*2602      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.509458       0.187363        -4.322095       32319.020838
HLA B*4601      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.413966       0.091860        -4.322106       25939.746416
HLA B*0801      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.382036       0.059757        -4.322279       24101.064499
HLA A*3201      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.626082       0.303280        -4.322802       42274.835964
HLA B*7301      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.611609       0.288570        -4.323040       40889.246121
HLA B*4403      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.626498       0.303280        -4.323218       42315.335637
HLA A*2601      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.364067       0.040386        -4.323681       23124.234437
HLA A*3001      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.309768       -0.014281       -4.324049       20406.494937
HLA A*6802      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.444627       0.120389        -4.324237       27837.261260
HLA A*2601      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.347219       0.022933        -4.324286       22244.323721
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HLA B*5801      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.347623       0.023284        -4.324340       22265.031718
HLA B*1503      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.347428       0.022933        -4.324495       22255.036500
HLA A*6801      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.651001       0.326268        -4.324732       44771.389081
HLA B*5401      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.135662       -0.189096       -4.324758       13666.653361
HLA A*2301      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.543925       0.219167        -4.324758       34988.485129
HLA A*0216      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.347872       0.022933        -4.324939       22277.803223
HLA A*2902      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.455772       0.130576        -4.325197       28560.937725
HLA B*3901      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.300533       -0.024958       -4.325490       19977.106746
HLA A*0201      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.385314       0.059757        -4.325556       24283.638357
HLA A*6901      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.383183       0.057558        -4.325625       24164.775996
HLA A*2601      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.383202       0.057558        -4.325644       24165.821849
HLA B*3501      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.448308       0.122444        -4.325865       28074.249060
HLA A*3101      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.348890       0.022933        -4.325957       22330.049745
HLA B*4403      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.652359       0.326268        -4.326090       44911.604557
HLA A*0301      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.366689       0.040386        -4.326303       23264.267825
HLA B*0803      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.457013       0.130576        -4.326437       28642.636428
HLA A*2301      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.539196       0.212403        -4.326792       34609.523997
HLA A*1101      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.518809       0.191859        -4.326950       33022.438869
HLA A*2301      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.514315       0.187363        -4.326952       32682.448091
HLA A*2402      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.561290       0.234317        -4.326973       36415.827505
HLA B*0801      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.449556       0.122444        -4.327112       28155.012530
HLA A*0250      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.546312       0.219167        -4.327145       35181.326983
HLA B*5801      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.350102       0.022933        -4.327169       22392.471226
HLA A*3002      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.542194       0.214819        -4.327374       34849.260684
HLA B*4002      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.632447       0.305034        -4.327413       42898.952323
HLA A*0219      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.458070       0.130576        -4.327494       28712.450442
HLA B*1801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.502708       0.174997        -4.327711       31820.582404
HLA A*6802      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.419724       0.091860        -4.327865       26285.988520
HLA A*3201      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.535439       0.207531        -4.327908       34311.428513
HLA A*8001      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.447789       0.119790        -4.327998       28040.703952
HLA B*7301      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.535545       0.207531        -4.328014       34319.782476
HLA B*2705      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.503615       0.174997        -4.328618       31887.100119
HLA B*5301      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.586791       0.257963        -4.328828       38618.152519
HLA A*0219      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.395428       0.066377        -4.329051       24855.831119
HLA B*4403      1:126-134       9       TAPDVRTVS       1.285972        -0.948450       -4.666855       0.337522        -4.329332       46436.009764
HLA B*1503      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.387137       0.057558        -4.329579       24385.797153
HLA B*3801      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.517012       0.187363        -4.329649       32886.055762
HLA B*1517      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.450115       0.120389        -4.329726       28191.286966
HLA A*3101      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.389773       0.059757        -4.330016       24534.266537
HLA A*6801      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.635095       0.305034        -4.330061       43161.303837
HLA A*2603      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.549247       0.219167        -4.330080       35419.850443
HLA A*2603      1:130-138       9       VRTVSRPLG       0.891121        -0.564853       -4.656350       0.326268        -4.330082       45326.308087
HLA B*3801      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.545072       0.214819        -4.330252       35080.977674
HLA B*5101      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.505271       0.174997        -4.330274       32008.948838
HLA A*3101      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.387849       0.057558        -4.330291       24425.803044
HLA B*4002      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.641079       0.310721        -4.330357       43760.139107
HLA A*8001      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.354338       0.023284        -4.331055       22611.956759
HLA B*1503      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.510588       0.179262        -4.331327       32403.229508
HLA B*5401      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.539064       0.207531        -4.331533       34599.040498
HLA A*8001      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.398102       0.066377        -4.331725       25009.326906
HLA A*2402      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.451640       0.119790        -4.331849       28290.441048
HLA B*0801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.424271       0.091860        -4.332411       26562.599082
HLA A*0216      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.399042       0.066377        -4.332665       25063.504579
HLA B*5301      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.567037       0.234317        -4.332720       36900.905518
HLA A*2902      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.454046       0.120389        -4.333656       28447.597253
HLA B*1502      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.581639       0.247860        -4.333779       38162.698197
HLA A*2902      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.393725       0.059757        -4.333968       24758.533267
HLA A*2403      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.426080       0.091860        -4.334220       26673.479415
HLA A*3301      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.622955       0.288570        -4.334385       41971.526677
HLA B*4501      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.594582       0.259962        -4.334621       39317.182255
HLA A*2601      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.394789       0.059757        -4.335032       24819.282913
HLA A*0216      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.146235       -0.189096       -4.335330       14003.444088
HLA B*4601      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.395175       0.059757        -4.335417       24841.312893
HLA A*0201      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.358913       0.022933        -4.335980       22851.388484
HLA A*0101      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.394230       0.057558        -4.336672       24787.347319
HLA A*2501      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.511751       0.174997        -4.336754       32490.118246
HLA B*0802      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.467374       0.130576        -4.336798       29334.198011
HLA A*0216      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.459337       0.122444        -4.336893       28796.296130
HLA B*3501      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.360012       0.022933        -4.337079       22909.317574
HLA B*1517      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.360066       0.022933        -4.337133       22912.168299
HLA A*0216      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.483146       0.145735        -4.337411       30419.096600
HLA B*7301      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.516676       0.179262        -4.337414       32860.624483
HLA A*0101      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.377864       0.040386        -4.337478       23870.611226
HLA B*4002      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.649537       0.311316        -4.338221       44620.747341
HLA B*0702      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.361163       0.022933        -4.338231       22970.127202
HLA A*0219      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.458763       0.120389        -4.338374       28758.309723
HLA B*4501      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.641901       0.303280        -4.338621       43843.075726
HLA B*5401      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.458505       0.119790        -4.338714       28741.201094
HLA A*6901      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.315182       -0.023878       -4.339059       20662.441131
HLA B*1502      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.469674       0.130576        -4.339099       29489.972328
HLA B*3501      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.398870       0.059757        -4.339113       25053.608406
HLA A*0201      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.396951       0.057558        -4.339393       24943.118833
HLA A*0202      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.531466       0.191859        -4.339607       33998.974722
HLA A*3002      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.462259       0.122444        -4.339816       28990.745963
HLA A*0203      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.431824       0.091860        -4.339964       27028.637996
HLA B*5701      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.399780       0.059757        -4.340022       25106.116266
HLA B*1503      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.486191       0.145735        -4.340456       30633.120875
HLA B*5101      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.486776       0.145735        -4.341041       30674.413406
HLA B*0801      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.363985       0.022933        -4.341052       23119.856368
HLA A*3301      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.644502       0.303280        -4.341222       44106.428616
HLA B*0802      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.487072       0.145735        -4.341337       30695.329626
HLA B*4403      1:167-175       9       TVYQMWLLG       0.746394        -0.486432       -4.601408       0.259962        -4.341446       39939.961291
HLA B*2705      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.487772       0.145735        -4.342037       30744.854919
HLA B*4801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.434016       0.091860        -4.342157       27165.407939
HLA B*1801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.462628       0.120389        -4.342239       29015.379789
HLA A*0202      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.529657       0.187363        -4.342294       33857.642667
HLA A*0250      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.365381       0.022933        -4.342448       23194.270929
HLA B*4501      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.647704       0.305034        -4.342670       44432.857270
HLA B*4402      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.400242       0.057558        -4.342685       25132.887326
HLA A*2603      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.646349       0.303280        -4.343069       44294.376085
HLA B*1503      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.462903       0.119790        -4.343113       29033.751091
HLA A*0212      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.367021       0.022933        -4.344088       23282.020448
HLA B*4403      1:215-223       9       GTGSPQPTG       1.137233        -0.826512       -4.654821       0.310721        -4.344099       45166.956949
HLA A*8001      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.475019       0.130576        -4.344444       29855.162778
HLA A*2301      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.464249       0.119790        -4.344459       29123.891482
HLA A*6901      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.385290       0.040386        -4.344904       24282.324675
HLA B*2705      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.475877       0.130576        -4.345301       29914.173310
HLA A*2403      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.403066       0.057558        -4.345509       25296.851145
HLA B*4403      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.603668       0.257963        -4.345705       40148.363189
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HLA A*3201      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.537607       0.191859        -4.345749       34483.185180
HLA A*2501      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.468201       0.122444        -4.345758       29390.111787
HLA A*0201      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.369206       0.023284        -4.345922       23399.452040
HLA B*5301      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.525637       0.179262        -4.346375       33545.691468
HLA B*0803      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.525787       0.179262        -4.346525       33557.308102
HLA B*7301      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.565987       0.219167        -4.346820       36811.778802
HLA B*4402      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.413331       0.066377        -4.346955       25901.884663
HLA B*3501      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.326015       -0.020998       -4.347013       21184.348122
HLA B*0802      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.468096       0.120389        -4.347706       29382.957782
HLA A*1101      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.467637       0.119790        -4.347847       29351.977209
HLA B*5701      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.414311       0.066377        -4.347934       25960.383300
HLA B*4403      1:11-19 9       ELATPYALN       0.932404        -0.621088       -4.659280       0.311316        -4.347964       45633.119064
HLA B*0801      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.405540       0.057558        -4.347983       25441.368762
HLA A*0212      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.440322       0.091860        -4.348463       27562.731146
HLA A*3301      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.535881       0.187363        -4.348518       34346.343017
HLA A*0216      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.469115       0.120389        -4.348726       29452.026841
HLA B*0702      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.471192       0.122444        -4.348749       29593.213840
HLA A*3101      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.372735       0.023284        -4.349451       23590.362464
HLA A*3201      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.597872       0.247860        -4.350012       39616.095022
HLA A*2603      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.416595       0.066377        -4.350218       26097.253241
HLA A*0301      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.156840       -0.194071       -4.350912       14349.621208
HLA A*0211      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.530632       0.179262        -4.351370       33933.741989
HLA B*5701      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.408971       0.057558        -4.351413       25643.111517
HLA B*4801      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.411304       0.059757        -4.351546       25781.237499
HLA A*2603      1:139-147       9       AGTATVVFS       1.346924        -1.058354       -4.640369       0.288570        -4.351800       43688.702753
HLA B*1503      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.474340       0.122444        -4.351897       29808.521956
HLA B*4601      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.409506       0.057558        -4.351949       25674.760649
HLA B*4002      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.609917       0.257963        -4.351954       40730.287376
HLA A*0212      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.412070       0.059757        -4.352312       25826.746022
HLA B*3801      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.571609       0.219167        -4.352442       37291.437207
HLA A*2902      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.375399       0.022933        -4.352466       23735.529789
HLA A*1101      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.375427       0.022933        -4.352494       23737.070718
HLA B*0802      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.472437       0.119790        -4.352647       29678.186483
HLA A*3101      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.393185       0.040386        -4.352799       24727.746014
HLA B*4801      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.419207       0.066377        -4.352831       26254.722187
HLA B*3901      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.473229       0.120389        -4.352840       29732.343106
HLA B*2705      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.412796       0.059757        -4.353038       25869.955556
HLA B*4001      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.393838       0.040386        -4.353452       24764.963266
HLA A*8001      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.473997       0.120389        -4.353608       29784.987175
HLA A*0203      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.411269       0.057558        -4.353711       25779.145479
HLA A*0101      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.377199       0.023284        -4.353915       23834.093315
HLA B*4402      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.394409       0.040386        -4.354023       24797.540771
HLA B*7301      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.566452       0.212403        -4.354049       36851.231161
HLA A*0219      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.446165       0.091860        -4.354306       27936.076938
HLA A*1101      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.474972       0.120389        -4.354583       29851.932691
HLA A*0211      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.546639       0.191859        -4.354780       35207.792396
HLA A*2501      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.474589       0.119790        -4.354799       29825.620503
HLA B*3901      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.485456       0.130576        -4.354880       30581.293847
HLA B*1503      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.165811       -0.189096       -4.354906       14649.094167
HLA B*1502      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.570021       0.214819        -4.355201       37155.308319
HLA B*0803      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.475597       0.120389        -4.355208       29894.921456
HLA A*3301      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.613423       0.257963        -4.355460       41060.374480
HLA B*4402      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.378923       0.023284        -4.355640       23928.923283
HLA B*0801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.354082       -0.001650       -4.355732       22598.626918
HLA B*7301      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.548197       0.191859        -4.356338       35334.300917
HLA B*7301      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.590656       0.234317        -4.356339       38963.359561
HLA A*0216      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.487319       0.130576        -4.356743       30712.770704
HLA A*3301      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.575989       0.219167        -4.356821       37669.387734
HLA A*2601      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.380166       0.023284        -4.356882       23997.501910
HLA B*3901      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.476866       0.119790        -4.357076       29982.382380
HLA B*1501      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.355546       -0.001650       -4.357195       22674.920944
HLA B*2705      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.479817       0.122444        -4.357374       30186.801001
HLA B*3901      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.397764       0.040386        -4.357378       24989.851626
HLA A*2902      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.380775       0.023284        -4.357491       24031.149848
HLA A*2402      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.536820       0.179262        -4.357559       34420.747455
HLA B*5801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.356103       -0.001650       -4.357752       22704.012097
HLA A*0101      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.356201       -0.001650       -4.357851       22709.171383
HLA A*2602      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.380927       0.022933        -4.357994       24039.601715
HLA A*0201      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.398617       0.040386        -4.358231       25038.974659
HLA B*5101      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.333303       -0.024958       -4.358261       21542.852457
HLA A*8001      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.398795       0.040386        -4.358409       25049.271589
HLA B*5101      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.478250       0.119790        -4.358460       30078.071355
HLA B*7301      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.504334       0.145735        -4.358599       31939.930573
HLA B*4801      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.416299       0.057558        -4.358741       26079.470213
HLA A*2402      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.578350       0.219167        -4.359183       37874.751652
HLA B*4403      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.607117       0.247860        -4.359257       40468.479592
HLA A*0212      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.382805       0.023284        -4.359521       24143.737829
HLA B*1509      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.534732       0.174997        -4.359734       34255.602050
HLA B*1509      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.567270       0.207531        -4.359739       36920.674163
HLA A*0211      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.479603       0.119790        -4.359813       30171.943699
HLA A*0216      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.419901       0.059757        -4.360143       26296.656005
HLA B*0803      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.506181       0.145735        -4.360445       32076.033841
HLA A*8001      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.420338       0.059757        -4.360580       26323.130053
HLA A*2501      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.506545       0.145735        -4.360810       32102.941928
HLA B*0802      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.483734       0.122444        -4.361290       30460.265419
HLA A*2301      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.536693       0.174997        -4.361696       34410.693453
HLA A*0203      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.421611       0.059757        -4.361854       26400.426948
HLA B*2705      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.428448       0.066377        -4.362071       26819.331704
HLA A*6801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.569706       0.207531        -4.362175       37128.383262
HLA A*3002      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.422264       0.059757        -4.362507       26440.161721
HLA B*3801      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.575077       0.212403        -4.362674       37590.401223
HLA B*4403      1:109-117       9       GVLTRPSPP       0.250080        0.054954        -4.667736       0.305034        -4.362702       46530.310510
HLA A*6901      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.386935       0.023284        -4.363651       24374.454288
HLA A*3301      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.576959       0.212403        -4.364555       37753.645946
HLA A*3201      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.456473       0.091860        -4.364613       28607.019289
HLA A*0202      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.579527       0.214819        -4.364707       37977.544894
HLA A*3002      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.484535       0.119790        -4.364744       30516.509532
HLA B*1501      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.422621       0.057558        -4.365064       26461.912491
HLA A*0301      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.363503       -0.001650       -4.365153       23094.230029
HLA B*5301      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.578094       0.212403        -4.365690       37852.424331
HLA A*0206      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.557914       0.191859        -4.366055       36133.828026
HLA A*2501      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.496722       0.130576        -4.366146       31384.964112
HLA A*0250      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.581498       0.214819        -4.366679       38150.312849
HLA B*3801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.541867       0.174997        -4.366870       34823.064776
HLA B*5801      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.352849       -0.014281       -4.367129       22534.533545
HLA B*4001      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.424975       0.057558        -4.367418       26605.744299
HLA B*1509      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.547055       0.179262        -4.367793       35241.521778
HLA B*5801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.346954       -0.020998       -4.367952       22230.729533
HLA B*0702      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.428121       0.059757        -4.368364       26799.171828
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HLA A*0219      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.392172       0.023284        -4.368888       24670.156428
HLA B*1509      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.488844       0.119790        -4.369053       30820.793320
HLA A*0250      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.582036       0.212403        -4.369633       38197.605210
HLA A*3301      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.577203       0.207531        -4.369672       37774.893199
HLA A*8001      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.392971       0.022933        -4.370038       24715.575542
HLA A*0202      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.436518       0.066377        -4.370142       27322.374053
HLA B*2705      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.427708       0.057558        -4.370150       26773.667396
HLA B*7301      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.585074       0.214819        -4.370255       38465.733633
HLA A*0101      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.393469       0.022933        -4.370536       24743.938011
HLA A*0211      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.516305       0.145735        -4.370569       32832.548455
HLA A*2501      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.491344       0.120389        -4.370954       30998.713141
HLA B*5101      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.493529       0.122444        -4.371085       31155.066764
HLA B*5701      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.411701       0.040386        -4.371315       25804.819322
HLA B*4001      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.394305       0.022933        -4.371372       24791.638788
HLA B*5301      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.579008       0.207531        -4.371477       37932.166624
HLA B*0803      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.492352       0.119790        -4.372561       31070.739819
HLA A*3002      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.564791       0.191859        -4.372932       36710.552086
HLA B*3801      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.580535       0.207531        -4.373004       38065.787150
HLA A*1101      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.396410       0.023284        -4.373127       24912.102047
HLA A*6801      1:128-136       9       PDVRTVSRP       0.500795        -0.197515       -4.676746       0.303280        -4.373467       47505.755116
HLA B*1801      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.519267       0.145735        -4.373532       33057.293558
HLA B*4601      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.396977       0.023284        -4.373693       24944.603211
HLA B*1503      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.397179       0.023284        -4.373895       24956.211400
HLA A*6901      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.372309       -0.001650       -4.373959       23567.274325
HLA B*4601      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.414562       0.040386        -4.374177       25975.415029
HLA A*2402      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.497293       0.122444        -4.374849       31426.250013
HLA B*0802      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.466940       0.091860        -4.375080       29304.854167
HLA B*1503      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.550121       0.174997        -4.375124       35491.203914
HLA A*0219      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.435912       0.059757        -4.376155       27284.265412
HLA A*0202      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.555600       0.179262        -4.376338       35941.792331
HLA B*5301      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.595877       0.219167        -4.376710       39434.555685
HLA A*2501      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.399817       0.022933        -4.376884       25108.289501
HLA B*5801      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.352400       -0.024958       -4.377358       22511.260889
HLA A*1101      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.499922       0.122444        -4.377478       31617.071033
HLA B*4801      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.418122       0.040386        -4.377736       26189.183891
HLA A*6801      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.592945       0.214819        -4.378125       39169.208399
HLA B*4001      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.401476       0.023284        -4.378192       25204.371012
HLA B*5101      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.508777       0.130576        -4.378201       32268.356318
HLA A*2403      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.401708       0.023284        -4.378425       25217.873560
HLA A*0212      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.436157       0.057558        -4.378599       27299.620636
HLA A*1101      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.438783       0.059757        -4.379026       27465.236069
HLA A*2501      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.419689       0.040386        -4.379303       26283.855542
HLA A*3201      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.566795       0.187363        -4.379432       36880.349376
HLA A*6901      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.365242       -0.014281       -4.379523       23186.868883
HLA A*0206      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.525338       0.145735        -4.379603       33522.651618
HLA B*1501      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.420034       0.040386        -4.379648       26304.766189
HLA B*4402      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.365505       -0.014281       -4.379786       23200.922240
HLA A*2301      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.525982       0.145735        -4.380247       33572.379414
HLA A*2501      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.472689       0.091860        -4.380829       29695.370916
HLA A*0206      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.555898       0.174997        -4.380901       35966.494837
HLA B*5301      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.595835       0.214819        -4.381015       39430.715813
HLA A*6802      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.422523       0.040386        -4.382137       26455.900621
HLA A*0301      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.368036       -0.014281       -4.382316       23336.495840
HLA A*2603      1:94-102        9       ASAAAIAVG       0.821433        -0.563470       -4.640299       0.257963        -4.382336       43681.612797
HLA B*3901      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.504903       0.122444        -4.382459       31981.773496
HLA A*0216      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.474352       0.091860        -4.382493       29809.328271
HLA B*0801      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.423108       0.040386        -4.382722       26491.562384
HLA A*0301      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.359115       -0.023878       -4.382992       22862.022577
HLA A*2402      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.570470       0.187363        -4.383107       37193.720325
HLA B*1503      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.475022       0.091860        -4.383162       29855.324292
HLA A*0211      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.559164       0.174997        -4.384167       36237.973184
HLA B*1502      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.592419       0.207531        -4.384888       39121.771307
HLA B*2705      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.476899       0.091860        -4.385039       29984.653285
HLA B*5701      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.408553       0.023284        -4.385269       25618.430105
HLA B*5801      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.361955       -0.023878       -4.385833       23012.042989
HLA B*5401      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.561069       0.174997        -4.386072       36397.313687
HLA B*3801      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.578324       0.191859        -4.386465       37872.497838
HLA A*2902      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.362688       -0.023878       -4.386566       23050.917479
HLA A*3301      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.601480       0.214819        -4.386661       39946.660046
HLA B*4501      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.634895       0.247860        -4.387035       43141.461081
HLA A*2501      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.444749       0.057558        -4.387191       27845.093379
HLA B*3501      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.427727       0.040386        -4.387341       26774.826161
HLA B*0702      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.427898       0.040386        -4.387512       26785.402215
HLA B*1502      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.508095       0.120389        -4.387706       32217.771222
HLA A*0202      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.533609       0.145735        -4.387873       34167.133998
HLA B*1501      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.199225       -0.189096       -4.388321       15820.680005
HLA B*1801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.519112       0.130576        -4.388536       33045.492470
HLA B*5701      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.411832       0.022933        -4.388900       25812.638174
HLA B*4002      1:99-107        9       IAVGLGAFG       0.719922        -0.472062       -4.636845       0.247860        -4.388985       43335.610774
HLA A*0301      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.368158       -0.020998       -4.389156       23343.061652
HLA B*1801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.481441       0.091860        -4.389581       30299.857493
HLA A*0211      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.520322       0.130576        -4.389746       33137.688656
HLA A*1101      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.482162       0.091860        -4.390302       30350.222399
HLA A*0301      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.365684       -0.024958       -4.390642       23210.463297
HLA A*2403      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.376630       -0.014281       -4.390911       23802.910299
HLA B*4402      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.414311       0.022933        -4.391378       25960.383300
HLA B*1517      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.451680       0.059757        -4.391922       28293.042986
HLA B*0801      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.415570       0.023284        -4.392287       26035.769885
HLA A*8001      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.450106       0.057558        -4.392548       28190.676926
HLA B*1502      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.605369       0.212403        -4.392965       40305.923042
HLA B*3501      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.204371       -0.189096       -4.393466       16009.232748
HLA B*0702      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.368900       -0.024958       -4.393858       23383.001328
HLA A*3301      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.513664       0.119790        -4.393873       32633.508837
HLA A*0212      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.205902       -0.189096       -4.394998       16065.800984
HLA B*0702      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.452995       0.057558        -4.395438       28378.887802
HLA A*0101      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.374555       -0.020998       -4.395553       23689.476561
HLA A*0201      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.394059       -0.001650       -4.395708       24777.560185
HLA B*5101      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.455568       0.059757        -4.395811       28547.498387
HLA B*0801      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.297041       -0.098967       -4.396008       19817.152687
HLA A*6802      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.419503       0.023284        -4.396220       26272.624715
HLA B*4601      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.394768       -0.001650       -4.396418       24818.074516
HLA B*4402      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.456294       0.059757        -4.396537       28595.259885
HLA A*6802      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.372702       -0.024958       -4.397659       23588.575835
HLA B*1801      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.520137       0.122444        -4.397693       33123.529255
HLA A*0203      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.438351       0.040386        -4.397965       27437.910238
HLA B*3501      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.421327       0.023284        -4.398043       26383.150974
HLA B*4402      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.373103       -0.024958       -4.398061       23610.407512
HLA A*0250      1:14-22 9       TPYALNAVS       1.157033        -0.969670       -4.585480       0.187363        -4.398118       38501.750982
HLA B*3801      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.577415       0.179262        -4.398153       37793.289896
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HLA B*4002	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.632517	0.234317	-4.398200	42905.915245
HLA B*5401	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.544132	0.145735	-4.398397	35005.146071
HLA B*4501	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.585972	0.187363	-4.398609	38545.308254
HLA A*2403	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.421616	0.022933	-4.398683	26400.712597
HLA B*4801	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.421881	0.022933	-4.398948	26416.856748
HLA B*0802	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.465443	0.066377	-4.399066	29204.040534
HLA B*1501	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.378098	-0.020998	-4.399096	23883.528456
HLA A*0212	1:3-11	9	EHTDFELLE	0.815912	-0.775526	-4.439970	0.040386	-4.399584	27540.373521
HLA B*1503	1:16-24	9	YALNAVSDD	0.579587	-0.829740	-4.149435	-0.250153	-4.399588	14107.006299
HLA A*0101	1:22-30	9	SDDERADID	0.941402	-0.955683	-4.385575	-0.014281	-4.399855	24298.225006
HLA A*0202	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.422851	0.022933	-4.399919	26475.945500
HLA A*6901	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.379238	-0.020998	-4.400236	23946.276250
HLA A*0216	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.458211	0.057558	-4.400654	28721.771825
HLA A*0202	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.461195	0.059757	-4.401438	28919.785914
HLA A*0219	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.459135	0.057558	-4.401577	28782.901755
HLA A*0250	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.581143	0.179262	-4.401882	38119.160842
HLA B*0803	1:37-45	9	PSPVAAAFN	0.822262	-0.699818	-4.524396	0.122444	-4.401953	33450.007557
HLA A*2601	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.400581	-0.001650	-4.402230	25152.474078
HLA B*1801	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.468688	0.066377	-4.402311	29423.042652
HLA B*1502	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.522249	0.119790	-4.402458	33285.017600
HLA B*7301	1:45-53	9	NDEVRAVRE	1.078509	-0.903512	-4.577701	0.174997	-4.402704	37818.241945
HLA A*2403	1:3-11	9	EHTDFELLE	0.815912	-0.775526	-4.443109	0.040386	-4.402723	27740.145720
HLA A*0250	1:15-23	9	PYALNAVSD	1.062946	-0.871087	-4.594632	0.191859	-4.402773	39321.649243
HLA B*4002	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.590941	0.187363	-4.403578	38988.873193
HLA B*3901	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.470600	0.066377	-4.404223	29552.897134
HLA B*1801	1:121-129	9	AEQVLTAPD	0.414330	-0.778826	-4.039770	-0.364496	-4.404266	10958.984137
HLA A*0219	1:3-11	9	EHTDFELLE	0.815912	-0.775526	-4.445024	0.040386	-4.404638	27862.723706
HLA B*3901	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.462464	0.057558	-4.404906	29004.393970
HLA B*3501	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.462525	0.057558	-4.404967	29008.473931
HLA A*2601	1:22-30	9	SDDERADID	0.941402	-0.955683	-4.391115	-0.014281	-4.405395	24610.171208
HLA B*4801	1:17-25	9	ALNAVSDDE	0.693197	-0.669913	-4.428786	0.023284	-4.405503	26840.232748
HLA A*0101	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.382351	-0.023878	-4.406229	24118.542301
HLA B*5101	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.498387	0.091860	-4.406528	31505.575800
HLA A*0211	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.466423	0.059757	-4.406665	29269.996991
HLA A*3101	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.382816	-0.023878	-4.406694	24144.390913
HLA B*4501	1:57-65	9	VVSAATTAE	0.760296	-0.525979	-4.641652	0.234317	-4.407334	43817.941198
HLA A*0101	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.382414	-0.024958	-4.407372	24122.065481
HLA A*3101	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.405832	-0.001650	-4.407481	25458.441226
HLA A*0201	1:22-30	9	SDDERADID	0.941402	-0.955683	-4.393283	-0.014281	-4.407564	24733.365175
HLA A*3002	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.538261	0.130576	-4.407685	34535.085156
HLA B*4601	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.387034	-0.020998	-4.408031	24379.993167
HLA B*1801	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.468979	0.059757	-4.409222	29442.787023
HLA A*2403	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.408061	-0.001650	-4.409711	25589.480565
HLA A*2601	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.386444	-0.023878	-4.410322	24346.910475
HLA A*0203	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.389491	-0.020998	-4.410489	24518.344386
HLA B*5301	1:15-23	9	PYALNAVSD	1.062946	-0.871087	-4.602488	0.191859	-4.410630	40039.477616
HLA A*6802	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.433567	0.022933	-4.410635	27137.352724
HLA A*0201	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.389646	-0.020998	-4.410644	24527.100290
HLA B*4001	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.409391	-0.001650	-4.411041	25667.955568
HLA A*0202	1:45-53	9	NDEVRAVRE	1.078509	-0.903512	-4.586044	0.174997	-4.411047	38551.773097
HLA A*0206	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.541930	0.130576	-4.411355	34828.151648
HLA A*0206	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.468944	0.057558	-4.411386	29440.397887
HLA A*2902	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.469291	0.057558	-4.411734	29463.979181
HLA A*2603	1:14-22	9	TPYALNAVS	1.157033	-0.969670	-4.599970	0.187363	-4.412607	39807.944648
HLA B*5701	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.412323	-0.001650	-4.413973	25841.840173
HLA A*0206	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.534671	0.120389	-4.414281	34250.784094
HLA B*0802	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.472000	0.057558	-4.414443	29648.338143
HLA B*5301	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.534997	0.120389	-4.414608	34276.549500
HLA A*3101	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.389801	-0.024958	-4.414759	24535.859321
HLA A*0203	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.413562	-0.001650	-4.415211	25915.620684
HLA A*3301	1:15-23	9	PYALNAVSD	1.062946	-0.871087	-4.607079	0.191859	-4.415220	40464.976864
HLA A*2402	1:45-53	9	NDEVRAVRE	1.078509	-0.903512	-4.590433	0.174997	-4.415436	38943.339897
HLA B*1502	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.594890	0.179262	-4.415628	39345.056040
HLA B*3501	1:16-24	9	YALNAVSDD	0.579587	-0.829740	-4.165909	-0.250153	-4.416062	14652.423044
HLA A*2602	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.595424	0.179262	-4.416162	39393.403213
HLA B*1509	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.536722	0.120389	-4.416332	34412.927422
HLA B*3901	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.508244	0.091860	-4.416384	32228.753652
HLA B*1501	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.392736	-0.023878	-4.416614	24702.208306
HLA A*2301	1:37-45	9	PSPVAAAFN	0.822262	-0.699818	-4.539102	0.122444	-4.416658	34602.035459
HLA A*2601	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.395816	-0.020998	-4.416814	24878.028128
HLA A*2601	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.391923	-0.024958	-4.416881	24656.013426
HLA A*2301	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.547607	0.130576	-4.417031	35286.353660
HLA A*0201	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.392376	-0.024958	-4.417334	24681.770426
HLA A*0211	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.538643	0.120389	-4.418254	34565.552037
HLA B*1502	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.441257	0.022933	-4.418324	27622.141388
HLA B*4001	1:22-30	9	SDDERADID	0.941402	-0.955683	-4.404215	-0.014281	-4.418496	25363.860936
HLA A*2902	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-4.229444	-0.189096	-4.418540	16960.717578
HLA A*1101	1:78-86	9	TKPEVRRQS	0.961360	-0.903802	-4.476178	0.057558	-4.418620	29934.895026
HLA B*0802	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.441577	0.022933	-4.418644	27642.471716
HLA B*4001	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.394991	-0.023878	-4.418869	24830.832782
HLA B*4001	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.394188	-0.024958	-4.419146	24784.933694
HLA A*2501	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.478903	0.059757	-4.419146	30123.341280
HLA B*1517	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.418218	-0.001650	-4.419868	26194.993439
HLA B*4001	1:121-129	9	AEQVLTAPD	0.414330	-0.778826	-4.055404	-0.364496	-4.419900	11360.665466
HLA A*6801	1:37-45	9	PSPVAAAFN	0.822262	-0.699818	-4.542365	0.122444	-4.419922	34863.026138
HLA B*2705	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.443041	0.022933	-4.420108	27735.794000
HLA A*2602	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.565902	0.145735	-4.420167	36804.610184
HLA B*1801	1:73-81	9	AILDATKPE	0.570602	-0.547669	-4.443177	0.022933	-4.420244	27744.498124
HLA A*3301	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.551267	0.130576	-4.420691	35585.025403
HLA A*0201	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.397087	-0.023878	-4.420965	24950.946552
HLA B*5301	1:45-53	9	NDEVRAVRE	1.078509	-0.903512	-4.596039	0.174997	-4.421042	39449.278656
HLA A*0211	1:37-45	9	PSPVAAAFN	0.822262	-0.699818	-4.543500	0.122444	-4.421056	34954.241525
HLA B*3801	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.566833	0.145735	-4.421097	36883.541812
HLA B*4501	1:195-203	9	TTATLTDLG	0.805893	-0.593490	-4.633870	0.212403	-4.421467	43039.822728
HLA B*1801	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.396525	-0.024958	-4.421483	24918.706736
HLA B*0801	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.396551	-0.024958	-4.421509	24920.189662
HLA B*0702	1:17-25	9	ALNAVSDDE	0.693197	-0.669913	-4.444843	0.023284	-4.421559	27851.119586
HLA A*2602	1:15-23	9	PYALNAVSD	1.062946	-0.871087	-4.613486	0.191859	-4.421628	41066.372484
HLA A*0216	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.400766	-0.020998	-4.421764	25163.226071
HLA B*4501	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.642216	0.219167	-4.423049	43874.870197
HLA A*2301	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.543986	0.120389	-4.423597	34993.406855
HLA A*0206	1:17-25	9	ALNAVSDDE	0.693197	-0.669913	-4.447425	0.023284	-4.424141	28017.200757
HLA A*0212	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.400341	-0.023878	-4.424219	25138.598553
HLA A*0206	1:37-45	9	PSPVAAAFN	0.822262	-0.699818	-4.547137	0.122444	-4.424693	35248.195255
HLA A*0212	1:38-46	9	SPVAAAFND	0.902542	-0.927500	-4.399881	-0.024958	-4.424838	25111.957262
HLA A*0250	1:45-53	9	NDEVRAVRE	1.078509	-0.903512	-4.599996	0.174997	-4.424998	39810.313641
HLA B*4601	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.401333	-0.023878	-4.425210	25196.054861
HLA B*2705	1:3-11	9	EHTDFELLE	0.815912	-0.775526	-4.465706	0.040386	-4.425320	29221.740845
HLA B*1509	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.556467	0.130576	-4.425891	36013.612763
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HLA B*5401      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.548408       0.122444        -4.425964       35351.509024
HLA B*5101      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.492455       0.066377        -4.426078       31078.136627
HLA B*0702      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.405397       -0.020998       -4.426395       25432.974413
HLA B*4403      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.639133       0.212403        -4.426730       43564.558823
HLA A*2603      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.634639       0.207531        -4.427108       43116.029013
HLA B*1502      1:15-23 9       PYALNAVSD       1.062946        -0.871087       -4.618977       0.191859        -4.427118       41588.866939
HLA B*0802      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.486884       0.059757        -4.427127       30682.047834
HLA B*0803      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.468081       0.040386        -4.427695       29382.004046
HLA A*0250      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.558288       0.130576        -4.427712       36164.922718
HLA B*4002      1:132-140       9       TVSRPLGAG       0.718172        -0.499005       -4.647011       0.219167        -4.427844       44362.002658
HLA A*0212      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.426277       -0.001650       -4.427927       26685.603417
HLA B*5401      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.520301       0.091860        -4.428441       33136.075254
HLA B*7301      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.559281       0.130576        -4.428706       36247.776681
HLA B*4002      1:195-203       9       TTATLTDLG       0.805893        -0.593490       -4.641488       0.212403        -4.429084       43801.350826
HLA A*0212      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.414807       -0.014281       -4.429088       25990.033649
HLA A*1101      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.235024       -0.194071       -4.429095       17180.043115
HLA B*4601      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.414915       -0.014281       -4.429196       25996.502201
HLA A*2402      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.521302       0.091860        -4.429442       33212.529141
HLA B*1517      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.469841       0.040386        -4.429455       29501.301665
HLA B*4501      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.604760       0.174997        -4.429763       40249.487490
HLA A*8001      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.428124       -0.001650       -4.429773       26799.316809
HLA B*1517      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.405113       -0.024958       -4.430071       25416.331523
HLA B*5701      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.409419       -0.020998       -4.430417       25669.621952
HLA A*2602      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.553288       0.122444        -4.430844       35750.970631
HLA B*4002      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.638746       0.207531        -4.431215       43525.689067
HLA B*4403      1:57-65 9       VVSAATTAE       0.760296        -0.525979       -4.665600       0.234317        -4.431283       46302.055249
HLA B*1503      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.471805       0.040386        -4.431419       29635.028411
HLA A*0219      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.429954       -0.001650       -4.431604       26912.495585
HLA B*1502      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.455321       0.023284        -4.432038       28531.286917
HLA B*4801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.411536       -0.020998       -4.432534       25795.049087
HLA A*3201      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.611893       0.179262        -4.432632       40916.020844
HLA B*1801      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.490343       0.057558        -4.432785       30927.355368
HLA B*4001      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.412063       -0.020998       -4.433061       25826.326866
HLA B*4002      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.648202       0.214819        -4.433383       44483.846392
HLA B*4601      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.239411       -0.194071       -4.433482       17354.445341
HLA B*4801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.239521       -0.194071       -4.433592       17358.858527
HLA B*1509      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.491647       0.057558        -4.434089       31020.353940
HLA A*6802      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.432658       -0.001650       -4.434308       27080.596660
HLA A*2402      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.580100       0.145735        -4.434365       38027.708846
HLA A*2603      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.580187       0.145735        -4.434452       38035.321459
HLA A*0202      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.556899       0.122444        -4.434455       36049.479267
HLA A*2902      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.240386       -0.194071       -4.434457       17393.451646
HLA B*4501      1:224-232       9       TILAELPLG       0.771690        -0.564159       -4.642331       0.207531        -4.434800       43886.502290
HLA A*0216      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.433217       -0.001650       -4.434867       27115.486837
HLA A*1101      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.475994       0.040386        -4.435609       29922.266022
HLA B*4601      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.410681       -0.024958       -4.435639       25744.303466
HLA A*6901      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.336686       -0.098967       -4.435653       21711.331851
HLA B*3801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.566285       0.130576        -4.435709       36837.079243
HLA A*3101      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.421914       -0.014281       -4.436195       26418.857595
HLA B*5701      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.412323       -0.023878       -4.436201       25841.840173
HLA A*2902      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.434594       -0.001650       -4.436244       27201.584620
HLA A*6802      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.412441       -0.023878       -4.436319       25848.831193
HLA A*6802      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.415930       -0.020998       -4.436928       26057.328952
HLA B*0803      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.460323       0.023284        -4.437040       28861.800122
HLA B*0801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.416130       -0.020998       -4.437127       26069.313925
HLA B*1517      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.461012       0.023284        -4.437728       28907.585167
HLA B*3801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.558781       0.120389        -4.438392       36206.032192
HLA A*2301      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.530303       0.091860        -4.438443       33908.050830
HLA B*4801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.437341       -0.001650       -4.438990       27374.156917
HLA B*5701      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.414144       -0.024958       -4.439102       25950.413776
HLA B*3901      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.498862       0.059757        -4.439105       31540.023837
HLA A*2403      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.415664       -0.023878       -4.439542       26041.404519
HLA A*3002      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.614880       0.174997        -4.439882       41198.327593
HLA B*1501      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.414990       -0.024958       -4.439948       26001.003013
HLA B*1502      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.614957       0.174997        -4.439960       41205.683237
HLA B*1501      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.425758       -0.014281       -4.440039       26653.717562
HLA B*0803      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.532530       0.091860        -4.440670       34082.397501
HLA A*0219      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.419687       -0.020998       -4.440685       26283.713350
HLA A*2301      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.500511       0.059757        -4.440754       31660.032452
HLA B*2705      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.246854       -0.194071       -4.440925       17654.438379
HLA A*6901      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.247206       -0.194071       -4.441278       17668.770477
HLA B*4403      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.616689       0.174997        -4.441691       41370.301891
HLA B*1509      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.564453       0.122444        -4.442009       36681.964820
HLA B*4501      1:141-149       9       TATVVFSRD       0.983382        -0.804120       -4.621780       0.179262        -4.442518       41858.149433
HLA B*4501      1:114-122       9       PSPPPTVAE       1.033102        -0.818283       -4.657401       0.214819        -4.442581       45436.049728
HLA B*4002      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.617720       0.174997        -4.442723       41468.670694
HLA A*3201      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.618009       0.174997        -4.443012       41496.273809
HLA A*8001      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.422342       -0.020998       -4.443340       26444.882407
HLA B*4402      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.419562       -0.023878       -4.443440       26276.178255
HLA B*5301      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.589350       0.145735        -4.443615       38846.337818
HLA A*6801      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.618895       0.174997        -4.443898       41580.992994
HLA A*0202      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.574647       0.130576        -4.444071       37553.204776
HLA B*5101      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.501646       0.057558        -4.444088       31742.867548
HLA B*5101      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.420368       -0.023878       -4.444246       26324.981386
HLA B*3901      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.467217       0.022933        -4.444284       29323.567389
HLA B*0802      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.484737       0.040386        -4.444351       30530.710656
HLA A*3101      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.345427       -0.098967       -4.444393       22152.694058
HLA A*8001      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.419644       -0.024958       -4.444602       26281.154019
HLA B*4402      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.442998       -0.001650       -4.444648       27733.093275
HLA A*3301      1:45-53 9       NDEVRAVRE       1.078509        -0.903512       -4.619987       0.174997        -4.444990       41685.725754
HLA A*0216      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.485538       0.040386        -4.445152       30587.084845
HLA B*7301      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.565684       0.120389        -4.445295       36786.097718
HLA A*0211      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.502945       0.057558        -4.445388       31837.973883
HLA A*0301      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.346705       -0.098967       -4.445671       22217.985014
HLA B*5101      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.486201       0.040386        -4.445815       30633.783770
HLA A*2501      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.422384       -0.023878       -4.446262       26447.457683
HLA A*0212      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.425377       -0.020998       -4.446375       26630.368422
HLA A*6802      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.432104       -0.014281       -4.446385       27046.044008
HLA B*5701      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.432759       -0.014281       -4.447040       27086.897023
HLA A*0203      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.422114       -0.024958       -4.447072       26431.008851
HLA A*2403      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.422628       -0.024958       -4.447586       26462.341962
HLA A*3002      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.593697       0.145735        -4.447961       39237.075471
HLA A*0250      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.594009       0.145735        -4.448274       39265.317304
HLA B*7301      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.571485       0.122444        -4.449041       37280.746385
HLA A*0219      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.424393       -0.024958       -4.449351       26570.072570
HLA B*2705      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.472769       0.023284        -4.449485       29700.833473
HLA A*3101      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.428652       -0.020998       -4.449650       26831.957471
HLA A*8001      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.426089       -0.023878       -4.449967       26674.056624
HLA B*3801      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.572420       0.122444        -4.449976       37361.103377
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HLA B*0803	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.510104	0.059757	-4.450347	32367.138259
HLA B*0802	1:17-25 9	ALNAVSDDE	0.693197	-0.669913	-4.474042	0.023284	-4.450758	29788.048869
HLA B*0801	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.436523	-0.014281	-4.450804	27322.669676
HLA A*2602	1:45-53 9	NDEVRAVRE	1.078509	-0.903512	-4.626312	0.174997	-4.451315	42297.254720
HLA A*0203	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.437688	-0.014281	-4.451969	27396.083184
HLA A*0101	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.353015	-0.098967	-4.451982	22543.190769
HLA B*0803	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.518431	0.066377	-4.452054	32993.689106
HLA B*3801	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.571978	0.119790	-4.452188	37323.124241
HLA B*4002	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.632376	0.179262	-4.453114	42891.990530
HLA A*2602	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.584122	0.130576	-4.453547	38381.547275
HLA B*4801	1:38-46 9	SPVAAAFND	0.902542	-0.927500	-4.428634	-0.024958	-4.453591	26830.796233
HLA B*1503	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.513466	0.059757	-4.453709	32618.682538
HLA A*2403	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.354747	-0.098967	-4.453714	22633.251883
HLA B*4002	1:15-23 9	PYALNAVSD	1.062946	-0.871087	-4.645620	0.191859	-4.453761	44220.153764
HLA B*3501	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.452185	-0.001650	-4.453834	28325.970510
HLA B*4801	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.430320	-0.023878	-4.454198	26935.217776
HLA B*4801	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.440111	-0.014281	-4.454392	27549.314394
HLA B*4403	1:114-122	9	PSPPPTVAE	1.033102	-0.818283	-4.669449	0.214819	-4.454629	46714.179510
HLA A*0203	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.431136	-0.023878	-4.455014	26985.828906
HLA B*4403	1:224-232	9	TILAELPLG	0.771690	-0.564159	-4.663046	0.207531	-4.455516	46030.572737
HLA B*4403	1:132-140	9	TVSRPLGAG	0.718172	-0.499005	-4.674968	0.219167	-4.455800	47311.603283
HLA B*5801	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.357287	-0.098967	-4.456254	22766.000967
HLA A*2501	1:17-25 9	ALNAVSDDE	0.693197	-0.669913	-4.479554	0.023284	-4.456270	30168.516130
HLA B*2705	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.454851	-0.001650	-4.456501	28500.433392
HLA B*1801	1:3-11  9	EHTDFELLE	0.815912	-0.775526	-4.497062	0.040386	-4.456676	31409.593201
HLA A*0206	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.548554	0.091860	-4.456694	35363.368373
HLA A*0211	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.548859	0.091860	-4.456999	35388.247668
HLA A*2403	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.436058	-0.020998	-4.457056	27293.418448
HLA A*2902	1:38-46 9	SPVAAAFND	0.902542	-0.927500	-4.432433	-0.024958	-4.457390	27066.536021
HLA A*6801	1:15-23 9	PYALNAVSD	1.062946	-0.871087	-4.649274	0.191859	-4.457415	44593.719481
HLA B*4403	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.638006	0.179262	-4.458744	43451.579447
HLA B*0702	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.457572	-0.001650	-4.459222	28679.539110
HLA B*0803	1:78-86 9	TKPEVRRQS	0.961360	-0.903802	-4.517002	0.057558	-4.459445	32885.344131
HLA A*1101	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.458037	-0.001650	-4.459687	28710.275888
HLA A*3002	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.552085	0.091860	-4.460225	35652.082348
HLA B*4501	1:15-23 9	PYALNAVSD	1.062946	-0.871087	-4.652446	0.191859	-4.460587	44920.595228
HLA B*1517	1:78-86 9	TKPEVRRQS	0.961360	-0.903802	-4.519281	0.057558	-4.461724	33058.366593
HLA B*4403	1:14-22 9	TPYALNAVS	1.157033	-0.969670	-4.649307	0.187363	-4.461944	44597.097068
HLA B*5301	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.554122	0.091860	-4.462262	35819.696724
HLA A*6801	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.608024	0.145735	-4.462289	40553.074863
HLA A*0250	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.582955	0.119790	-4.463164	38278.488846
HLA B*3901	1:17-25 9	ALNAVSDDE	0.693197	-0.669913	-4.486544	0.023284	-4.463260	30657.989232
HLA A*0250	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.529671	0.066377	-4.463294	33858.741681
HLA B*4402	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.442378	-0.020998	-4.463376	27693.512845
HLA B*2705	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.439594	-0.023878	-4.463472	27516.545376
HLA A*2603	1:141-149	9	TATVVFSRD	0.983382	-0.804120	-4.642961	0.179262	-4.463699	43950.177296
HLA A*8001	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.450047	-0.014281	-4.464328	28186.864473
HLA B*1517	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.440614	-0.023878	-4.464491	27581.227153
HLA B*5301	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.584426	0.119790	-4.464635	38408.342173
HLA A*3002	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.585415	0.120389	-4.465025	38495.919298
HLA A*6802	1:156-164	9	VMNNVAPPS	0.722767	-0.916838	-4.271467	-0.194071	-4.465538	18683.881806
HLA A*0216	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.451703	-0.014281	-4.465984	28294.573650
HLA B*1509	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.558064	0.091860	-4.466205	36146.340912
HLA B*5101	1:73-81 9	AILDATKPE	0.570602	-0.547669	-4.489361	0.022933	-4.466428	30857.497314
HLA B*4601	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-4.277698	-0.189096	-4.466794	18953.872092
HLA A*0201	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-4.277707	-0.189096	-4.466803	18954.282250
HLA B*5301	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.597726	0.130576	-4.467150	39602.809492
HLA A*2402	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.597900	0.130576	-4.467324	39618.666930
HLA A*2402	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.527631	0.059757	-4.467874	33700.121067
HLA B*4403	1:15-23 9	PYALNAVSD	1.062946	-0.871087	-4.661395	0.191859	-4.469536	45855.843940
HLA B*3801	1:78-86 9	TKPEVRRQS	0.961360	-0.903802	-4.527192	0.057558	-4.469634	33666.045603
HLA B*5401	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.536447	0.066377	-4.470070	34391.152410
HLA A*3301	1:37-45 9	PSPVAAAFN	0.822262	-0.699818	-4.592621	0.122444	-4.470177	39139.976964
HLA A*2603	1:15-23 9	PYALNAVSD	1.062946	-0.871087	-4.662471	0.191859	-4.470612	45969.603179
HLA B*0803	1:73-81 9	AILDATKPE	0.570602	-0.547669	-4.493970	0.022933	-4.471038	31186.769429
HLA A*1101	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.457250	-0.014281	-4.471531	28658.291006
HLA A*0219	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.447791	-0.023878	-4.471669	28040.855649
HLA B*3901	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.458432	-0.014281	-4.472713	28736.381410
HLA A*2603	1:45-53 9	NDEVRAVRE	1.078509	-0.903512	-4.647718	0.174997	-4.472721	44434.299554
HLA B*4501	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.539127	0.066377	-4.472751	34604.094645
HLA B*7301	1:101-109	9	VGLGAFGLG	0.679122	-0.619365	-4.532913	0.059757	-4.473156	34112.465021
HLA A*0250	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.593824	0.120389	-4.473434	39248.539630
HLA A*0219	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.459257	-0.014281	-4.473538	28790.999934
HLA A*3001	1:210-218	9	FTVEPGTGS	0.737044	-0.926140	-4.284528	-0.189096	-4.473624	19254.307278
HLA B*0802	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.450185	-0.023878	-4.474063	28195.862690
HLA A*0250	1:37-45 9	PSPVAAAFN	0.822262	-0.699818	-4.596629	0.122444	-4.474185	39502.882514
HLA A*0202	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.594932	0.120389	-4.474543	39348.887570
HLA A*3201	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.620323	0.145735	-4.474588	41717.986898
HLA A*0211	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.473227	-0.001650	-4.474876	29732.182258
HLA B*5101	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.473798	-0.001650	-4.475447	29771.293978
HLA B*1509	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.451821	-0.023878	-4.475698	28302.228210
HLA B*1517	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.376914	-0.098967	-4.475881	23818.496704
HLA B*3501	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.461672	-0.014281	-4.475953	28951.563286
HLA A*2902	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.454990	-0.020998	-4.475988	28509.531711
HLA B*5101	1:17-25 9	ALNAVSDDE	0.693197	-0.669913	-4.499515	0.023284	-4.476232	31587.494117
HLA A*3002	1:174-182	9	LGGAKGPRS	1.138498	-1.140148	-4.474860	-0.001650	-4.476509	29844.181906
HLA A*2601	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.377676	-0.098967	-4.476642	23860.282472
HLA A*3201	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.608200	0.130576	-4.477624	40569.532275
HLA A*2402	1:179-187	9	GPRSAGTMG	0.871076	-0.750687	-4.598090	0.120389	-4.477701	39636.031674
HLA A*2301	1:197-205	9	ATLTDLGAS	0.977434	-0.911057	-4.544844	0.066377	-4.478467	35062.573436
HLA A*2902	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.464480	-0.014281	-4.478760	29139.336164
HLA B*0702	1:22-30 9	SDDERADID	0.941402	-0.955683	-4.464886	-0.014281	-4.479167	29166.620750
HLA B*2705	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.459022	-0.020998	-4.480020	28775.428535
HLA B*5301	1:37-45 9	PSPVAAAFN	0.822262	-0.699818	-4.603111	0.122444	-4.480667	40096.920202
HLA B*1509	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.459985	-0.020998	-4.480983	28839.324842
HLA B*7301	1:3-11  9	EHTDFELLE	0.815912	-0.775526	-4.521396	0.040386	-4.481010	33219.716963
HLA B*7301	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.572962	0.091860	-4.481103	37407.822150
HLA B*5701	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.382654	-0.098967	-4.481621	24135.379920
HLA B*4601	1:207-215	9	ALAFTVEPG	0.423556	-0.522523	-4.382964	-0.098967	-4.481931	24152.621279
HLA A*2301	1:78-86 9	TKPEVRRQS	0.961360	-0.903802	-4.540131	0.057558	-4.482573	34684.123287
HLA B*3801	1:3-11  9	EHTDFELLE	0.815912	-0.775526	-4.523933	0.040386	-4.483547	33414.377263
HLA B*4501	1:176-184	9	GAKGPRSAG	0.805226	-0.674650	-4.614494	0.130576	-4.483918	41161.791748
HLA A*3301	1:158-166	9	NNVAPPSRG	0.751363	-0.605628	-4.629822	0.145735	-4.484087	42640.502227
HLA A*3201	1:171-179	9	MWLLGGAKG	0.611310	-0.491520	-4.604368	0.119790	-4.484578	40213.140452
HLA A*1101	1:220-228	9	QPTGTILAE	0.859570	-0.883448	-4.461052	-0.023878	-4.484930	28910.243866
HLA A*0202	1:193-201	9	PSTTATLTD	1.083413	-0.991553	-4.576867	0.091860	-4.485008	37745.681308
HLA A*0206	1:214-222	9	PGTGSPQPT	0.698667	-0.719665	-4.464266	-0.020998	-4.485264	29124.994402
HLA A*3001	1:186-194	9	MGTAAVTPS	0.673053	-1.083427	-4.075027	-0.410374	-4.485401	11885.752162
HLA A*1101	1:38-46 9	SPVAAAFND	0.902542	-0.927500	-4.460713	-0.024958	-4.485671	28887.730861
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HLA B*3801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.577617       0.091860        -4.485757       37810.877332
HLA A*0250      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.297394       -0.189096       -4.486489       19833.240503
HLA A*0216      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.461733       -0.024958       -4.486691       28955.635816
HLA A*3001      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.237609       -0.250153       -4.487762       17282.584259
HLA B*1517      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.467543       -0.020998       -4.488541       29345.626259
HLA B*1509      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.555287       0.066377        -4.488910       35915.940964
HLA A*6801      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.620617       0.130576        -4.490041       41746.207649
HLA B*1502      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.612739       0.122444        -4.490296       40995.784901
HLA A*1101      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.469313       -0.020998       -4.490310       29465.413788
HLA A*3201      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.613270       0.122444        -4.490827       41045.938434
HLA A*2501      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.466916       -0.024958       -4.491874       29303.268850
HLA A*2501      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.490270       -0.001650       -4.491920       30922.169083
HLA B*4501      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.638788       0.145735        -4.493053       43529.927718
HLA B*2705      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.394416       -0.098967       -4.493382       24797.943231
HLA A*2602      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.613792       0.120389        -4.493403       41095.264031
HLA A*2301      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.534767       0.040386        -4.494381       34258.381948
HLA A*2301      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.517451       0.022933        -4.494518       32919.341751
HLA B*3801      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.561020       0.066377        -4.494643       36393.178908
HLA B*0802      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.470154       -0.024958       -4.495111       29522.535940
HLA B*1801      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.518647       0.023284        -4.495363       33010.114476
HLA B*1502      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.561814       0.066377        -4.495437       36459.786262
HLA B*0802      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.494156       -0.001650       -4.495806       31200.100918
HLA A*2602      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.588643       0.091860        -4.496783       38783.132824
HLA B*4002      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.642660       0.145735        -4.496925       43919.753836
HLA B*1517      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.247547       -0.250153       -4.497700       17682.635897
HLA B*1503      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.473969       -0.023878       -4.497847       29783.053636
HLA A*2501      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.477266       -0.020998       -4.498263       30009.969295
HLA A*2602      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.618364       0.119790        -4.498573       41530.185685
HLA A*3002      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.521626       0.022933        -4.498693       33237.333701
HLA B*7301      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.566647       0.066377        -4.500270       36867.781846
HLA A*0211      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.479686       -0.020998       -4.500683       30177.657181
HLA B*1517      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.486504       -0.014281       -4.500785       30655.169804
HLA B*1509      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.524086       0.023284        -4.500802       33426.129254
HLA A*3001      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.270793       -0.230021       -4.500814       18654.895006
HLA B*4002      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.631643       0.130576        -4.501067       42819.654830
HLA A*0211      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.541515       0.040386        -4.501129       34794.817900
HLA A*0206      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.541987       0.040386        -4.501601       34832.673936
HLA B*4403      1:158-166       9       NNVAPPSRG       0.751363        -0.605628       -4.648021       0.145735        -4.502286       44465.319995
HLA A*0206      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.500789       -0.001650       -4.502438       31680.249622
HLA B*5401      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.560066       0.057558        -4.502508       36313.332105
HLA B*5801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.313619       -0.189096       -4.502715       20588.239975
HLA B*5301      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.544423       0.040386        -4.504037       35028.636320
HLA A*0250      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.597153       0.091860        -4.505293       39550.567758
HLA A*2603      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.636469       0.130576        -4.505893       43298.116468
HLA B*5401      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.546526       0.040386        -4.506140       35198.651011
HLA B*3901      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.504574       -0.001650       -4.506223       31957.560168
HLA B*2705      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.481476       -0.024958       -4.506434       30302.316376
HLA A*3201      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.627341       0.120389        -4.506952       42397.598231
HLA A*2902      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.407993       -0.098967       -4.506960       25585.466229
HLA B*4501      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.626986       0.119790        -4.507196       42362.978062
HLA B*5801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.313262       -0.194071       -4.507333       20571.317159
HLA B*0802      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.486518       -0.020998       -4.507516       30656.164867
HLA A*0216      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.483705       -0.023878       -4.507583       30458.288043
HLA B*4002      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.628166       0.120389        -4.507777       42478.182290
HLA B*1503      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.486788       -0.020998       -4.507786       30675.243143
HLA A*2603      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.630499       0.122444        -4.508055       42706.989961
HLA A*3301      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.548979       0.040386        -4.508593       35398.012787
HLA B*1502      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.568409       0.059757        -4.508652       37017.673686
HLA B*4001      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.410164       -0.098967       -4.509131       25713.681450
HLA B*0802      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.495223       -0.014281       -4.509503       31276.825346
HLA A*2402      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.550487       0.040386        -4.510101       35521.169099
HLA B*5101      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.489497       -0.020998       -4.510495       30867.181101
HLA A*2501      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.496992       -0.014281       -4.511273       31404.495942
HLA B*1503      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.510316       -0.001650       -4.511965       32382.901333
HLA A*3301      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.632496       0.120389        -4.512107       42903.826250
HLA A*2402      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.579428       0.066377        -4.513051       37968.916793
HLA B*3501      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.414137       -0.098967       -4.513104       25949.992613
HLA B*1509      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.573630       0.059757        -4.513872       37465.340021
HLA A*2301      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.537960       0.023284        -4.514676       34511.179068
HLA A*0250      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.575382       0.059757        -4.515625       37616.847309
HLA B*5101      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.503331       -0.014281       -4.517612       31866.233763
HLA A*1101      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.418895       -0.098967       -4.517862       26235.838309
HLA B*4601      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.268117       -0.250153       -4.518270       18540.299509
HLA A*0206      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.504818       -0.014281       -4.519099       31975.545460
HLA B*1502      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.495977       -0.023878       -4.519855       31331.187068
HLA A*3002      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.561227       0.040386        -4.520841       36410.508742
HLA B*5401      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.519627       -0.001650       -4.521276       33084.666838
HLA B*1801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.520379       -0.001650       -4.522028       33141.991445
HLA B*4002      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.641988       0.119790        -4.522198       43851.852493
HLA A*0301      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.333606       -0.189096       -4.522702       21557.891937
HLA A*2603      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.563174       0.040386        -4.522789       36574.169241
HLA B*2705      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.508509       -0.014281       -4.522790       32248.461675
HLA B*4002      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.645926       0.122444        -4.523482       44251.264099
HLA B*0803      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.509444       -0.014281       -4.523725       32317.971801
HLA B*4501      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.644375       0.120389        -4.523986       44093.545510
HLA A*8001      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.425093       -0.098967       -4.524060       26612.941979
HLA A*2603      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.644067       0.119790        -4.524277       44062.307684
HLA B*3901      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.503288       -0.020998       -4.524286       31863.130844
HLA A*0206      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.499365       -0.024958       -4.524323       31576.559381
HLA A*2402      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.582036       0.057558        -4.524478       38197.605210
HLA B*1502      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.616912       0.091860        -4.525052       41391.569186
HLA A*0101      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.336233       -0.189096       -4.525329       21688.674693
HLA B*1801      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.511314       -0.014281       -4.525595       32457.441852
HLA A*0219      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.336724       -0.189096       -4.525820       21713.211227
HLA A*0206      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.502142       -0.023878       -4.526020       31779.122294
HLA A*2603      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.618451       0.091860        -4.526591       41538.499444
HLA B*0803      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.502734       -0.023878       -4.526612       31822.476064
HLA A*0250      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.584322       0.057558        -4.526764       38399.200726
HLA B*5301      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.587092       0.059757        -4.527335       38644.903530
HLA A*0202      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.117017       -0.410374       -4.527391       13092.321643
HLA B*3801      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.550990       0.023284        -4.527706       35562.316349
HLA A*2301      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.526602       -0.001650       -4.528252       33620.362103
HLA B*0702      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.429512       -0.098967       -4.528479       26885.137900
HLA B*5401      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.551732       0.022933        -4.528800       35623.163011
HLA B*1503      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.504308       -0.024958       -4.529266       31938.029923
HLA B*3801      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.506568       -0.023878       -4.530446       32104.678709
HLA A*2603      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.553535       0.022933        -4.530602       35771.284322
HLA B*5301      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.597435       0.066377        -4.531058       39576.251796
HLA A*0202      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.588626       0.057558        -4.531069       38781.664165
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HLA B*4403      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.654689       0.122444        -4.532246       45153.275521
HLA B*4403      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.572641       0.040386        -4.532255       37380.107435
HLA A*6801      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.599396       0.066377        -4.533020       39755.432312
HLA B*4402      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.434293       -0.098967       -4.533260       27182.754973
HLA B*4501      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.573691       0.040386        -4.533305       37470.610158
HLA B*4501      1:37-45 9       PSPVAAAFN       0.822262        -0.699818       -4.656120       0.122444        -4.533677       45302.283846
HLA A*0202      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.574069       0.040386        -4.533683       37503.260983
HLA A*2501      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.344684       -0.189096       -4.533780       22114.855826
HLA B*1509      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.557042       0.022933        -4.534109       36061.377675
HLA A*3301      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.600522       0.066377        -4.534145       39858.585625
HLA B*0803      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.532918       -0.001650       -4.534567       34112.834112
HLA A*3301      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.626491       0.091860        -4.534631       42314.648878
HLA B*1502      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.592545       0.057558        -4.534988       39133.201776
HLA B*0803      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.514244       -0.020998       -4.535242       32677.144269
HLA A*6801      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.655735       0.119790        -4.535944       45262.108497
HLA B*1801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.515102       -0.020998       -4.536100       32741.732617
HLA B*0803      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.511519       -0.024958       -4.536476       32472.721879
HLA B*4403      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.657177       0.120389        -4.536788       45412.704349
HLA B*4403      1:171-179       9       MWLLGGAKG       0.611310        -0.491520       -4.656797       0.119790        -4.537006       45372.921997
HLA B*3801      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.597080       0.059757        -4.537322       39543.935424
HLA B*4403      1:176-184       9       GAKGPRSAG       0.805226        -0.674650       -4.668854       0.130576        -4.538279       46650.285457
HLA B*5401      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.561805       0.023284        -4.538521       36458.997297
HLA A*0101      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.345354       -0.194071       -4.539425       22148.979217
HLA A*2603      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.660227       0.120389        -4.539838       45732.716251
HLA A*2602      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.580699       0.040386        -4.540313       38080.205099
HLA B*3801      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.563870       0.022933        -4.540937       36632.783370
HLA B*0801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.346951       -0.194071       -4.541023       22230.609267
HLA B*4801      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.442667       -0.098967       -4.541634       27711.946694
HLA A*2403      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.291579       -0.250153       -4.541732       19569.453737
HLA A*6801      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.634035       0.091860        -4.542175       43056.124662
HLA A*0250      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.583763       0.040386        -4.543377       38349.791512
HLA A*2602      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.519829       -0.023878       -4.543707       33100.063076
HLA A*3002      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.601354       0.057558        -4.543796       39934.991972
HLA B*4403      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.635952       0.091860        -4.544092       43246.614759
HLA B*3901      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.446473       -0.098967       -4.545440       27955.882126
HLA B*5401      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.136489       -0.410374       -4.546863       13692.703305
HLA A*2602      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.604854       0.057558        -4.547297       40258.198243
HLA A*0211      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.533672       -0.014281       -4.547953       34172.125054
HLA A*0216      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.298557       -0.250153       -4.548710       19886.423018
HLA A*6801      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.572053       0.023284        -4.548770       37329.586047
HLA A*0202      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.528123       -0.020998       -4.549120       33738.246225
HLA B*4002      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.615732       0.066377        -4.549356       41279.311939
HLA B*5301      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.607251       0.057558        -4.549693       40480.960526
HLA A*2301      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.530171       -0.020998       -4.551169       33897.779813
HLA A*0211      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.529126       -0.023878       -4.553004       33816.272425
HLA A*0202      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.551777       -0.001650       -4.553427       35626.824829
HLA A*3201      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.613423       0.059757        -4.553666       41060.374480
HLA B*7301      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.577109       0.023284        -4.553826       37766.719764
HLA B*7301      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.576926       0.022933        -4.553993       37750.786652
HLA A*3201      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.611882       0.057558        -4.554324       40914.914104
HLA A*6801      1:179-187       9       GPRSAGTMG       0.871076        -0.750687       -4.675127       0.120389        -4.554738       47329.011121
HLA A*2402      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.578420       0.023284        -4.555137       37880.899097
HLA B*4002      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.647298       0.091860        -4.555438       44391.291532
HLA B*5401      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.534487       -0.020998       -4.555485       34236.334294
HLA B*4403      1:197-205       9       ATLTDLGAS       0.977434        -0.911057       -4.622078       0.066377        -4.555702       41886.918204
HLA A*2902      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.325928       -0.230021       -4.555950       21180.108163
HLA A*2603      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.615798       0.059757        -4.556041       41285.565275
HLA A*2403      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.362002       -0.194071       -4.556073       23014.532975
HLA A*2402      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.579083       0.022933        -4.556150       37938.733875
HLA B*1502      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.535763       -0.020998       -4.556761       34337.053778
HLA A*0211      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.531973       -0.024958       -4.556931       34038.726971
HLA A*6901      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.307348       -0.250153       -4.557501       20293.102371
HLA A*3301      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.618011       0.059757        -4.558254       41496.498300
HLA A*0250      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.557322       -0.001650       -4.558972       36084.600628
HLA B*4501      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.582997       0.023284        -4.559713       38282.216510
HLA A*6801      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.583068       0.022933        -4.560135       38288.430091
HLA B*0802      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.461327       -0.098967       -4.560293       28928.548600
HLA A*3301      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.618129       0.057558        -4.560571       41507.724391
HLA A*2301      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.536181       -0.024958       -4.561139       34370.134922
HLA B*1509      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.559794       -0.001650       -4.561443       36290.550926
HLA B*1509      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.547322       -0.014281       -4.561603       35263.262892
HLA A*2403      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.372598       -0.189096       -4.561694       23582.961593
HLA B*4501      1:193-201       9       PSTTATLTD       1.083413        -0.991553       -4.656036       0.091860        -4.564176       45293.461813
HLA A*2301      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.540619       -0.023878       -4.564497       34723.173804
HLA A*2301      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.550638       -0.014281       -4.564918       35533.469826
HLA A*3301      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.588077       0.022933        -4.565144       38732.600973
HLA B*0803      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.466338       -0.098967       -4.565305       29264.297039
HLA A*2603      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.623178       0.057558        -4.565620       41993.103045
HLA B*4001      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.376884       -0.189096       -4.565979       23816.821642
HLA A*6801      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.624877       0.057558        -4.567319       42157.674401
HLA A*2601      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.373357       -0.194071       -4.567428       23624.206348
HLA B*3801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.566024       -0.001650       -4.567674       36814.965302
HLA B*1503      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.553422       -0.014281       -4.567703       35761.996631
HLA B*1502      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.373651       -0.194071       -4.567722       23640.187293
HLA B*3801      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.555522       -0.014281       -4.569803       35935.376347
HLA B*3901      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.376179       -0.194071       -4.570250       23778.199083
HLA B*2705      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.056776       -0.513782       -4.570558       11396.614831
HLA B*1502      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.613087       0.040386        -4.572701       41028.621878
HLA B*4002      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.630344       0.057558        -4.572786       42691.744038
HLA A*0250      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.552395       -0.020998       -4.573393       35677.550784
HLA B*5401      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.559253       -0.014281       -4.573534       36245.423600
HLA A*3201      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.613937       0.040386        -4.573551       41109.050234
HLA A*2602      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.633967       0.059757        -4.574209       43049.370254
HLA B*1502      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.475687       -0.098967       -4.574654       29901.067760
HLA A*2602      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.598208       0.023284        -4.574924       39646.754451
HLA B*3801      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.550031       -0.024958       -4.574989       35483.908532
HLA A*2501      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.345076       -0.230021       -4.575098       22134.844553
HLA B*1801      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.477061       -0.098967       -4.576028       29995.848116
HLA B*5701      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.386949       -0.189096       -4.576045       24375.245479
HLA B*4501      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.635823       0.059757        -4.576065       43233.748907
HLA A*0202      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.551465       -0.024958       -4.576422       35601.200005
HLA A*0301      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.347118       -0.230021       -4.577140       22239.149732
HLA B*2705      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.388591       -0.189096       -4.577687       24467.595276
HLA B*5301      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.601422       0.023284        -4.578138       39941.257736
HLA B*4403      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.565665       -0.014281       -4.579946       36784.505683
HLA A*8001      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.386138       -0.194071       -4.580210       24329.793664
HLA B*4002      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.640113       0.059757        -4.580356       43662.948084
HLA B*1501      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.330244       -0.250153       -4.580397       21391.644746
HLA B*1502      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.578932       -0.001650       -4.580582       37925.600510
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HLA A*3101      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.391676       -0.189096       -4.580772       24642.011841
HLA B*1509      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.556321       -0.024958       -4.581279       36001.535350
HLA A*3002      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.557926       -0.023878       -4.581804       36134.805439
HLA B*5301      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.604951       0.022933        -4.582018       40267.128721
HLA B*4001      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.388594       -0.194071       -4.582665       24467.727643
HLA B*4403      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.642867       0.059757        -4.583109       43940.667702
HLA B*5801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.353377       -0.230021       -4.583399       22561.979844
HLA A*2601      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.353499       -0.230021       -4.583521       22568.327743
HLA A*2402      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.581968       -0.001650       -4.583618       38191.612981
HLA B*4002      1:3-11  9       EHTDFELLE       0.815912        -0.775526       -4.624550       0.040386        -4.584164       42125.984817
HLA A*2501      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.485665       -0.098967       -4.584632       30596.021678
HLA B*5701      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.392771       -0.194071       -4.586842       24704.212931
HLA B*7301      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.586336       -0.001650       -4.587985       38577.643315
HLA A*6802      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.337972       -0.250153       -4.588124       21775.675384
HLA A*0202      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.573966       -0.014281       -4.588246       37494.334952
HLA B*4801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.399260       -0.189096       -4.588356       25076.117694
HLA B*1502      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.566179       -0.024958       -4.591137       36828.112531
HLA B*7301      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.566739       -0.024958       -4.591696       36875.561240
HLA A*6901      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.362096       -0.230021       -4.592118       23019.513757
HLA B*4501      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.651017       0.057558        -4.593459       44773.084570
HLA B*5301      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.572594       -0.020998       -4.593591       37376.063209
HLA A*3201      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.569758       -0.023878       -4.593636       37132.802454
HLA B*1501      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.363696       -0.230021       -4.593718       23104.477154
HLA B*4403      1:78-86 9       TKPEVRRQS       0.961360        -0.903802       -4.651858       0.057558        -4.594300       44859.882434
HLA B*5301      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.593220       -0.001650       -4.594869       39194.008673
HLA B*5101      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.496139       -0.098967       -4.595106       31342.884630
HLA B*1801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.401051       -0.194071       -4.595122       25179.703225
HLA A*8001      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.406083       -0.189096       -4.595179       25473.182318
HLA B*3801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.574847       -0.020998       -4.595845       37570.477234
HLA A*2402      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.574875       -0.020998       -4.595873       37572.916339
HLA B*1517      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.401849       -0.194071       -4.595921       25226.060443
HLA A*3002      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.571548       -0.024958       -4.596506       37286.192270
HLA A*6801      1:101-109       9       VGLGAFGLG       0.679122        -0.619365       -4.656731       0.059757        -4.596974       45366.049568
HLA A*0203      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.187022       -0.410374       -4.597396       15382.322818
HLA B*4002      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.620359       0.022933        -4.597426       41721.372381
HLA B*4002      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.583608       -0.014281       -4.597889       38336.101060
HLA A*0206      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.187614       -0.410374       -4.597988       15403.307717
HLA A*2402      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.573284       -0.024958       -4.598242       37435.557414
HLA A*6801      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.573550       -0.024958       -4.598508       37458.449421
HLA B*5801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.348443       -0.250153       -4.598596       22307.108949
HLA A*3301      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.621996       0.023284        -4.598713       41878.987829
HLA B*5401      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.405508       -0.194071       -4.599579       25439.441945
HLA B*4403      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.575044       -0.024958       -4.600002       37587.554292
HLA B*1509      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.501848       -0.098967       -4.600815       31757.639368
HLA B*4501      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.623904       0.022933        -4.600971       42063.359763
HLA B*0801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.350835       -0.250153       -4.600988       22430.299067
HLA B*0702      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.410197       -0.194071       -4.604268       25715.629038
HLA B*4002      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.628622       0.023284        -4.605338       42522.787331
HLA A*0203      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.355240       -0.250153       -4.605393       22658.979605
HLA A*2603      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.628962       0.023284        -4.605679       42556.156734
HLA B*4402      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.417159       -0.189096       -4.606254       26131.159227
HLA A*0250      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.583690       -0.023878       -4.607568       38343.360539
HLA A*0212      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.357599       -0.250153       -4.607752       22782.387346
HLA A*3002      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.508915       -0.098967       -4.607882       32278.657488
HLA B*4403      1:73-81 9       AILDATKPE       0.570602        -0.547669       -4.631368       0.022933        -4.608435       42792.560404
HLA A*0202      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.584656       -0.023878       -4.608534       38428.710489
HLA A*6801      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.585170       -0.023878       -4.609048       38474.266489
HLA B*0801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.420843       -0.189096       -4.609938       26353.764987
HLA B*1801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.422008       -0.189096       -4.611104       26424.575137
HLA A*2402      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.587912       -0.023878       -4.611790       38717.936014
HLA B*4402      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.417838       -0.194071       -4.611909       26172.046150
HLA A*0250      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.597688       -0.014281       -4.611969       39599.381691
HLA A*0301      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.362176       -0.250153       -4.612329       23023.748269
HLA A*6802      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.382454       -0.230021       -4.612476       24124.284044
HLA A*2402      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.599053       -0.014281       -4.613334       39724.044127
HLA B*0801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.383382       -0.230021       -4.613404       24175.890496
HLA B*0702      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.424562       -0.189096       -4.613658       26580.423949
HLA A*2603      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.383960       -0.230021       -4.613982       24208.085981
HLA B*4403      1:17-25 9       ALNAVSDDE       0.693197        -0.669913       -4.637519       0.023284        -4.614236       43402.947559
HLA A*2602      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.384506       -0.230021       -4.614527       24238.488486
HLA B*1501      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.204822       -0.410374       -4.615196       16025.870156
HLA A*0101      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.385253       -0.230021       -4.615274       24280.222931
HLA A*2602      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.592743       -0.024958       -4.617701       39150.989145
HLA A*0250      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.592832       -0.024958       -4.617790       39159.038468
HLA A*2602      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.518828       -0.098967       -4.617795       33023.868082
HLA A*3002      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.604316       -0.014281       -4.618597       40208.354666
HLA A*3002      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.598656       -0.020998       -4.619654       39687.742172
HLA B*5101      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.431101       -0.189096       -4.620196       26983.639140
HLA B*7301      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.605930       -0.014281       -4.620211       40358.070835
HLA A*3201      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.606219       -0.014281       -4.620500       40384.934692
HLA B*7301      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.597317       -0.023878       -4.621195       39565.548087
HLA B*5301      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.607122       -0.014281       -4.621402       40468.917454
HLA A*0101      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.372084       -0.250153       -4.622237       23555.037854
HLA B*7301      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.602383       -0.020998       -4.623381       40029.731391
HLA A*2301      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.524991       -0.098967       -4.623957       33495.821994
HLA A*2603      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.600809       -0.023878       -4.624686       39884.901233
HLA A*3201      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.600557       -0.024958       -4.625515       39861.820214
HLA A*2602      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.624270       -0.001650       -4.625920       42098.873813
HLA A*3001      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.261787       -0.364496       -4.626283       18272.048237
HLA A*8001      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.396575       -0.230021       -4.626596       24921.537853
HLA B*1502      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.612699       -0.014281       -4.626980       40992.014769
HLA A*2501      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.433048       -0.194071       -4.627119       27104.927086
HLA A*0219      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.377107       -0.250153       -4.627260       23829.065193
HLA B*4001      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.397343       -0.230021       -4.627365       24965.663913
HLA A*3201      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.626312       -0.001650       -4.627962       42297.254720
HLA B*4501      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.604880       -0.023878       -4.628758       40260.594030
HLA A*3201      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.607852       -0.020998       -4.628850       40537.062728
HLA A*3301      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.605223       -0.023878       -4.629101       40292.406173
HLA A*0201      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.399540       -0.230021       -4.629561       25092.266314
HLA B*4501      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.617370       -0.014281       -4.631651       41435.257367
HLA A*0201      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.381630       -0.250153       -4.631783       24078.518604
HLA B*0802      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.443160       -0.189096       -4.632256       27743.447481
HLA A*2402      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.533376       -0.098967       -4.632343       34148.839698
HLA A*2603      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.611384       -0.020998       -4.632381       40868.015831
HLA A*2601      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.382802       -0.250153       -4.632955       24143.607215
HLA B*4501      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.608310       -0.024958       -4.633268       40579.848990
HLA A*0211      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.384928       -0.250153       -4.635081       24262.102938
HLA B*0702      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.406772       -0.230021       -4.636793       25513.591814
HLA A*2603      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.635402       -0.001650       -4.637052       43191.902899
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HLA A*0203      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.407293       -0.230021       -4.637315       25544.251928
HLA B*5401      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.387391       -0.250153       -4.637544       24400.049157
HLA B*4402      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.387445       -0.250153       -4.637598       24403.085382
HLA B*5401      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.540460       -0.098967       -4.639426       34710.402454
HLA A*1101      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.450559       -0.189096       -4.639655       28220.126426
HLA A*0206      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.390666       -0.250153       -4.640819       24584.754927
HLA B*4601      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.411384       -0.230021       -4.641405       25785.980038
HLA B*4002      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.640390       -0.001650       -4.642040       43690.829964
HLA A*3301      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.640670       -0.001650       -4.642320       43718.966163
HLA A*2602      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.621576       -0.020998       -4.642574       41838.453097
HLA B*5701      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.414158       -0.230021       -4.644180       25951.256123
HLA B*4801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.394418       -0.250153       -4.644571       24798.077385
HLA B*7301      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.450839       -0.194071       -4.644910       28238.299738
HLA B*5101      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.396175       -0.250153       -4.646328       24898.628520
HLA B*3501      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.416884       -0.230021       -4.646905       26114.624559
HLA B*5701      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.396840       -0.250153       -4.646993       24936.777482
HLA A*3101      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.398358       -0.250153       -4.648511       25024.078703
HLA A*2602      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.634831       -0.014281       -4.649112       43135.159997
HLA A*3002      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.419562       -0.230021       -4.649584       26276.178255
HLA B*4501      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.648221       -0.001650       -4.649871       44485.771655
HLA A*3301      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.626963       -0.024958       -4.651921       42360.686333
HLA B*1501      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.290585       -0.364496       -4.655081       19524.722530
HLA A*2403      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.425575       -0.230021       -4.655596       26642.472829
HLA B*4002      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.633520       -0.023878       -4.657398       43005.143447
HLA A*3001      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.143707       -0.513782       -4.657489       13922.166260
HLA B*4002      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.637550       -0.020998       -4.658548       43406.000133
HLA B*3901      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.469623       -0.189096       -4.658718       29486.462713
HLA B*4501      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.637804       -0.020998       -4.658801       43431.368282
HLA B*4002      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.634495       -0.024958       -4.659453       43101.802931
HLA A*3301      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.639197       -0.020998       -4.660195       43570.922632
HLA A*3301      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.646156       -0.014281       -4.660437       44274.730974
HLA B*4001      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.410387       -0.250153       -4.660540       25726.900123
HLA B*4801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.431286       -0.230021       -4.661308       26995.173906
HLA B*4501      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.564657       -0.098967       -4.663624       36699.233630
HLA B*5101      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.469919       -0.194071       -4.663990       29506.568895
HLA B*4403      1:220-228       9       QPTGTILAE       0.859570        -0.883448       -4.640357       -0.023878       -4.664235       43687.521014
HLA A*0203      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -3.958351       -0.706171       -4.664522       9085.550466
HLA A*0212      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.434587       -0.230021       -4.664609       27201.143151
HLA A*3101      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.435210       -0.230021       -4.665231       27240.167237
HLA B*4403      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.664672       -0.001650       -4.666322       46203.217741
HLA A*2603      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.652359       -0.014281       -4.666639       44911.604557
HLA B*4402      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.437071       -0.230021       -4.667092       27357.131731
HLA A*2902      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.417995       -0.250153       -4.668148       26181.534257
HLA B*1509      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.474244       -0.194071       -4.668315       29801.910997
HLA A*6801      1:174-182       9       LGGAKGPRS       1.138498        -1.140148       -4.667132       -0.001650       -4.668782       46465.662440
HLA A*0216      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.439742       -0.230021       -4.669763       27525.925246
HLA B*2705      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.420967       -0.250153       -4.671120       26361.322331
HLA A*2603      1:38-46 9       SPVAAAFND       0.902542        -0.927500       -4.647570       -0.024958       -4.672528       44419.157902
HLA B*0802      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.478473       -0.194071       -4.672544       30093.533636
HLA A*8001      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.426535       -0.250153       -4.676688       26701.488421
HLA B*3801      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.577852       -0.098967       -4.676819       37831.338132
HLA A*6801      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.578495       -0.098967       -4.677462       37887.457471
HLA A*0219      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.447495       -0.230021       -4.677517       28021.748224
HLA B*0803      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.483729       -0.194071       -4.677800       30459.935847
HLA B*7301      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.579717       -0.098967       -4.678684       37994.190340
HLA B*5401      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.448708       -0.230021       -4.678729       28100.080294
HLA B*0803      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.493578       -0.189096       -4.682674       31158.606419
HLA B*4403      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.665927       -0.020998       -4.686925       46336.886313
HLA A*6801      1:22-30 9       SDDERADID       0.941402        -0.955683       -4.673887       -0.014281       -4.688168       47194.012416
HLA B*1801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.438612       -0.250153       -4.688765       27454.391588
HLA B*1509      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.499778       -0.189096       -4.688874       31606.639019
HLA A*6801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.496691       -0.194071       -4.690762       31382.756930
HLA A*3301      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.507003       -0.189096       -4.696099       32136.826102
HLA B*1503      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.286069       -0.410374       -4.696443       19322.760038
HLA A*6801      1:214-222       9       PGTGSPQPT       0.698667        -0.719665       -4.676168       -0.020998       -4.697166       47442.574952
HLA B*5301      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.600280       -0.098967       -4.699247       39836.381867
HLA A*2501      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.449220       -0.250153       -4.699373       28133.239837
HLA B*1503      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.189329       -0.513782       -4.703111       15464.259030
HLA B*3901      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.453169       -0.250153       -4.703322       28390.251047
HLA B*0802      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.473777       -0.230021       -4.703798       29769.844479
HLA B*0702      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.457567       -0.250153       -4.707720       28679.228805
HLA B*1503      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.479937       -0.230021       -4.709958       30195.130820
HLA A*2301      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.480536       -0.230021       -4.710557       30236.814404
HLA A*0202      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.004721       -0.706171       -4.710892       10109.290604
HLA B*0803      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.481398       -0.230021       -4.711420       30296.907097
HLA B*5101      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.482519       -0.230021       -4.712540       30375.189746
HLA A*3201      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.524817       -0.189096       -4.713912       33482.415235
HLA A*3301      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.520012       -0.194071       -4.714083       33114.033302
HLA B*0801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.307334       -0.410374       -4.717709       20292.443682
HLA B*5801      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.353269       -0.364496       -4.717765       22556.365884
HLA A*3301      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.618827       -0.098967       -4.717794       41574.469998
HLA A*1101      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.488731       -0.230021       -4.718752       30812.790980
HLA A*2402      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.524965       -0.194071       -4.719036       33493.828758
HLA A*0206      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.489189       -0.230021       -4.719211       30845.313419
HLA B*3801      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.526083       -0.194071       -4.720154       33580.190105
HLA B*0802      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.470189       -0.250153       -4.720342       29524.931742
HLA B*5801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.310121       -0.410374       -4.720495       20423.061189
HLA B*1517      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.492208       -0.230021       -4.722230       31060.488066
HLA B*3901      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.492915       -0.230021       -4.722937       31111.107441
HLA A*2301      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.529532       -0.194071       -4.723603       33847.936256
HLA A*2402      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.493634       -0.230021       -4.723656       31162.652232
HLA B*3801      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.535542       -0.189096       -4.724638       34319.596810
HLA A*1101      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.475203       -0.250153       -4.725356       29867.763460
HLA A*3002      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.537074       -0.189096       -4.726170       34440.864274
HLA A*6901      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.316171       -0.410374       -4.726545       20709.554781
HLA B*4002      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.630147       -0.098967       -4.729113       42672.348006
HLA B*1801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.216090       -0.513782       -4.729872       16447.115784
HLA A*0301      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.366241       -0.364496       -4.730736       23240.241532
HLA B*1801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.502461       -0.230021       -4.732483       31802.512225
HLA A*2301      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.544750       -0.189096       -4.733845       35054.986871
HLA A*0202      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.504534       -0.230021       -4.734555       31954.621226
HLA B*4601      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.324906       -0.410374       -4.735280       21130.323578
HLA B*2705      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.505535       -0.230021       -4.735556       32028.349179
HLA A*3101      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.371139       -0.364496       -4.735635       23503.866599
HLA A*6801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.505715       -0.230021       -4.735737       32041.693734
HLA A*6901      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.371405       -0.364496       -4.735901       23518.239316
HLA A*0212      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.376313       -0.364496       -4.740809       23785.532546
HLA B*1801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.333851       -0.410374       -4.744225       21570.024434
HLA A*2403      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.379847       -0.364496       -4.744342       23979.852363
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HLA A*0101      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.384919       -0.364496       -4.749415       24261.577923
HLA B*1509      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.520014       -0.230021       -4.750036       33114.212446
HLA B*4601      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.387452       -0.364496       -4.751948       24403.481439
HLA A*0202      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.501829       -0.250153       -4.751982       31756.264955
HLA B*1502      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.503265       -0.250153       -4.753418       31861.407130
HLA A*0201      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.388986       -0.364496       -4.753482       24489.843037
HLA A*2601      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.389341       -0.364496       -4.753837       24509.856798
HLA B*4501      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.560144       -0.194071       -4.754215       36319.815570
HLA B*4403      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.655265       -0.098967       -4.754232       45213.162383
HLA A*6801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.504818       -0.250153       -4.754971       31975.545460
HLA B*0803      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.505600       -0.250153       -4.755753       32033.201102
HLA A*3002      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.506228       -0.250153       -4.756381       32079.504585
HLA A*0250      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.506310       -0.250153       -4.756463       32085.579289
HLA A*3101      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.346498       -0.410374       -4.756872       22207.410210
HLA B*7301      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.569464       -0.189096       -4.758560       37107.700400
HLA B*0702      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.394378       -0.364496       -4.758874       24795.796857
HLA A*2402      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.572643       -0.189096       -4.761739       37380.309657
HLA B*5301      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.572883       -0.189096       -4.761978       37400.942129
HLA A*2603      1:207-215       9       ALAFTVEPG       0.423556        -0.522523       -4.663286       -0.098967       -4.762253       46055.979817
HLA A*2301      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.513753       -0.250153       -4.763906       32640.218186
HLA A*0301      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.353802       -0.410374       -4.764177       22584.083128
HLA B*1517      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.356591       -0.410374       -4.766966       22729.574324
HLA B*4801      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.402611       -0.364496       -4.767106       25270.315559
HLA B*5301      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.518316       -0.250153       -4.768469       32984.944147
HLA A*0101      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.358722       -0.410374       -4.769097       22841.377176
HLA B*3901      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.405797       -0.364496       -4.770292       25456.375400
HLA A*0201      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.360961       -0.410374       -4.771336       22959.442826
HLA B*4002      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.577875       -0.194071       -4.771946       37833.384821
HLA B*4801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.363682       -0.410374       -4.774056       23103.727210
HLA A*0211      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.544508       -0.230021       -4.774529       35035.459022
HLA A*0203      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.410150       -0.364496       -4.774646       25712.846815
HLA A*2602      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.581254       -0.194071       -4.775325       38128.854434
HLA A*2403      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.365364       -0.410374       -4.775739       23193.392597
HLA B*2705      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.412154       -0.364496       -4.776650       25831.776426
HLA B*5701      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.412382       -0.364496       -4.776878       25845.335447
HLA A*8001      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.413832       -0.364496       -4.778328       25931.748773
HLA A*6802      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.419600       -0.364496       -4.784096       26278.452773
HLA A*2402      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.534158       -0.250153       -4.784311       34210.414042
HLA B*0801      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.420175       -0.364496       -4.784671       26313.305927
HLA B*5701      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.376780       -0.410374       -4.787155       23811.153077
HLA A*2601      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.377088       -0.410374       -4.787462       23828.033914
HLA B*5301      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.594888       -0.194071       -4.788959       39344.843189
HLA B*3801      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.562167       -0.230021       -4.792188       36489.384780
HLA B*4001      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.383949       -0.410374       -4.794323       24207.431175
HLA B*0802      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.431046       -0.364496       -4.795542       26980.281843
HLA B*0702      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.386467       -0.410374       -4.796842       24348.227652
HLA B*4002      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.608503       -0.189096       -4.797599       40597.854647
HLA A*2602      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.549585       -0.250153       -4.799738       35447.454108
HLA A*0216      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.389634       -0.410374       -4.800009       24526.436855
HLA A*0250      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.570387       -0.230021       -4.800409       37186.678506
HLA A*0219      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.438290       -0.364496       -4.802786       27434.051172
HLA B*7301      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.557928       -0.250153       -4.808081       36135.000925
HLA A*3201      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.578533       -0.230021       -4.808554       37890.737084
HLA B*2705      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.399566       -0.410374       -4.809940       25093.759569
HLA A*0212      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.399751       -0.410374       -4.810126       25104.486463
HLA A*3201      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.560475       -0.250153       -4.810628       36347.530690
HLA B*1502      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.582776       -0.230021       -4.812798       38262.753820
HLA B*5301      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.586293       -0.230021       -4.816315       38573.886884
HLA B*3501      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.452965       -0.364496       -4.817461       28376.892026
HLA A*0211      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.113502       -0.706171       -4.819673       12986.790560
HLA B*1503      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.455366       -0.364496       -4.819862       28534.219739
HLA B*1509      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.570500       -0.250153       -4.820653       37196.336198
HLA A*2902      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.456360       -0.364496       -4.820856       28599.591735
HLA A*1101      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.456604       -0.364496       -4.821100       28615.687207
HLA B*7301      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.592278       -0.230021       -4.822299       39109.074701
HLA A*0212      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.116542       -0.706171       -4.822713       13078.022200
HLA B*4403      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.628944       -0.194071       -4.823015       42554.314981
HLA B*1517      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.459943       -0.364496       -4.824439       28836.516663
HLA B*4501      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.636756       -0.189096       -4.825851       43326.702937
HLA A*3301      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.596269       -0.230021       -4.826291       39470.198991
HLA B*3801      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.576144       -0.250153       -4.826296       37682.840092
HLA A*1101      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.416538       -0.410374       -4.826913       26093.865063
HLA B*4403      1:210-218       9       FTVEPGTGS       0.737044        -0.926140       -4.639300       -0.189096       -4.828396       43581.295276
HLA A*6801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.418411       -0.410374       -4.828785       26206.266401
HLA B*3901      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.421320       -0.410374       -4.831694       26382.722788
HLA A*2501      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.468065       -0.364496       -4.832561       29380.891393
HLA A*3301      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.585953       -0.250153       -4.836106       38543.640084
HLA A*0216      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.472668       -0.364496       -4.837163       29693.925113
HLA B*4402      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.427762       -0.410374       -4.838136       26776.998982
HLA A*0219      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.429430       -0.410374       -4.839804       26880.047785
HLA A*2902      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.431084       -0.410374       -4.841458       26982.617310
HLA A*8001      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.434068       -0.410374       -4.844442       27168.641292
HLA A*2603      1:156-164       9       VMNNVAPPS       0.722767        -0.916838       -4.652528       -0.194071       -4.846599       44929.101574
HLA B*0803      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.488181       -0.364496       -4.852677       30773.809313
HLA B*5101      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.447798       -0.410374       -4.858173       28041.310747
HLA B*4002      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.610105       -0.250153       -4.860258       40747.918898
HLA A*3201      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.496595       -0.364496       -4.861091       31375.796835
HLA A*0211      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.450773       -0.410374       -4.861147       28234.022612
HLA A*0206      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.497429       -0.364496       -4.861925       31436.112287
HLA B*1501      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.161474       -0.706171       -4.867645       14503.526788
HLA B*0802      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.457485       -0.410374       -4.867859       28673.799019
HLA B*4403      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.618921       -0.250153       -4.869074       41583.467502
HLA B*5801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.355412       -0.513782       -4.869194       22667.929900
HLA A*2501      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.459795       -0.410374       -4.870169       28826.690189
HLA B*0801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.358837       -0.513782       -4.872620       22847.432875
HLA B*5101      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.509815       -0.364496       -4.874311       32345.607800
HLA B*4002      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.645944       -0.230021       -4.875966       44253.179296
HLA A*0216      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.170576       -0.706171       -4.876747       14810.697995
HLA B*7301      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.512903       -0.364496       -4.877398       32576.358790
HLA B*4501      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.650441       -0.230021       -4.880463       44713.780612
HLA A*0301      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.367695       -0.513782       -4.881477       23318.197079
HLA A*6901      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.370608       -0.513782       -4.884390       23475.147511
HLA A*2603      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.637453       -0.250153       -4.887606       43396.373513
HLA B*1502      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.478600       -0.410374       -4.888974       30102.326265
HLA B*1509      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.525357       -0.364496       -4.889853       33524.102480
HLA A*2601      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.380375       -0.513782       -4.894157       24009.059012
HLA A*0101      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.381865       -0.513782       -4.895647       24091.548340
HLA A*0211      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.533303       -0.364496       -4.897799       34143.113193
HLA B*4403      1:39-47 9       PVAAAFNDE       0.566007        -0.796028       -4.667797       -0.230021       -4.897818       46536.855790
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HLA B*4501      1:16-24 9       YALNAVSDD       0.579587        -0.829740       -4.649685       -0.250153       -4.899838       44635.957710
HLA A*2301      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.535418       -0.364496       -4.899913       34309.757964
HLA B*5401      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.537906       -0.364496       -4.902402       34506.885197
HLA A*0202      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.539806       -0.364496       -4.904302       34658.239008
HLA A*0201      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.394594       -0.513782       -4.908376       24808.141040
HLA B*4001      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.397844       -0.513782       -4.911626       24994.448588
HLA B*0702      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.398010       -0.513782       -4.911793       25004.050853
HLA B*4601      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.398680       -0.513782       -4.912462       25042.632294
HLA B*1501      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.398880       -0.513782       -4.912662       25054.150561
HLA B*3901      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.399937       -0.513782       -4.913719       25115.217943
HLA A*3101      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.405510       -0.513782       -4.919292       25439.579570
HLA B*3501      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.406236       -0.513782       -4.920018       25482.141354
HLA B*5701      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.408943       -0.513782       -4.922725       25641.446855
HLA A*6802      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.409330       -0.513782       -4.923112       25664.345442
HLA A*3002      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.561443       -0.364496       -4.925939       36428.635120
HLA B*4801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.416254       -0.513782       -4.930036       26076.789697
HLA B*0803      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.519866       -0.410374       -4.930241       33102.928283
HLA A*0203      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.417227       -0.513782       -4.931009       26135.259182
HLA A*3001      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.225774       -0.706171       -4.931945       16817.999180
HLA A*0212      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.421660       -0.513782       -4.935442       26403.426410
HLA B*3801      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.571163       -0.364496       -4.935659       37253.125818
HLA A*2301      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.526144       -0.410374       -4.936518       33584.913730
HLA A*0201      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.234108       -0.706171       -4.940279       17143.833897
HLA B*5301      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.531750       -0.410374       -4.942124       34021.237621
HLA B*1509      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.431911       -0.513782       -4.945693       27034.048749
HLA A*2402      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.582887       -0.364496       -4.947382       38272.483928
HLA B*4402      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.435583       -0.513782       -4.949366       27263.608557
HLA B*1502      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.585384       -0.364496       -4.949880       38493.212030
HLA A*0250      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.541014       -0.410374       -4.951388       34754.746701
HLA A*2403      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.439686       -0.513782       -4.953468       27522.351586
HLA A*8001      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.440689       -0.513782       -4.954471       27586.002331
HLA B*0802      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.443872       -0.513782       -4.957654       27788.961734
HLA A*0250      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.593293       -0.364496       -4.957788       39200.582317
HLA A*3002      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.550189       -0.410374       -4.960563       35496.772452
HLA A*2602      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.603593       -0.364496       -4.968088       40141.413448
HLA A*0219      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.454457       -0.513782       -4.968239       28474.542216
HLA B*1517      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.456644       -0.513782       -4.970426       28618.319059
HLA B*5301      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.607112       -0.364496       -4.971608       40468.041734
HLA B*1509      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.561666       -0.410374       -4.972040       36447.362045
HLA B*3801      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.566506       -0.410374       -4.976880       36855.816751
HLA A*2902      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.464679       -0.513782       -4.978462       29152.738695
HLA A*0216      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.469247       -0.513782       -4.983029       29460.950796
HLA B*4501      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.575730       -0.410374       -4.986104       37646.977810
HLA A*3301      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.624571       -0.364496       -4.989067       42128.035939
HLA A*3201      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.581157       -0.410374       -4.991532       38120.398184
HLA A*2501      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.478180       -0.513782       -4.991962       30073.190181
HLA B*4002      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.582170       -0.410374       -4.992544       38209.385781
HLA A*2402      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.583220       -0.410374       -4.993595       38301.896309
HLA A*3101      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.287914       -0.706171       -4.994084       19404.993710
HLA B*0803      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.494055       -0.513782       -5.007837       31192.843831
HLA A*2603      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.647554       -0.364496       -5.012050       44417.475815
HLA B*5101      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.498343       -0.513782       -5.012125       31502.337575
HLA A*1101      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.501555       -0.513782       -5.015337       31736.170964
HLA B*7301      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.606048       -0.410374       -5.016422       40368.988946
HLA A*2602      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.607326       -0.410374       -5.017700       40487.969052
HLA A*3301      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.611250       -0.410374       -5.021624       40855.415562
HLA A*0301      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.321889       -0.706171       -5.028060       20984.664663
HLA A*6801      1:121-129       9       AEQVLTAPD       0.414330        -0.778826       -4.675990       -0.364496       -5.040486       47423.072872
HLA A*0206      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.532027       -0.513782       -5.045810       34042.962587
HLA A*3301      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.538437       -0.513782       -5.052219       34549.100323
HLA A*2603      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.643452       -0.410374       -5.053826       43999.898408
HLA A*0250      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.348537       -0.706171       -5.054708       22311.936631
HLA B*4403      1:186-194       9       MGTAAVTPS       0.673053        -1.083427       -4.644575       -0.410374       -5.054949       44113.826174
HLA B*5801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.349733       -0.706171       -5.055904       22373.460197
HLA B*3801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.542804       -0.513782       -5.056587       34898.313139
HLA A*2301      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.543556       -0.513782       -5.057338       34958.780185
HLA B*0801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.353387       -0.706171       -5.059558       22562.468081
HLA B*5401      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.550518       -0.513782       -5.064300       35523.667340
HLA B*1502      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.551895       -0.513782       -5.065677       35636.462992
HLA A*0211      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.552644       -0.513782       -5.066426       35698.015880
HLA B*4601      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.361441       -0.706171       -5.067612       22984.795253
HLA A*0206      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.363792       -0.706171       -5.069963       23109.602422
HLA A*8001      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.366311       -0.706171       -5.072482       23244.013652
HLA B*2705      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.367425       -0.706171       -5.073596       23303.694472
HLA A*2902      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.369391       -0.706171       -5.075562       23409.454664
HLA A*2603      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.565757       -0.513782       -5.079539       36792.267505
HLA A*3002      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.568113       -0.513782       -5.081895       36992.449334
HLA A*2602      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.570028       -0.513782       -5.083810       37155.911342
HLA B*4001      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.378275       -0.706171       -5.084446       23893.220965
HLA A*6901      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.380819       -0.706171       -5.086990       24033.620086
HLA A*0101      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.382863       -0.706171       -5.089034       24147.003424
HLA A*2601      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.385368       -0.706171       -5.091539       24286.660097
HLA A*3201      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.387088       -0.706171       -5.093259       24383.026896
HLA A*0219      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.395005       -0.706171       -5.101176       24831.638788
HLA A*0202      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.591953       -0.513782       -5.105735       39079.888142
HLA A*2402      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.593403       -0.513782       -5.107185       39210.550912
HLA A*0250      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.596420       -0.513782       -5.110202       39483.867239
HLA B*5701      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.407810       -0.706171       -5.113981       25574.672173
HLA B*0702      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.416137       -0.706171       -5.122308       26069.737024
HLA B*5301      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.612053       -0.513782       -5.125835       40931.075491
HLA A*2403      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.421357       -0.706171       -5.127528       26385.006528
HLA B*4801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.422988       -0.706171       -5.129159       26484.254255
HLA A*6802      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.424938       -0.706171       -5.131109       26603.441452
HLA B*4501      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.621411       -0.513782       -5.135193       41822.612199
HLA A*3201      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.622910       -0.513782       -5.136692       41967.212734
HLA B*4402      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.430781       -0.706171       -5.136952       26963.793366
HLA B*4002      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.628551       -0.513782       -5.142333       42515.886584
HLA A*6801      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.638769       -0.513782       -5.152551       43528.043822
HLA B*3501      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.451583       -0.706171       -5.157754       28286.768131
HLA B*1503      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.452551       -0.706171       -5.158722       28349.886097
HLA B*1502      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.454938       -0.706171       -5.161109       28506.138778
HLA B*4403      1:30-38 9       DRRVAAAPS       0.485396        -0.999178       -4.648169       -0.513782       -5.161952       44480.477382
HLA A*1101      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.459527       -0.706171       -5.165698       28808.917461
HLA B*0802      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.464778       -0.706171       -5.170949       29159.363397
HLA B*1517      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.466933       -0.706171       -5.173104       29304.378563
HLA A*2501      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.482030       -0.706171       -5.188201       30341.029076
HLA B*3901      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.484478       -0.706171       -5.190649       30512.547607
HLA B*1801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.502844       -0.706171       -5.209015       31830.568428
HLA B*5101      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.511021       -0.706171       -5.217192       32435.500377
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HLA A*3002      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.521659       -0.706171       -5.227830       33239.851140
HLA B*0803      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.522970       -0.706171       -5.229141       33340.344486
HLA A*2301      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.535314       -0.706171       -5.241485       34301.592009
HLA B*1509      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.540673       -0.706171       -5.246844       34727.494589
HLA B*5401      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.548241       -0.706171       -5.254412       35337.933042
HLA B*3801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.558151       -0.706171       -5.264322       36153.576901
HLA A*2402      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.575615       -0.706171       -5.281786       37636.999499
HLA B*4002      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.603767       -0.706171       -5.309938       40157.486549
HLA B*7301      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.606454       -0.706171       -5.312625       40406.788405
HLA A*3301      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.607789       -0.706171       -5.313960       40531.142033
HLA B*5301      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.609957       -0.706171       -5.316128       40734.033436
HLA B*4501      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.617046       -0.706171       -5.323217       41404.334811
HLA A*2603      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.627884       -0.706171       -5.334055       42450.614968
HLA A*2602      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.628930       -0.706171       -5.335100       42552.933719
HLA A*6801      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.659212       -0.706171       -5.365383       45625.960392
HLA B*4403      1:107-115       9       GLGVLTRPS       0.455750        -1.161921       -4.659586       -0.706171       -5.365757       45665.223467
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