NetMHCII 2.0 Server - prediction results

Technical University of Denmark

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# Input is in FSA format
        NetMHCII version 2.0.

Strong binder threshold  50.00. Weak binder threshold 500.00.

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0101   82  GASYLAGDAAAAATY  YLAGDAAAA        0.8902          3.3         SB     0.20     Sequence
   DRB1_0101   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.8810          3.6         SB     0.80     Sequence
   DRB1_0101   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.8807          3.6         SB     0.80     Sequence
   DRB1_0101   13  SAAVEALTARLAAAH  VEALTARLA        0.8770          3.8         SB     0.80     Sequence
   DRB1_0101   12  ASAAVEALTARLAAA  VEALTARLA        0.8678          4.2         SB     1.00     Sequence
   DRB1_0101   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.8667          4.2         SB     2.00     Sequence
   DRB1_0101   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.8665          4.2         SB     2.00     Sequence
   DRB1_0101   14  AAVEALTARLAAAHA  VEALTARLA        0.8580          4.6         SB     2.00     Sequence
   DRB1_0101   11  AASAAVEALTARLAA  VEALTARLA        0.8538          4.9         SB     2.00     Sequence
   DRB1_0101   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.8472          5.2         SB     4.00     Sequence
   DRB1_0101   79  GESGASYLAGDAAAA  YLAGDAAAA        0.8428          5.5         SB     4.00     Sequence
   DRB1_0101   15  AVEALTARLAAAHAS  VEALTARLA        0.8341          6.0         SB     4.00     Sequence
   DRB1_0101   10  AAASAAVEALTARLA  VEALTARLA        0.8335          6.1         SB     4.00     Sequence
   DRB1_0101   16  VEALTARLAAAHASA  VEALTARLA        0.8202          7.0         SB     8.00     Sequence
   DRB1_0101   17  EALTARLAAAHASAA  TARLAAAHA        0.8196          7.0         SB     8.00     Sequence
   DRB1_0101   20  TARLAAAHASAAPVI  LAAAHASAA        0.8106          7.8         SB     8.00     Sequence
   DRB1_0101   18  ALTARLAAAHASAAP  TARLAAAHA        0.8097          7.8         SB     8.00     Sequence
   DRB1_0101   44  PVSLQTAAGFSAQGV  LQTAAGFSA        0.7936          9.3         SB     8.00     Sequence
   DRB1_0101   19  LTARLAAAHASAAPV  LAAAHASAA        0.7886          9.9         SB     8.00     Sequence
   DRB1_0101   31  APVITAVVPPAADPV  ITAVVPPAA        0.7855         10.2         SB     8.00     Sequence
   DRB1_0101   21  ARLAAAHASAAPVIT  LAAAHASAA        0.7753         11.4         SB    16.00     Sequence
   DRB1_0101   22  RLAAAHASAAPVITA  LAAAHASAA        0.7744         11.5         SB    16.00     Sequence
   DRB1_0101   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.7685         12.2         SB    16.00     Sequence
   DRB1_0101   45  VSLQTAAGFSAQGVE  LQTAAGFSA        0.7657         12.6         SB    16.00     Sequence
   DRB1_0101   23  LAAAHASAAPVITAV  AHASAAPVI        0.7516         14.7         SB    16.00     Sequence
   DRB1_0101   32  PVITAVVPPAADPVS  ITAVVPPAA        0.7237         19.9         SB    16.00     Sequence
   DRB1_0101   51  AGFSAQGVEHAVVTA  FSAQGVEHA        0.7170         21.4         SB    16.00     Sequence
   DRB1_0101   43  DPVSLQTAAGFSAQG  LQTAAGFSA        0.7145         22.0         SB    16.00     Sequence
   DRB1_0101   49  TAAGFSAQGVEHAVV  FSAQGVEHA        0.7126         22.4         SB    16.00     Sequence
   DRB1_0101   30  AAPVITAVVPPAADP  ITAVVPPAA        0.7054         24.2         SB    32.00     Sequence
   DRB1_0101   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.7040         24.6         SB    32.00     Sequence
   DRB1_0101    5  VPEGLAAASAAVEAL  GLAAASAAV        0.7027         24.9         SB    32.00     Sequence
   DRB1_0101   29  SAAPVITAVVPPAAD  ITAVVPPAA        0.7001         25.7         SB    32.00     Sequence
   DRB1_0101   28  ASAAPVITAVVPPAA  ITAVVPPAA        0.6972         26.5         SB    32.00     Sequence
   DRB1_0101    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.6943         27.3         SB    32.00     Sequence
   DRB1_0101    3  RVVPEGLAAASAAVE  PEGLAAASA        0.6906         28.4         SB    32.00     Sequence
   DRB1_0101    4  VVPEGLAAASAAVEA  GLAAASAAV        0.6775         32.8         SB    32.00     Sequence
   DRB1_0101    6  PEGLAAASAAVEALT  GLAAASAAV        0.6738         34.1         SB    32.00     Sequence
   DRB1_0101   42  ADPVSLQTAAGFSAQ  LQTAAGFSA        0.6731         34.4         SB    32.00     Sequence
   DRB1_0101   33  VITAVVPPAADPVSL  ITAVVPPAA        0.6714         35.0         SB    32.00     Sequence
   DRB1_0101    2  LRVVPEGLAAASAAV  PEGLAAASA        0.6698         35.6         SB    32.00     Sequence
   DRB1_0101   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.6652         37.4         SB    32.00     Sequence
   DRB1_0101    1  TLRVVPEGLAAASAA  VVPEGLAAA        0.6564         41.2         SB    32.00     Sequence
   DRB1_0101   24  AAAHASAAPVITAVV  AHASAAPVI        0.6556         41.5         SB    32.00     Sequence
   DRB1_0101   52  GFSAQGVEHAVVTAE  FSAQGVEHA        0.6483         44.9         SB    32.00     Sequence
   DRB1_0101    7  EGLAAASAAVEALTA  GLAAASAAV        0.6472         45.5         SB    32.00     Sequence
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   DRB1_0101   48  QTAAGFSAQGVEHAV  FSAQGVEHA        0.6384         50.0          WB    32.00     Sequence
   DRB1_0101   41  AADPVSLQTAAGFSA  LQTAAGFSA        0.6192         61.6          WB    32.00     Sequence
   DRB1_0101    8  GLAAASAAVEALTAR  GLAAASAAV        0.6083         69.3          WB    32.00     Sequence
   DRB1_0101    9  LAAASAAVEALTARL  SAAVEALTA        0.6049         71.9          WB    32.00     Sequence
   DRB1_0101   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.6029         73.4          WB    32.00     Sequence
   DRB1_0101   25  AAHASAAPVITAVVP  AHASAAPVI        0.5892         85.2          WB    50.00     Sequence
   DRB1_0101   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.5816         92.5          WB    50.00     Sequence
   DRB1_0101   86  LAGDAAAAATYGVVG  DAAAAATYG        0.5331        156.3          WB    50.00     Sequence
   DRB1_0101   26  AHASAAPVITAVVPP  AHASAAPVI        0.5169        186.2          WB    50.00     Sequence
   DRB1_0101   76  VGVGESGASYLAGDA  GESGASYLA        0.4967        231.8          WB    50.00     Sequence
   DRB1_0101   87  AGDAAAAATYGVVGG  AAAAATYGV        0.4785        282.0          WB    50.00     Sequence
   DRB1_0101   27  HASAAPVITAVVPPA  VITAVVPPA        0.4663        322.2          WB    50.00     Sequence
   DRB1_0101   40  PAADPVSLQTAAGFS  PVSLQTAAG        0.4507        381.4          WB    50.00     Sequence
   DRB1_0101   74  AGVGVGESGASYLAG  GESGASYLA        0.4475        394.7          WB    50.00     Sequence
   DRB1_0101   77  GVGESGASYLAGDAA  GESGASYLA        0.4434        412.5          WB    50.00     Sequence
   DRB1_0101   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.4407        424.9          WB    50.00     Sequence
   DRB1_0101   75  GVGVGESGASYLAGD  GESGASYLA        0.4389        433.2          WB    50.00     Sequence
   DRB1_0101   78  VGESGASYLAGDAAA  GESGASYLA        0.4292        481.1          WB    50.00     Sequence
   DRB1_0101   35  TAVVPPAADPVSLQT  VVPPAADPV        0.4267        494.4          WB    50.00     Sequence
   DRB1_0101   73  RAGVGVGESGASYLA  GESGASYLA        0.4124        576.9                50.00     Sequence
   DRB1_0101   39  PPAADPVSLQTAAGF  PVSLQTAAG        0.3835        788.9                50.00     Sequence
   DRB1_0101   60  HAVVTAEGVEELGRA  VTAEGVEEL        0.3828        794.8                50.00     Sequence
   DRB1_0101   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.3773        843.4                50.00     Sequence
   DRB1_0101   36  AVVPPAADPVSLQTA  VVPPAADPV        0.3673        939.6                50.00     Sequence
   DRB1_0101   54  SAQGVEHAVVTAEGV  AQGVEHAVV        0.3550       1073.9                50.00     Sequence
   DRB1_0101   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.3548       1076.1                50.00     Sequence
   DRB1_0101   64  TAEGVEELGRAGVGV  GVEELGRAG        0.3515       1115.4                50.00     Sequence
   DRB1_0101   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.3419       1236.9                50.00     Sequence
   DRB1_0101   56  QGVEHAVVTAEGVEE  HAVVTAEGV        0.3336       1353.6                50.00     Sequence
   DRB1_0101   65  AEGVEELGRAGVGVG  VEELGRAGV        0.3228       1520.3                50.00     Sequence
   DRB1_0101   72  GRAGVGVGESGASYL  VGVGESGAS        0.3122       1705.6                50.00     Sequence
   DRB1_0101   37  VVPPAADPVSLQTAA  VVPPAADPV        0.3105       1738.2                50.00     Sequence
   DRB1_0101   67  GVEELGRAGVGVGES  ELGRAGVGV        0.3081       1784.0                50.00     Sequence
   DRB1_0101   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.2991       1965.1                50.00     Sequence
   DRB1_0101   66  EGVEELGRAGVGVGE  GVEELGRAG        0.2928       2104.7                50.00     Sequence
   DRB1_0101   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.2767       2504.2                50.00     Sequence
   DRB1_0101   68  VEELGRAGVGVGESG  ELGRAGVGV        0.2612       2960.5                50.00     Sequence
   DRB1_0101   63  VTAEGVEELGRAGVG  GVEELGRAG        0.2591       3030.0                50.00     Sequence
   DRB1_0101   62  VVTAEGVEELGRAGV  VTAEGVEEL        0.2580       3068.1                50.00     Sequence
   DRB1_0101   71  LGRAGVGVGESGASY  VGVGESGAS        0.2572       3093.6                50.00     Sequence
   DRB1_0101   70  ELGRAGVGVGESGAS  VGVGESGAS        0.2489       3382.9                50.00     Sequence
   DRB1_0101   69  EELGRAGVGVGESGA  GRAGVGVGE        0.2350       3934.8                50.00     Sequence
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Allele: DRB1_0101. Number of high binders 46. Number of weak binders 19. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0301   83  ASYLAGDAAAAATYG  ASYLAGDAA        0.4185        539.9                16.00     Sequence
   DRB1_0301   15  AVEALTARLAAAHAS  VEALTARLA        0.3913        724.5                32.00     Sequence
   DRB1_0301   16  VEALTARLAAAHASA  VEALTARLA        0.3908        729.1                32.00     Sequence
   DRB1_0301   82  GASYLAGDAAAAATY  ASYLAGDAA        0.3899        735.6                32.00     Sequence
   DRB1_0301   14  AAVEALTARLAAAHA  VEALTARLA        0.3620        995.2                32.00     Sequence
   DRB1_0301   81  SGASYLAGDAAAAAT  ASYLAGDAA        0.3440       1208.7                32.00     Sequence
   DRB1_0301   13  SAAVEALTARLAAAH  AVEALTARL        0.3372       1302.0                32.00     Sequence
   DRB1_0301    1  TLRVVPEGLAAASAA  TLRVVPEGL        0.3188       1588.1                32.00     Sequence
   DRB1_0301    0  MTLRVVPEGLAAASA  TLRVVPEGL        0.2922       2118.6                50.00     Sequence
   DRB1_0301   80  ESGASYLAGDAAAAA  ASYLAGDAA        0.2912       2141.1                50.00     Sequence
   DRB1_0301   17  EALTARLAAAHASAA  TARLAAAHA        0.2748       2556.2                50.00     Sequence
   DRB1_0301   12  ASAAVEALTARLAAA  AVEALTARL        0.2642       2866.6                50.00     Sequence
   DRB1_0301   84  SYLAGDAAAAATYGV  SYLAGDAAA        0.2547       3178.0                50.00     Sequence
   DRB1_0301   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.2236       4450.6                50.00     Sequence
   DRB1_0301   18  ALTARLAAAHASAAP  TARLAAAHA        0.2202       4614.5                50.00     Sequence
   DRB1_0301    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.2198       4637.6                50.00     Sequence
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DRB1_0301   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.2142      4927.5                50.00     Sequence
DRB1_0301   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.2068      5337.1                50.00     Sequence
DRB1_0301   20  TARLAAAHASAAPVI  TARLAAAHA        0.2044      5474.4                50.00     Sequence
DRB1_0301   11  AASAAVEALTARLAA  AAVEALTAR        0.1963      5975.2                50.00     Sequence
DRB1_0301   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.1863      6662.1                50.00     Sequence
DRB1_0301   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.1852      6741.0                50.00     Sequence
DRB1_0301   79  GESGASYLAGDAAAA  ASYLAGDAA        0.1833      6884.2                50.00     Sequence
DRB1_0301   19  LTARLAAAHASAAPV  TARLAAAHA        0.1822      6963.5                50.00     Sequence
DRB1_0301    3  RVVPEGLAAASAAVE  VPEGLAAAS        0.1786      7236.9                50.00     Sequence
DRB1_0301   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.1744      7577.8                50.00     Sequence
DRB1_0301   31  APVITAVVPPAADPV  VITAVVPPA        0.1712      7845.6                50.00     Sequence
DRB1_0301    7  EGLAAASAAVEALTA  LAAASAAVE        0.1670      8210.6                50.00     Sequence
DRB1_0301    9  LAAASAAVEALTARL  LAAASAAVE        0.1661      8289.2                50.00     Sequence
DRB1_0301   73  RAGVGVGESGASYLA  VGVGESGAS        0.1657      8323.9                50.00     Sequence
DRB1_0301   52  GFSAQGVEHAVVTAE  FSAQGVEHA        0.1636      8512.7                50.00     Sequence
DRB1_0301    8  GLAAASAAVEALTAR  LAAASAAVE        0.1625      8615.1                50.00     Sequence
DRB1_0301   21  ARLAAAHASAAPVIT  LAAAHASAA        0.1613      8727.7                50.00     Sequence
DRB1_0301    5  VPEGLAAASAAVEAL  GLAAASAAV        0.1605      8808.9                50.00     Sequence
DRB1_0301   32  PVITAVVPPAADPVS  ITAVVPPAA        0.1570      9142.4                50.00     Sequence
DRB1_0301   22  RLAAAHASAAPVITA  LAAAHASAA        0.1570      9145.8                50.00     Sequence
DRB1_0301   23  LAAAHASAAPVITAV  LAAAHASAA        0.1559      9259.6                50.00     Sequence
DRB1_0301    6  PEGLAAASAAVEALT  LAAASAAVE        0.1550      9346.2                50.00     Sequence
DRB1_0301   30  AAPVITAVVPPAADP  APVITAVVP        0.1531      9545.2                50.00     Sequence
DRB1_0301    4  VVPEGLAAASAAVEA  VVPEGLAAA        0.1520      9655.7                50.00     Sequence
DRB1_0301   75  GVGVGESGASYLAGD  GVGVGESGA        0.1494      9932.6                50.00     Sequence
DRB1_0301   10  AAASAAVEALTARLA  AAVEALTAR        0.1436     10568.4                50.00     Sequence
DRB1_0301   72  GRAGVGVGESGASYL  RAGVGVGES        0.1418     10786.1                50.00     Sequence
DRB1_0301   74  AGVGVGESGASYLAG  GVGVGESGA        0.1417     10788.0                50.00     Sequence
DRB1_0301   55  AQGVEHAVVTAEGVE  VEHAVVTAE        0.1394     11065.6                50.00     Sequence
DRB1_0301   56  QGVEHAVVTAEGVEE  VEHAVVTAE        0.1393     11082.4                50.00     Sequence
DRB1_0301   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.1388     11132.8                50.00     Sequence
DRB1_0301   51  AGFSAQGVEHAVVTA  FSAQGVEHA        0.1377     11265.6                50.00     Sequence
DRB1_0301   29  SAAPVITAVVPPAAD  APVITAVVP        0.1347     11647.3                50.00     Sequence
DRB1_0301   33  VITAVVPPAADPVSL  ITAVVPPAA        0.1292     12353.0                50.00     Sequence
DRB1_0301   76  VGVGESGASYLAGDA  VGVGESGAS        0.1275     12578.5                50.00     Sequence
DRB1_0301   54  SAQGVEHAVVTAEGV  SAQGVEHAV        0.1216     13409.9                50.00     Sequence
DRB1_0301   78  VGESGASYLAGDAAA  VGESGASYL        0.1198     13679.4                50.00     Sequence
DRB1_0301   71  LGRAGVGVGESGASY  RAGVGVGES        0.1190     13800.4                50.00     Sequence
DRB1_0301   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.1160     14249.2                50.00     Sequence
DRB1_0301   28  ASAAPVITAVVPPAA  APVITAVVP        0.1156     14316.1                50.00     Sequence
DRB1_0301   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.1156     14316.9                50.00     Sequence
DRB1_0301   25  AAHASAAPVITAVVP  AAHASAAPV        0.1131     14711.2                50.00     Sequence
DRB1_0301   68  VEELGRAGVGVGESG  VEELGRAGV        0.1104     15140.1                50.00     Sequence
DRB1_0301   62  VVTAEGVEELGRAGV  VTAEGVEEL        0.1077     15589.1                50.00     Sequence
DRB1_0301   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1068     15747.2                50.00     Sequence
DRB1_0301   24  AAAHASAAPVITAVV  AAHASAAPV        0.1059     15905.3                50.00     Sequence
DRB1_0301   37  VVPPAADPVSLQTAA  VVPPAADPV        0.1039     16245.8                50.00     Sequence
DRB1_0301   45  VSLQTAAGFSAQGVE  SLQTAAGFS        0.1038     16268.5                50.00     Sequence
DRB1_0301   46  SLQTAAGFSAQGVEH  SLQTAAGFS        0.1027     16461.5                50.00     Sequence
DRB1_0301   67  GVEELGRAGVGVGES  VEELGRAGV        0.1024     16507.5                50.00     Sequence
DRB1_0301   77  GVGESGASYLAGDAA  VGESGASYL        0.0988     17171.8                50.00     Sequence
DRB1_0301   27  HASAAPVITAVVPPA  HASAAPVIT        0.0963     17630.4                50.00     Sequence
DRB1_0301   42  ADPVSLQTAAGFSAQ  ADPVSLQTA        0.0961     17675.1                50.00     Sequence
DRB1_0301   43  DPVSLQTAAGFSAQG  DPVSLQTAA        0.0954     17816.0                50.00     Sequence
DRB1_0301   44  PVSLQTAAGFSAQGV  SLQTAAGFS        0.0952     17852.3                50.00     Sequence
DRB1_0301   63  VTAEGVEELGRAGVG  VTAEGVEEL        0.0948     17929.3                50.00     Sequence
DRB1_0301   66  EGVEELGRAGVGVGE  VEELGRAGV        0.0933     18216.0                50.00     Sequence
DRB1_0301   65  AEGVEELGRAGVGVG  VEELGRAGV        0.0933     18227.2                50.00     Sequence
DRB1_0301   70  ELGRAGVGVGESGAS  RAGVGVGES        0.0923     18413.6                50.00     Sequence
DRB1_0301   36  AVVPPAADPVSLQTA  VVPPAADPV        0.0883     19224.9                50.00     Sequence
DRB1_0301   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.0877     19359.5                50.00     Sequence
DRB1_0301   41  AADPVSLQTAAGFSA  ADPVSLQTA        0.0867     19561.2                50.00     Sequence
DRB1_0301   49  TAAGFSAQGVEHAVV  FSAQGVEHA        0.0823     20515.6                50.00     Sequence
DRB1_0301   39  PPAADPVSLQTAAGF  PPAADPVSL        0.0791     21254.0                50.00     Sequence
DRB1_0301   40  PAADPVSLQTAAGFS  ADPVSLQTA        0.0785     21377.0                50.00     Sequence
DRB1_0301   35  TAVVPPAADPVSLQT  VVPPAADPV        0.0778     21543.0                50.00     Sequence
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   DRB1_0301   64  TAEGVEELGRAGVGV  AEGVEELGR        0.0738      22490.9                 50.00     Sequence
   DRB1_0301   38  VPPAADPVSLQTAAG  PPAADPVSL        0.0737      22524.3                 50.00     Sequence
   DRB1_0301   48  QTAAGFSAQGVEHAV  FSAQGVEHA        0.0734      22593.6                 50.00     Sequence
   DRB1_0301   69  EELGRAGVGVGESGA  LGRAGVGVG        0.0713      23107.6                 50.00     Sequence
   DRB1_0301   26  AHASAAPVITAVVPP  HASAAPVIT        0.0689      23733.0                 50.00     Sequence
   DRB1_0301   87  AGDAAAAATYGVVGG  GDAAAAATY        0.0469      30100.5                 50.00     Sequence
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Allele: DRB1_0301. Number of high binders 0. Number of weak binders 0. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
   DRB1_0401   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.5243        172.0         WB   16.00     Sequence
   DRB1_0401   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.5173        185.5         WB   16.00     Sequence
   DRB1_0401   82  GASYLAGDAAAAATY  YLAGDAAAA        0.4917        244.6         WB   16.00     Sequence
   DRB1_0401   18  ALTARLAAAHASAAP  LTARLAAAH        0.4865        258.8         WB   32.00     Sequence
   DRB1_0401   17  EALTARLAAAHASAA  LTARLAAAH        0.4739        296.6         WB   32.00     Sequence
   DRB1_0401   19  LTARLAAAHASAAPV  LTARLAAAH        0.4622        336.6         WB   32.00     Sequence
   DRB1_0401    2  LRVVPEGLAAASAAV  RVVPEGLAA        0.4614        339.5         WB   32.00     Sequence
   DRB1_0401    0  MTLRVVPEGLAAASA  RVVPEGLAA        0.4594        346.8         WB   32.00     Sequence
   DRB1_0401   16  VEALTARLAAAHASA  LTARLAAAH        0.4533        370.8         WB   32.00     Sequence
   DRB1_0401    1  TLRVVPEGLAAASAA  RVVPEGLAA        0.4523        374.6         WB   32.00     Sequence
   DRB1_0401   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.4321        466.2         WB   32.00     Sequence
   DRB1_0401   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.4297        478.2         WB   32.00     Sequence
   DRB1_0401   20  TARLAAAHASAAPVI  TARLAAAHA        0.4111        585.2              32.00     Sequence
   DRB1_0401   15  AVEALTARLAAAHAS  VEALTARLA        0.4006        655.7              32.00     Sequence
   DRB1_0401    3  RVVPEGLAAASAAVE  RVVPEGLAA        0.3872        758.2              32.00     Sequence
   DRB1_0401   14  AAVEALTARLAAAHA  VEALTARLA        0.3709        904.4              50.00     Sequence
   DRB1_0401   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.3561       1060.8              50.00     Sequence
   DRB1_0401   13  SAAVEALTARLAAAH  SAAVEALTA        0.3497       1137.0              50.00     Sequence
   DRB1_0401   44  PVSLQTAAGFSAQGV  LQTAAGFSA        0.3462       1180.3              50.00     Sequence
   DRB1_0401   21  ARLAAAHASAAPVIT  RLAAAHASA        0.3307       1396.9              50.00     Sequence
   DRB1_0401   43  DPVSLQTAAGFSAQG  PVSLQTAAG        0.3267       1457.8              50.00     Sequence
   DRB1_0401   52  GFSAQGVEHAVVTAE  GFSAQGVEH        0.3107       1734.1              50.00     Sequence
   DRB1_0401   12  ASAAVEALTARLAAA  SAAVEALTA        0.3067       1810.9              50.00     Sequence
   DRB1_0401   42  ADPVSLQTAAGFSAQ  PVSLQTAAG        0.3047       1849.7              50.00     Sequence
   DRB1_0401   51  AGFSAQGVEHAVVTA  GFSAQGVEH        0.3010       1925.6              50.00     Sequence
   DRB1_0401   22  RLAAAHASAAPVITA  RLAAAHASA        0.2977       1996.2              50.00     Sequence
   DRB1_0401   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.2882       2210.8              50.00     Sequence
   DRB1_0401   79  GESGASYLAGDAAAA  YLAGDAAAA        0.2800       2418.0              50.00     Sequence
   DRB1_0401   45  VSLQTAAGFSAQGVE  LQTAAGFSA        0.2626       2919.0              50.00     Sequence
   DRB1_0401   41  AADPVSLQTAAGFSA  PVSLQTAAG        0.2621       2932.7              50.00     Sequence
   DRB1_0401    5  VPEGLAAASAAVEAL  PEGLAAASA        0.2611       2965.7              50.00     Sequence
   DRB1_0401    4  VVPEGLAAASAAVEA  PEGLAAASA        0.2593       3025.1              50.00     Sequence
   DRB1_0401   49  TAAGFSAQGVEHAVV  GFSAQGVEH        0.2588       3038.7              50.00     Sequence
   DRB1_0401   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.2564       3118.8              50.00     Sequence
   DRB1_0401    6  PEGLAAASAAVEALT  PEGLAAASA        0.2545       3183.2              50.00     Sequence
   DRB1_0401   11  AASAAVEALTARLAA  SAAVEALTA        0.2471       3449.0              50.00     Sequence
   DRB1_0401   32  PVITAVVPPAADPVS  PVITAVVPP        0.2282       4232.9              50.00     Sequence
   DRB1_0401   31  APVITAVVPPAADPV  PVITAVVPP        0.2186       4696.8              50.00     Sequence
   DRB1_0401   48  QTAAGFSAQGVEHAV  GFSAQGVEH        0.2163       4816.8              50.00     Sequence
   DRB1_0401   10  AAASAAVEALTARLA  SAAVEALTA        0.2152       4871.3              50.00     Sequence
   DRB1_0401   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.2144       4913.6              50.00     Sequence
   DRB1_0401   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.2080       5265.8              50.00     Sequence
   DRB1_0401   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.2054       5417.9              50.00     Sequence
   DRB1_0401   27  HASAAPVITAVVPPA  HASAAPVIT        0.2050       5442.7              50.00     Sequence
   DRB1_0401   26  AHASAAPVITAVVPP  HASAAPVIT        0.2015       5648.8              50.00     Sequence
   DRB1_0401   76  VGVGESGASYLAGDA  VGVGESGAS        0.2014       5660.2              50.00     Sequence
   DRB1_0401   30  AAPVITAVVPPAADP  PVITAVVPP        0.1992       5792.8              50.00     Sequence
   DRB1_0401   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.1985       5834.9              50.00     Sequence
   DRB1_0401   73  RAGVGVGESGASYLA  VGVGESGAS        0.1978       5881.7              50.00     Sequence
   DRB1_0401   25  AAHASAAPVITAVVP  HASAAPVIT        0.1937       6150.7              50.00     Sequence
   DRB1_0401   75  GVGVGESGASYLAGD  VGVGESGAS        0.1920       6261.5              50.00     Sequence
   DRB1_0401   24  AAAHASAAPVITAVV  HASAAPVIT        0.1908       6346.3              50.00     Sequence
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   DRB1_0401    7  EGLAAASAAVEALTA  GLAAASAAV        0.1832      6886.2                 50.00     Sequence
   DRB1_0401    8  GLAAASAAVEALTAR  GLAAASAAV        0.1825      6937.6                 50.00     Sequence
   DRB1_0401   56  QGVEHAVVTAEGVEE  QGVEHAVVT        0.1782      7270.3                 50.00     Sequence
   DRB1_0401   54  SAQGVEHAVVTAEGV  QGVEHAVVT        0.1782      7273.1                 50.00     Sequence
   DRB1_0401   74  AGVGVGESGASYLAG  VGVGESGAS        0.1779      7294.2                 50.00     Sequence
   DRB1_0401   29  SAAPVITAVVPPAAD  PVITAVVPP        0.1754      7495.3                 50.00     Sequence
   DRB1_0401   77  GVGESGASYLAGDAA  GVGESGASY        0.1743      7582.9                 50.00     Sequence
   DRB1_0401   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.1718      7793.8                 50.00     Sequence
   DRB1_0401   72  GRAGVGVGESGASYL  RAGVGVGES        0.1699      7958.7                 50.00     Sequence
   DRB1_0401   23  LAAAHASAAPVITAV  LAAAHASAA        0.1698      7960.9                 50.00     Sequence
   DRB1_0401   55  AQGVEHAVVTAEGVE  QGVEHAVVT        0.1698      7964.4                 50.00     Sequence
   DRB1_0401   70  ELGRAGVGVGESGAS  ELGRAGVGV        0.1669      8217.1                 50.00     Sequence
   DRB1_0401   78  VGESGASYLAGDAAA  GESGASYLA        0.1636      8519.7                 50.00     Sequence
   DRB1_0401   28  ASAAPVITAVVPPAA  PVITAVVPP        0.1630      8569.4                 50.00     Sequence
   DRB1_0401   33  VITAVVPPAADPVSL  ITAVVPPAA        0.1580      9044.9                 50.00     Sequence
   DRB1_0401   69  EELGRAGVGVGESGA  ELGRAGVGV        0.1575      9098.7                 50.00     Sequence
   DRB1_0401   71  LGRAGVGVGESGASY  RAGVGVGES        0.1555      9293.1                 50.00     Sequence
   DRB1_0401   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.1529      9563.0                 50.00     Sequence
   DRB1_0401    9  LAAASAAVEALTARL  SAAVEALTA        0.1495      9924.5                 50.00     Sequence
   DRB1_0401   68  VEELGRAGVGVGESG  ELGRAGVGV        0.1455     10358.4                 50.00     Sequence
   DRB1_0401   58  VEHAVVTAEGVEELG  EHAVVTAEG        0.1403     10959.6                 50.00     Sequence
   DRB1_0401   67  GVEELGRAGVGVGES  ELGRAGVGV        0.1377     11265.9                 50.00     Sequence
   DRB1_0401   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.1273     12609.6                 50.00     Sequence
   DRB1_0401   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1271     12636.2                 50.00     Sequence
   DRB1_0401   66  EGVEELGRAGVGVGE  ELGRAGVGV        0.1152     14382.6                 50.00     Sequence
   DRB1_0401   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.1072     15673.3                 50.00     Sequence
   DRB1_0401   65  AEGVEELGRAGVGVG  ELGRAGVGV        0.1057     15928.4                 50.00     Sequence
   DRB1_0401   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.1023     16532.4                 50.00     Sequence
   DRB1_0401   64  TAEGVEELGRAGVGV  ELGRAGVGV        0.0930     18270.1                 50.00     Sequence
   DRB1_0401   35  TAVVPPAADPVSLQT  TAVVPPAAD        0.0815     20711.2                 50.00     Sequence
   DRB1_0401   62  VVTAEGVEELGRAGV  VVTAEGVEE        0.0763     21893.6                 50.00     Sequence
   DRB1_0401   63  VTAEGVEELGRAGVG  EGVEELGRA        0.0743     22373.7                 50.00     Sequence
   DRB1_0401   61  AVVTAEGVEELGRAG  VVTAEGVEE        0.0641     24977.0                 50.00     Sequence
   DRB1_0401   37  VVPPAADPVSLQTAA  PPAADPVSL        0.0620     25564.8                 50.00     Sequence
   DRB1_0401   36  AVVPPAADPVSLQTA  PPAADPVSL        0.0564     27150.3                 50.00     Sequence
   DRB1_0401   87  AGDAAAAATYGVVGG  AGDAAAAAT        0.0349     34273.4                 50.00     Sequence
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Allele: DRB1_0401. Number of high binders 0. Number of weak binders 12. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404   31  APVITAVVPPAADPV  VITAVVPPA        0.4719       303.0          WB    32.00     Sequence
   DRB1_0404   30  AAPVITAVVPPAADP  VITAVVPPA        0.4652       325.7          WB    32.00     Sequence
   DRB1_0404   29  SAAPVITAVVPPAAD  VITAVVPPA        0.4478       393.3          WB    32.00     Sequence
   DRB1_0404   32  PVITAVVPPAADPVS  VITAVVPPA        0.4450       405.2          WB    32.00     Sequence
   DRB1_0404    0  MTLRVVPEGLAAASA  TLRVVPEGL        0.4001       658.7                50.00     Sequence
   DRB1_0404   28  ASAAPVITAVVPPAA  VITAVVPPA        0.3973       679.4                50.00     Sequence
   DRB1_0404    1  TLRVVPEGLAAASAA  TLRVVPEGL        0.3925       715.8                50.00     Sequence
   DRB1_0404   16  VEALTARLAAAHASA  LTARLAAAH        0.3849       777.2                50.00     Sequence
   DRB1_0404   18  ALTARLAAAHASAAP  LTARLAAAH        0.3801       818.4                50.00     Sequence
   DRB1_0404   17  EALTARLAAAHASAA  LTARLAAAH        0.3785       832.5                50.00     Sequence
   DRB1_0404   15  AVEALTARLAAAHAS  ALTARLAAA        0.3778       838.6                50.00     Sequence
   DRB1_0404   33  VITAVVPPAADPVSL  VITAVVPPA        0.3691       921.6                50.00     Sequence
   DRB1_0404   14  AAVEALTARLAAAHA  AVEALTARL        0.3686       926.6                50.00     Sequence
   DRB1_0404   13  SAAVEALTARLAAAH  AVEALTARL        0.3570      1050.9                50.00     Sequence
   DRB1_0404   19  LTARLAAAHASAAPV  RLAAAHASA        0.3493      1141.5                50.00     Sequence
   DRB1_0404   27  HASAAPVITAVVPPA  VITAVVPPA        0.3448      1199.4                50.00     Sequence
   DRB1_0404   12  ASAAVEALTARLAAA  AVEALTARL        0.3374      1299.3                50.00     Sequence
   DRB1_0404   11  AASAAVEALTARLAA  AVEALTARL        0.3116      1716.1                50.00     Sequence
   DRB1_0404   82  GASYLAGDAAAAATY  SYLAGDAAA        0.3023      1897.8                50.00     Sequence
   DRB1_0404   20  TARLAAAHASAAPVI  RLAAAHASA        0.3023      1899.7                50.00     Sequence
   DRB1_0404   83  ASYLAGDAAAAATYG  SYLAGDAAA        0.2992      1963.5                50.00     Sequence
   DRB1_0404   84  SYLAGDAAAAATYGV  SYLAGDAAA        0.2954      2046.7                50.00     Sequence
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DRB1_0404    2  LRVVPEGLAAASAAV  RVVPEGLAA         0.2927       2105.8                 50.00      Sequence
DRB1_0404    3  RVVPEGLAAASAAVE  RVVPEGLAA         0.2887       2200.4                 50.00      Sequence
DRB1_0404   26  AHASAAPVITAVVPP  PVITAVVPP         0.2842       2310.4                 50.00      Sequence
DRB1_0404   81  SGASYLAGDAAAAAT  SYLAGDAAA         0.2810       2390.1                 50.00      Sequence
DRB1_0404   21  ARLAAAHASAAPVIT  RLAAAHASA         0.2776       2481.1                 50.00      Sequence
DRB1_0404   43  DPVSLQTAAGFSAQG  PVSLQTAAG         0.2751       2548.4                 50.00      Sequence
DRB1_0404   22  RLAAAHASAAPVITA  RLAAAHASA         0.2747       2558.9                 50.00      Sequence
DRB1_0404   10  AAASAAVEALTARLA  AVEALTARL         0.2694       2710.3                 50.00      Sequence
DRB1_0404   44  PVSLQTAAGFSAQGV  VSLQTAAGF         0.2651       2840.2                 50.00      Sequence
DRB1_0404   42  ADPVSLQTAAGFSAQ  PVSLQTAAG         0.2635       2890.3                 50.00      Sequence
DRB1_0404   57  GVEHAVVTAEGVEEL  HAVVTAEGV         0.2562       3126.0                 50.00      Sequence
DRB1_0404   58  VEHAVVTAEGVEELG  HAVVTAEGV         0.2520       3273.4                 50.00      Sequence
DRB1_0404    4  VVPEGLAAASAAVEA  EGLAAASAA         0.2479       3420.4                 50.00      Sequence
DRB1_0404   41  AADPVSLQTAAGFSA  PVSLQTAAG         0.2469       3459.5                 50.00      Sequence
DRB1_0404   56  QGVEHAVVTAEGVEE  HAVVTAEGV         0.2440       3569.4                 50.00      Sequence
DRB1_0404    7  EGLAAASAAVEALTA  EGLAAASAA         0.2432       3597.6                 50.00      Sequence
DRB1_0404    6  PEGLAAASAAVEALT  EGLAAASAA         0.2417       3656.1                 50.00      Sequence
DRB1_0404   80  ESGASYLAGDAAAAA  SYLAGDAAA         0.2409       3689.8                 50.00      Sequence
DRB1_0404    5  VPEGLAAASAAVEAL  EGLAAASAA         0.2372       3840.7                 50.00      Sequence
DRB1_0404    9  LAAASAAVEALTARL  SAAVEALTA         0.2327       4031.0                 50.00      Sequence
DRB1_0404   55  AQGVEHAVVTAEGVE  VEHAVVTAE         0.2295       4173.8                 50.00      Sequence
DRB1_0404   23  LAAAHASAAPVITAV  LAAAHASAA         0.2290       4195.2                 50.00      Sequence
DRB1_0404   25  AAHASAAPVITAVVP  HASAAPVIT         0.2286       4217.0                 50.00      Sequence
DRB1_0404    8  GLAAASAAVEALTAR  GLAAASAAV         0.2242       4418.8                 50.00      Sequence
DRB1_0404   45  VSLQTAAGFSAQGVE  VSLQTAAGF         0.2176       4749.3                 50.00      Sequence
DRB1_0404   24  AAAHASAAPVITAVV  HASAAPVIT         0.2175       4754.2                 50.00      Sequence
DRB1_0404   40  PAADPVSLQTAAGFS  DPVSLQTAA         0.2161       4823.8                 50.00      Sequence
DRB1_0404   59  EHAVVTAEGVEELGR  HAVVTAEGV         0.2100       5153.5                 50.00      Sequence
DRB1_0404   34  ITAVVPPAADPVSLQ  ITAVVPPAA         0.2055       5412.4                 50.00      Sequence
DRB1_0404   60  HAVVTAEGVEELGRA  HAVVTAEGV         0.2038       5509.8                 50.00      Sequence
DRB1_0404   54  SAQGVEHAVVTAEGV  VEHAVVTAE         0.1982       5856.8                 50.00      Sequence
DRB1_0404   79  GESGASYLAGDAAAA  SYLAGDAAA         0.1945       6098.8                 50.00      Sequence
DRB1_0404   35  TAVVPPAADPVSLQT  VVPPAADPV         0.1931       6191.7                 50.00      Sequence
DRB1_0404   39  PPAADPVSLQTAAGF  DPVSLQTAA         0.1795       7168.1                 50.00      Sequence
DRB1_0404   85  YLAGDAAAAATYGVV  YLAGDAAAA         0.1792       7197.0                 50.00      Sequence
DRB1_0404   46  SLQTAAGFSAQGVEH  LQTAAGFSA         0.1781       7280.9                 50.00      Sequence
DRB1_0404   36  AVVPPAADPVSLQTA  VVPPAADPV         0.1746       7556.1                 50.00      Sequence
DRB1_0404   53  FSAQGVEHAVVTAEG  FSAQGVEHA         0.1703       7920.8                 50.00      Sequence
DRB1_0404   47  LQTAAGFSAQGVEHA  TAAGFSAQG         0.1673       8178.9                 50.00      Sequence
DRB1_0404   37  VVPPAADPVSLQTAA  VVPPAADPV         0.1644       8440.4                 50.00      Sequence
DRB1_0404   38  VPPAADPVSLQTAAG  DPVSLQTAA         0.1643       8455.4                 50.00      Sequence
DRB1_0404   48  QTAAGFSAQGVEHAV  QTAAGFSAQ         0.1516       9697.2                 50.00      Sequence
DRB1_0404   52  GFSAQGVEHAVVTAE  FSAQGVEHA         0.1488       9991.3                 50.00      Sequence
DRB1_0404   78  VGESGASYLAGDAAA  SYLAGDAAA         0.1435      10590.2                 50.00      Sequence
DRB1_0404   49  TAAGFSAQGVEHAVV  TAAGFSAQG         0.1423      10723.2                 50.00      Sequence
DRB1_0404   51  AGFSAQGVEHAVVTA  FSAQGVEHA         0.1324      11941.0                 50.00      Sequence
DRB1_0404   50  AAGFSAQGVEHAVVT  FSAQGVEHA         0.1199      13657.5                 50.00      Sequence
DRB1_0404   75  GVGVGESGASYLAGD  VGVGESGAS         0.1029      16425.8                 50.00      Sequence
DRB1_0404   70  ELGRAGVGVGESGAS  LGRAGVGVG         0.1025      16501.7                 50.00      Sequence
DRB1_0404   76  VGVGESGASYLAGDA  VGVGESGAS         0.0994      17053.1                 50.00      Sequence
DRB1_0404   87  AGDAAAAATYGVVGG  AAAATYGVV         0.0983      17253.2                 50.00      Sequence
DRB1_0404   61  AVVTAEGVEELGRAG  AVVTAEGVE         0.0981      17302.1                 50.00      Sequence
DRB1_0404   69  EELGRAGVGVGESGA  LGRAGVGVG         0.0970      17497.2                 50.00      Sequence
DRB1_0404   71  LGRAGVGVGESGASY  LGRAGVGVG         0.0965      17602.6                 50.00      Sequence
DRB1_0404   68  VEELGRAGVGVGESG  LGRAGVGVG         0.0957      17761.0                 50.00      Sequence
DRB1_0404   74  AGVGVGESGASYLAG  VGVGESGAS         0.0941      18068.6                 50.00      Sequence
DRB1_0404   77  GVGESGASYLAGDAA  VGESGASYL         0.0923      18420.9                 50.00      Sequence
DRB1_0404   67  GVEELGRAGVGVGES  ELGRAGVGV         0.0886      19160.9                 50.00      Sequence
DRB1_0404   86  LAGDAAAAATYGVVG  LAGDAAAAA         0.0857      19776.3                 50.00      Sequence
DRB1_0404   73  RAGVGVGESGASYLA  VGVGESGAS         0.0843      20087.1                 50.00      Sequence
DRB1_0404   62  VVTAEGVEELGRAGV  VVTAEGVEE         0.0820      20584.6                 50.00      Sequence
DRB1_0404   66  EGVEELGRAGVGVGE  ELGRAGVGV         0.0819      20606.4                 50.00      Sequence
DRB1_0404   72  GRAGVGVGESGASYL  AGVGVGESG         0.0778      21542.5                 50.00      Sequence
DRB1_0404   65  AEGVEELGRAGVGVG  ELGRAGVGV         0.0778      21548.8                 50.00      Sequence
DRB1_0404   63  VTAEGVEELGRAGVG  VTAEGVEEL         0.0732      22647.0                 50.00      Sequence
DRB1_0404   64  TAEGVEELGRAGVGV  GVEELGRAG         0.0714      23086.1                 50.00      Sequence
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Allele: DRB1_0404. Number of high binders 0. Number of weak binders 4. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.4167        550.8               50.00     Sequence
   DRB1_0405   56  QGVEHAVVTAEGVEE  GVEHAVVTA        0.4118        580.9               50.00     Sequence
   DRB1_0405   55  AQGVEHAVVTAEGVE  GVEHAVVTA        0.4032        637.0               50.00     Sequence
   DRB1_0405   54  SAQGVEHAVVTAEGV  GVEHAVVTA        0.3914        723.7               50.00     Sequence
   DRB1_0405   57  GVEHAVVTAEGVEEL  GVEHAVVTA        0.3839        784.9               50.00     Sequence
   DRB1_0405    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.3812        808.4               50.00     Sequence
   DRB1_0405   53  FSAQGVEHAVVTAEG  GVEHAVVTA        0.3327       1366.1               50.00     Sequence
   DRB1_0405    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.3292       1419.2               50.00     Sequence
   DRB1_0405   52  GFSAQGVEHAVVTAE  FSAQGVEHA        0.3124       1702.7               50.00     Sequence
   DRB1_0405   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.3072       1800.1               50.00     Sequence
   DRB1_0405   51  AGFSAQGVEHAVVTA  FSAQGVEHA        0.3070       1804.2               50.00     Sequence
   DRB1_0405   29  SAAPVITAVVPPAAD  PVITAVVPP        0.3061       1821.7               50.00     Sequence
   DRB1_0405   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.3061       1822.9               50.00     Sequence
   DRB1_0405   43  DPVSLQTAAGFSAQG  SLQTAAGFS        0.2989       1969.9               50.00     Sequence
   DRB1_0405   30  AAPVITAVVPPAADP  PVITAVVPP        0.2974       2001.7               50.00     Sequence
   DRB1_0405   49  TAAGFSAQGVEHAVV  FSAQGVEHA        0.2947       2061.1               50.00     Sequence
   DRB1_0405   31  APVITAVVPPAADPV  PVITAVVPP        0.2936       2085.1               50.00     Sequence
   DRB1_0405   12  ASAAVEALTARLAAA  AVEALTARL        0.2896       2178.9               50.00     Sequence
   DRB1_0405   13  SAAVEALTARLAAAH  AVEALTARL        0.2874       2231.9               50.00     Sequence
   DRB1_0405   11  AASAAVEALTARLAA  AVEALTARL        0.2867       2248.7               50.00     Sequence
   DRB1_0405   42  ADPVSLQTAAGFSAQ  SLQTAAGFS        0.2864       2255.8               50.00     Sequence
   DRB1_0405   28  ASAAPVITAVVPPAA  APVITAVVP        0.2812       2385.3               50.00     Sequence
   DRB1_0405   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.2800       2416.8               50.00     Sequence
   DRB1_0405   48  QTAAGFSAQGVEHAV  AGFSAQGVE        0.2797       2423.8               50.00     Sequence
   DRB1_0405   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.2772       2491.2               50.00     Sequence
   DRB1_0405   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.2749       2553.5               50.00     Sequence
   DRB1_0405    3  RVVPEGLAAASAAVE  GLAAASAAV        0.2749       2554.5               50.00     Sequence
   DRB1_0405   14  AAVEALTARLAAAHA  AVEALTARL        0.2730       2606.6               50.00     Sequence
   DRB1_0405   45  VSLQTAAGFSAQGVE  SLQTAAGFS        0.2713       2655.9               50.00     Sequence
   DRB1_0405   82  GASYLAGDAAAAATY  SYLAGDAAA        0.2709       2666.4               50.00     Sequence
   DRB1_0405   46  SLQTAAGFSAQGVEH  SLQTAAGFS        0.2705       2678.9               50.00     Sequence
   DRB1_0405    4  VVPEGLAAASAAVEA  GLAAASAAV        0.2703       2685.2               50.00     Sequence
   DRB1_0405   32  PVITAVVPPAADPVS  PVITAVVPP        0.2701       2689.4               50.00     Sequence
   DRB1_0405   41  AADPVSLQTAAGFSA  PVSLQTAAG        0.2698       2697.7               50.00     Sequence
   DRB1_0405   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.2652       2837.3               50.00     Sequence
   DRB1_0405   47  LQTAAGFSAQGVEHA  TAAGFSAQG        0.2637       2882.4               50.00     Sequence
   DRB1_0405   10  AAASAAVEALTARLA  AVEALTARL        0.2611       2965.3               50.00     Sequence
   DRB1_0405   27  HASAAPVITAVVPPA  VITAVVPPA        0.2549       3172.6               50.00     Sequence
   DRB1_0405   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.2542       3196.1               50.00     Sequence
   DRB1_0405    6  PEGLAAASAAVEALT  GLAAASAAV        0.2530       3237.1               50.00     Sequence
   DRB1_0405   40  PAADPVSLQTAAGFS  PVSLQTAAG        0.2500       3343.2               50.00     Sequence
   DRB1_0405    9  LAAASAAVEALTARL  LAAASAAVE        0.2488       3387.1               50.00     Sequence
   DRB1_0405   80  ESGASYLAGDAAAAA  ASYLAGDAA        0.2479       3419.3               50.00     Sequence
   DRB1_0405    5  VPEGLAAASAAVEAL  GLAAASAAV        0.2475       3436.8               50.00     Sequence
   DRB1_0405    7  EGLAAASAAVEALTA  GLAAASAAV        0.2459       3496.8               50.00     Sequence
   DRB1_0405    8  GLAAASAAVEALTAR  GLAAASAAV        0.2437       3580.8               50.00     Sequence
   DRB1_0405   25  AAHASAAPVITAVVP  AAHASAAPV        0.2399       3728.3               50.00     Sequence
   DRB1_0405   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.2393       3754.2               50.00     Sequence
   DRB1_0405   26  AHASAAPVITAVVPP  AHASAAPVI        0.2384       3790.6               50.00     Sequence
   DRB1_0405   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.2331       4012.8               50.00     Sequence
   DRB1_0405   61  AVVTAEGVEELGRAG  AVVTAEGVE        0.2329       4024.1               50.00     Sequence
   DRB1_0405   15  AVEALTARLAAAHAS  AVEALTARL        0.2311       4103.8               50.00     Sequence
   DRB1_0405   24  AAAHASAAPVITAVV  AAHASAAPV        0.2240       4428.7               50.00     Sequence
   DRB1_0405   79  GESGASYLAGDAAAA  GASYLAGDA        0.2233       4462.6               50.00     Sequence
   DRB1_0405   73  RAGVGVGESGASYLA  GVGESGASY        0.2219       4533.6               50.00     Sequence
   DRB1_0405   71  LGRAGVGVGESGASY  LGRAGVGVG        0.2206       4595.7               50.00     Sequence
   DRB1_0405   72  GRAGVGVGESGASYL  GVGVGESGA        0.2157       4847.4               50.00     Sequence
   DRB1_0405   78  VGESGASYLAGDAAA  VGESGASYL        0.2140       4937.6               50.00     Sequence
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   DRB1_0405   74  AGVGVGESGASYLAG  GVGESGASY         0.2130       4992.5                 50.00     Sequence
   DRB1_0405   23  LAAAHASAAPVITAV  AAHASAAPV         0.2106       5118.6                 50.00     Sequence
   DRB1_0405   75  GVGVGESGASYLAGD  VGESGASYL         0.2067       5342.7                 50.00     Sequence
   DRB1_0405   38  VPPAADPVSLQTAAG  PAADPVSLQ         0.2040       5501.1                 50.00     Sequence
   DRB1_0405   33  VITAVVPPAADPVSL  VITAVVPPA         0.2022       5610.0                 50.00     Sequence
   DRB1_0405   76  VGVGESGASYLAGDA  VGESGASYL         0.2021       5615.5                 50.00     Sequence
   DRB1_0405   77  GVGESGASYLAGDAA  VGESGASYL         0.2010       5680.0                 50.00     Sequence
   DRB1_0405   22  RLAAAHASAAPVITA  AAHASAAPV         0.2009       5690.9                 50.00     Sequence
   DRB1_0405   62  VVTAEGVEELGRAGV  VVTAEGVEE         0.1991       5799.5                 50.00     Sequence
   DRB1_0405   70  ELGRAGVGVGESGAS  LGRAGVGVG         0.1961       5990.6                 50.00     Sequence
   DRB1_0405   63  VTAEGVEELGRAGVG  TAEGVEELG         0.1935       6164.8                 50.00     Sequence
   DRB1_0405   16  VEALTARLAAAHASA  VEALTARLA         0.1906       6355.3                 50.00     Sequence
   DRB1_0405   64  TAEGVEELGRAGVGV  TAEGVEELG         0.1886       6496.4                 50.00     Sequence
   DRB1_0405   21  ARLAAAHASAAPVIT  AAHASAAPV         0.1870       6611.7                 50.00     Sequence
   DRB1_0405   69  EELGRAGVGVGESGA  LGRAGVGVG         0.1809       7060.1                 50.00     Sequence
   DRB1_0405   17  EALTARLAAAHASAA  TARLAAAHA         0.1795       7167.0                 50.00     Sequence
   DRB1_0405   34  ITAVVPPAADPVSLQ  ITAVVPPAA         0.1766       7400.7                 50.00     Sequence
   DRB1_0405   67  GVEELGRAGVGVGES  GVEELGRAG         0.1745       7569.8                 50.00     Sequence
   DRB1_0405   37  VVPPAADPVSLQTAA  PAADPVSLQ         0.1732       7676.4                 50.00     Sequence
   DRB1_0405   19  LTARLAAAHASAAPV  LTARLAAAH         0.1712       7841.2                 50.00     Sequence
   DRB1_0405   20  TARLAAAHASAAPVI  AAHASAAPV         0.1673       8182.9                 50.00     Sequence
   DRB1_0405   18  ALTARLAAAHASAAP  LTARLAAAH         0.1669       8216.2                 50.00     Sequence
   DRB1_0405   66  EGVEELGRAGVGVGE  GVEELGRAG         0.1645       8428.9                 50.00     Sequence
   DRB1_0405   85  YLAGDAAAAATYGVV  YLAGDAAAA         0.1644       8441.2                 50.00     Sequence
   DRB1_0405   68  VEELGRAGVGVGESG  LGRAGVGVG         0.1566       9185.3                 50.00     Sequence
   DRB1_0405   35  TAVVPPAADPVSLQT  TAVVPPAAD         0.1509       9770.8                 50.00     Sequence
   DRB1_0405   65  AEGVEELGRAGVGVG  GVEELGRAG         0.1504       9823.8                 50.00     Sequence
   DRB1_0405   36  AVVPPAADPVSLQTA  VPPAADPVS         0.1435      10584.9                 50.00     Sequence
   DRB1_0405   86  LAGDAAAAATYGVVG  LAGDAAAAA         0.1157      14298.2                 50.00     Sequence
   DRB1_0405   87  AGDAAAAATYGVVGG  AAAATYGVV         0.1015      16682.3                 50.00     Sequence
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Allele: DRB1_0405. Number of high binders 0. Number of weak binders 0. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701    2  LRVVPEGLAAASAAV  GLAAASAAV         0.7459         15.6          SB     8.00     Sequence
   DRB1_0701   20  TARLAAAHASAAPVI  AHASAAPVI         0.7454         15.7          SB     8.00     Sequence
   DRB1_0701   21  ARLAAAHASAAPVIT  AHASAAPVI         0.7118         22.6          SB     8.00     Sequence
   DRB1_0701    3  RVVPEGLAAASAAVE  GLAAASAAV         0.6883         29.1          SB    16.00     Sequence
   DRB1_0701   22  RLAAAHASAAPVITA  AHASAAPVI         0.6631         38.3          SB    16.00     Sequence
   DRB1_0701    4  VVPEGLAAASAAVEA  GLAAASAAV         0.6507         43.8          SB    16.00     Sequence
   DRB1_0701   19  LTARLAAAHASAAPV  AAHASAAPV         0.6274         56.3          WB    16.00     Sequence
   DRB1_0701    9  LAAASAAVEALTARL  AVEALTARL         0.6250         57.8          WB    16.00     Sequence
   DRB1_0701   23  LAAAHASAAPVITAV  AHASAAPVI         0.6151         64.3          WB    16.00     Sequence
   DRB1_0701    5  VPEGLAAASAAVEAL  GLAAASAAV         0.6131         65.8          WB    16.00     Sequence
   DRB1_0701   72  GRAGVGVGESGASYL  VGESGASYL         0.6083         69.3          WB    16.00     Sequence
   DRB1_0701   10  AAASAAVEALTARLA  AVEALTARL         0.6033         73.1          WB    16.00     Sequence
   DRB1_0701    6  PEGLAAASAAVEALT  GLAAASAAV         0.5921         82.5          WB    32.00     Sequence
   DRB1_0701   73  RAGVGVGESGASYLA  VGESGASYL         0.5861         88.1          WB    32.00     Sequence
   DRB1_0701    7  EGLAAASAAVEALTA  GLAAASAAV         0.5699        105.0          WB    32.00     Sequence
   DRB1_0701   24  AAAHASAAPVITAVV  AHASAAPVI         0.5675        107.8          WB    32.00     Sequence
   DRB1_0701   11  AASAAVEALTARLAA  AVEALTARL         0.5465        135.2          WB    32.00     Sequence
   DRB1_0701   74  AGVGVGESGASYLAG  VGESGASYL         0.5407        143.9          WB    32.00     Sequence
   DRB1_0701    8  GLAAASAAVEALTAR  GLAAASAAV         0.5353        152.6          WB    32.00     Sequence
   DRB1_0701   25  AAHASAAPVITAVVP  AHASAAPVI         0.5262        168.4          WB    32.00     Sequence
   DRB1_0701   75  GVGVGESGASYLAGD  VGESGASYL         0.4972        230.5          WB    32.00     Sequence
   DRB1_0701   31  APVITAVVPPAADPV  VVPPAADPV         0.4955        234.6          WB    32.00     Sequence
   DRB1_0701   12  ASAAVEALTARLAAA  AVEALTARL         0.4776        284.9          WB    32.00     Sequence
   DRB1_0701   76  VGVGESGASYLAGDA  VGESGASYL         0.4758        290.4          WB    32.00     Sequence
   DRB1_0701   32  PVITAVVPPAADPVS  VVPPAADPV         0.4602        344.0          WB    32.00     Sequence
   DRB1_0701   77  GVGESGASYLAGDAA  VGESGASYL         0.4552        363.0          WB    32.00     Sequence
   DRB1_0701   26  AHASAAPVITAVVPP  AHASAAPVI         0.4523        374.5          WB    50.00     Sequence
   DRB1_0701   13  SAAVEALTARLAAAH  AVEALTARL         0.4389        433.1          WB    50.00     Sequence
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   DRB1_0701    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.4368        443.2          WB    50.00     Sequence
   DRB1_0701   33  VITAVVPPAADPVSL  VVPPAADPV        0.4332        460.5          WB    50.00     Sequence
   DRB1_0701   78  VGESGASYLAGDAAA  VGESGASYL        0.4261        497.5          WB    50.00     Sequence
   DRB1_0701   57  GVEHAVVTAEGVEEL  VTAEGVEEL        0.4178        543.9                50.00     Sequence
   DRB1_0701    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.4048        626.4                50.00     Sequence
   DRB1_0701   14  AAVEALTARLAAAHA  AVEALTARL        0.4001        659.0                50.00     Sequence
   DRB1_0701   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.3839        785.6                50.00     Sequence
   DRB1_0701   15  AVEALTARLAAAHAS  AVEALTARL        0.3827        795.2                50.00     Sequence
   DRB1_0701   34  ITAVVPPAADPVSLQ  VVPPAADPV        0.3813        807.9                50.00     Sequence
   DRB1_0701   17  EALTARLAAAHASAA  LAAAHASAA        0.3793        825.7                50.00     Sequence
   DRB1_0701   35  TAVVPPAADPVSLQT  VVPPAADPV        0.3631        983.5                50.00     Sequence
   DRB1_0701   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.3569       1051.2                50.00     Sequence
   DRB1_0701   58  VEHAVVTAEGVEELG  VTAEGVEEL        0.3540       1085.3                50.00     Sequence
   DRB1_0701   85  YLAGDAAAAATYGVV  AAAAATYGV        0.3466       1175.5                50.00     Sequence
   DRB1_0701   84  SYLAGDAAAAATYGV  AAAAATYGV        0.3408       1251.8                50.00     Sequence
   DRB1_0701   36  AVVPPAADPVSLQTA  VVPPAADPV        0.3398       1265.0                50.00     Sequence
   DRB1_0701   27  HASAAPVITAVVPPA  VITAVVPPA        0.3396       1268.5                50.00     Sequence
   DRB1_0701   49  TAAGFSAQGVEHAVV  AQGVEHAVV        0.3383       1285.9                50.00     Sequence
   DRB1_0701   56  QGVEHAVVTAEGVEE  VVTAEGVEE        0.3338       1350.2                50.00     Sequence
   DRB1_0701   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.3264       1463.0                50.00     Sequence
   DRB1_0701   18  ALTARLAAAHASAAP  LAAAHASAA        0.3226       1524.3                50.00     Sequence
   DRB1_0701   37  VVPPAADPVSLQTAA  VVPPAADPV        0.3160       1637.0                50.00     Sequence
   DRB1_0701   50  AAGFSAQGVEHAVVT  AQGVEHAVV        0.3058       1828.5                50.00     Sequence
   DRB1_0701   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.3057       1830.1                50.00     Sequence
   DRB1_0701   59  EHAVVTAEGVEELGR  VTAEGVEEL        0.3024       1896.3                50.00     Sequence
   DRB1_0701   86  LAGDAAAAATYGVVG  AAAAATYGV        0.3008       1930.6                50.00     Sequence
   DRB1_0701   28  ASAAPVITAVVPPAA  VITAVVPPA        0.3003       1941.1                50.00     Sequence
   DRB1_0701   54  SAQGVEHAVVTAEGV  HAVVTAEGV        0.2962       2027.3                50.00     Sequence
   DRB1_0701   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.2933       2094.0                50.00     Sequence
   DRB1_0701   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.2779       2473.2                50.00     Sequence
   DRB1_0701   51  AGFSAQGVEHAVVTA  AQGVEHAVV        0.2758       2530.4                50.00     Sequence
   DRB1_0701   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.2701       2690.9                50.00     Sequence
   DRB1_0701   60  HAVVTAEGVEELGRA  VTAEGVEEL        0.2647       2852.8                50.00     Sequence
   DRB1_0701   29  SAAPVITAVVPPAAD  VITAVVPPA        0.2608       2976.3                50.00     Sequence
   DRB1_0701   47  LQTAAGFSAQGVEHA  FSAQGVEHA        0.2596       3012.6                50.00     Sequence
   DRB1_0701   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.2535       3220.5                50.00     Sequence
   DRB1_0701   87  AGDAAAAATYGVVGG  AAAAATYGV        0.2444       3550.7                50.00     Sequence
   DRB1_0701   52  GFSAQGVEHAVVTAE  AQGVEHAVV        0.2402       3717.8                50.00     Sequence
   DRB1_0701   16  VEALTARLAAAHASA  RLAAAHASA        0.2320       4061.0                50.00     Sequence
   DRB1_0701   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.2265       4309.8                50.00     Sequence
   DRB1_0701   30  AAPVITAVVPPAADP  VITAVVPPA        0.2228       4487.3                50.00     Sequence
   DRB1_0701   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.2121       5041.2                50.00     Sequence
   DRB1_0701   53  FSAQGVEHAVVTAEG  AQGVEHAVV        0.2100       5155.3                50.00     Sequence
   DRB1_0701   48  QTAAGFSAQGVEHAV  FSAQGVEHA        0.2021       5614.3                50.00     Sequence
   DRB1_0701   62  VVTAEGVEELGRAGV  VTAEGVEEL        0.1982       5857.8                50.00     Sequence
   DRB1_0701   82  GASYLAGDAAAAATY  GDAAAAATY        0.1865       6645.3                50.00     Sequence
   DRB1_0701   83  ASYLAGDAAAAATYG  GDAAAAATY        0.1685       8071.7                50.00     Sequence
   DRB1_0701   65  AEGVEELGRAGVGVG  LGRAGVGVG        0.1595       8902.8                50.00     Sequence
   DRB1_0701   63  VTAEGVEELGRAGVG  VTAEGVEEL        0.1417      10794.2                50.00     Sequence
   DRB1_0701   66  EGVEELGRAGVGVGE  LGRAGVGVG        0.1358      11503.0                50.00     Sequence
   DRB1_0701   67  GVEELGRAGVGVGES  LGRAGVGVG        0.1315      12052.4                50.00     Sequence
   DRB1_0701   71  LGRAGVGVGESGASY  GVGESGASY        0.1273      12606.1                50.00     Sequence
   DRB1_0701   69  EELGRAGVGVGESGA  GVGVGESGA        0.1240      13067.8                50.00     Sequence
   DRB1_0701   70  ELGRAGVGVGESGAS  LGRAGVGVG        0.1184      13885.3                50.00     Sequence
   DRB1_0701   68  VEELGRAGVGVGESG  LGRAGVGVG        0.1062      15853.2                50.00     Sequence
   DRB1_0701   64  TAEGVEELGRAGVGV  ELGRAGVGV        0.1027      16462.2                50.00     Sequence
   DRB1_0701   79  GESGASYLAGDAAAA  YLAGDAAAA        0.0979      17331.7                50.00     Sequence
   DRB1_0701   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.0765      21853.8                50.00     Sequence
   DRB1_0701   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.0664      24372.1                50.00     Sequence
   DRB1_0701   38  VPPAADPVSLQTAAG  AADPVSLQT        0.0442      30989.5                50.00     Sequence
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Allele: DRB1_0701. Number of high binders 6. Number of weak binders 25. Number of peptides 88

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     Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802   16  VEALTARLAAAHASA  VEALTARLA         0.3845        780.2                32.00     Sequence
   DRB1_0802   15  AVEALTARLAAAHAS  VEALTARLA         0.3754        860.9                32.00     Sequence
   DRB1_0802   14  AAVEALTARLAAAHA  VEALTARLA         0.3494       1141.2                32.00     Sequence
   DRB1_0802   17  EALTARLAAAHASAA  ALTARLAAA         0.3399       1264.2                32.00     Sequence
   DRB1_0802    0  MTLRVVPEGLAAASA  MTLRVVPEG         0.3372       1302.0                32.00     Sequence
   DRB1_0802   18  ALTARLAAAHASAAP  ALTARLAAA         0.3358       1321.5                32.00     Sequence
   DRB1_0802   31  APVITAVVPPAADPV  VITAVVPPA         0.3306       1397.2                32.00     Sequence
   DRB1_0802   32  PVITAVVPPAADPVS  VITAVVPPA         0.3283       1432.4                32.00     Sequence
   DRB1_0802   13  SAAVEALTARLAAAH  VEALTARLA         0.3256       1476.2                32.00     Sequence
   DRB1_0802   19  LTARLAAAHASAAPV  RLAAAHASA         0.3110       1728.3                50.00     Sequence
   DRB1_0802   30  AAPVITAVVPPAADP  VITAVVPPA         0.3101       1745.3                50.00     Sequence
   DRB1_0802   52  GFSAQGVEHAVVTAE  FSAQGVEHA         0.2967       2017.3                50.00     Sequence
   DRB1_0802   29  SAAPVITAVVPPAAD  VITAVVPPA         0.2908       2150.9                50.00     Sequence
   DRB1_0802   33  VITAVVPPAADPVSL  VITAVVPPA         0.2879       2219.1                50.00     Sequence
   DRB1_0802   28  ASAAPVITAVVPPAA  VITAVVPPA         0.2863       2256.8                50.00     Sequence
   DRB1_0802   12  ASAAVEALTARLAAA  VEALTARLA         0.2826       2350.0                50.00     Sequence
   DRB1_0802   20  TARLAAAHASAAPVI  RLAAAHASA         0.2822       2359.3                50.00     Sequence
   DRB1_0802   21  ARLAAAHASAAPVIT  RLAAAHASA         0.2813       2381.9                50.00     Sequence
   DRB1_0802   51  AGFSAQGVEHAVVTA  GFSAQGVEH         0.2812       2385.1                50.00     Sequence
   DRB1_0802   22  RLAAAHASAAPVITA  RLAAAHASA         0.2685       2736.7                50.00     Sequence
   DRB1_0802   44  PVSLQTAAGFSAQGV  PVSLQTAAG         0.2682       2745.9                50.00     Sequence
   DRB1_0802   67  GVEELGRAGVGVGES  GVEELGRAG         0.2615       2953.2                50.00     Sequence
   DRB1_0802   11  AASAAVEALTARLAA  VEALTARLA         0.2615       2953.9                50.00     Sequence
   DRB1_0802    2  LRVVPEGLAAASAAV  RVVPEGLAA         0.2591       3031.2                50.00     Sequence
   DRB1_0802   46  SLQTAAGFSAQGVEH  LQTAAGFSA         0.2579       3070.4                50.00     Sequence
   DRB1_0802   43  DPVSLQTAAGFSAQG  PVSLQTAAG         0.2575       3082.1                50.00     Sequence
   DRB1_0802   47  LQTAAGFSAQGVEHA  LQTAAGFSA         0.2544       3189.7                50.00     Sequence
   DRB1_0802   50  AAGFSAQGVEHAVVT  GFSAQGVEH         0.2479       3422.2                50.00     Sequence
   DRB1_0802   66  EGVEELGRAGVGVGE  GVEELGRAG         0.2474       3440.9                50.00     Sequence
   DRB1_0802   49  TAAGFSAQGVEHAVV  GFSAQGVEH         0.2450       3528.2                50.00     Sequence
   DRB1_0802   65  AEGVEELGRAGVGVG  GVEELGRAG         0.2388       3773.7                50.00     Sequence
   DRB1_0802   45  VSLQTAAGFSAQGVE  LQTAAGFSA         0.2361       3885.1                50.00     Sequence
   DRB1_0802   27  HASAAPVITAVVPPA  VITAVVPPA         0.2349       3936.0                50.00     Sequence
   DRB1_0802   42  ADPVSLQTAAGFSAQ  PVSLQTAAG         0.2315       4084.5                50.00     Sequence
   DRB1_0802    1  TLRVVPEGLAAASAA  RVVPEGLAA         0.2300       4153.0                50.00     Sequence
   DRB1_0802   53  FSAQGVEHAVVTAEG  FSAQGVEHA         0.2228       4488.2                50.00     Sequence
   DRB1_0802    3  RVVPEGLAAASAAVE  RVVPEGLAA         0.2210       4574.2                50.00     Sequence
   DRB1_0802   48  QTAAGFSAQGVEHAV  FSAQGVEHA         0.2200       4626.0                50.00     Sequence
   DRB1_0802   10  AAASAAVEALTARLA  VEALTARLA         0.2147       4897.3                50.00     Sequence
   DRB1_0802   79  GESGASYLAGDAAAA  GESGASYLA         0.2145       4912.1                50.00     Sequence
   DRB1_0802   41  AADPVSLQTAAGFSA  PVSLQTAAG         0.2139       4940.7                50.00     Sequence
   DRB1_0802   63  VTAEGVEELGRAGVG  GVEELGRAG         0.2122       5032.5                50.00     Sequence
   DRB1_0802   77  GVGESGASYLAGDAA  GESGASYLA         0.2111       5095.9                50.00     Sequence
   DRB1_0802   75  GVGVGESGASYLAGD  GESGASYLA         0.2090       5213.0                50.00     Sequence
   DRB1_0802   76  VGVGESGASYLAGDA  GESGASYLA         0.2087       5229.6                50.00     Sequence
   DRB1_0802   73  RAGVGVGESGASYLA  GESGASYLA         0.2034       5534.2                50.00     Sequence
   DRB1_0802   74  AGVGVGESGASYLAG  GESGASYLA         0.1996       5766.7                50.00     Sequence
   DRB1_0802   64  TAEGVEELGRAGVGV  GVEELGRAG         0.1973       5912.5                50.00     Sequence
   DRB1_0802   62  VVTAEGVEELGRAGV  GVEELGRAG         0.1956       6020.6                50.00     Sequence
   DRB1_0802   78  VGESGASYLAGDAAA  GESGASYLA         0.1894       6438.3                50.00     Sequence
   DRB1_0802   82  GASYLAGDAAAAATY  YLAGDAAAA         0.1877       6564.0                50.00     Sequence
   DRB1_0802   71  LGRAGVGVGESGASY  LGRAGVGVG         0.1783       7266.1                50.00     Sequence
   DRB1_0802    4  VVPEGLAAASAAVEA  GLAAASAAV         0.1760       7443.5                50.00     Sequence
   DRB1_0802    8  GLAAASAAVEALTAR  GLAAASAAV         0.1742       7595.1                50.00     Sequence
   DRB1_0802   81  SGASYLAGDAAAAAT  YLAGDAAAA         0.1730       7693.0                50.00     Sequence
   DRB1_0802   80  ESGASYLAGDAAAAA  YLAGDAAAA         0.1695       7990.9                50.00     Sequence
   DRB1_0802   83  ASYLAGDAAAAATYG  YLAGDAAAA         0.1678       8140.6                50.00     Sequence
   DRB1_0802   55  AQGVEHAVVTAEGVE  GVEHAVVTA         0.1660       8300.5                50.00     Sequence
   DRB1_0802   56  QGVEHAVVTAEGVEE  GVEHAVVTA         0.1652       8369.5                50.00     Sequence
   DRB1_0802    7  EGLAAASAAVEALTA  GLAAASAAV         0.1647       8418.3                50.00     Sequence
   DRB1_0802   84  SYLAGDAAAAATYGV  YLAGDAAAA         0.1644       8441.9                50.00     Sequence
   DRB1_0802    6  PEGLAAASAAVEALT  GLAAASAAV         0.1644       8442.5                50.00     Sequence
   DRB1_0802   85  YLAGDAAAAATYGVV  YLAGDAAAA         0.1636       8514.9                50.00     Sequence
   DRB1_0802   70  ELGRAGVGVGESGAS  LGRAGVGVG         0.1633       8541.6                50.00     Sequence
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   DRB1_0802   72  GRAGVGVGESGASYL  GVGESGASY        0.1611       8752.7                 50.00     Sequence
   DRB1_0802   26  AHASAAPVITAVVPP  HASAAPVIT        0.1604       8814.9                 50.00     Sequence
   DRB1_0802   61  AVVTAEGVEELGRAG  GVEELGRAG        0.1590       8947.6                 50.00     Sequence
   DRB1_0802   54  SAQGVEHAVVTAEGV  GVEHAVVTA        0.1587       8982.9                 50.00     Sequence
   DRB1_0802   40  PAADPVSLQTAAGFS  PVSLQTAAG        0.1585       8998.2                 50.00     Sequence
   DRB1_0802    5  VPEGLAAASAAVEAL  GLAAASAAV        0.1545       9392.6                 50.00     Sequence
   DRB1_0802   23  LAAAHASAAPVITAV  HASAAPVIT        0.1505       9808.0                 50.00     Sequence
   DRB1_0802   69  EELGRAGVGVGESGA  LGRAGVGVG        0.1505       9816.1                 50.00     Sequence
   DRB1_0802   57  GVEHAVVTAEGVEEL  GVEHAVVTA        0.1498       9884.0                 50.00     Sequence
   DRB1_0802   24  AAAHASAAPVITAVV  HASAAPVIT        0.1416      10809.3                 50.00     Sequence
   DRB1_0802   68  VEELGRAGVGVGESG  LGRAGVGVG        0.1388      11141.8                 50.00     Sequence
   DRB1_0802   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1328      11886.6                 50.00     Sequence
   DRB1_0802   25  AAHASAAPVITAVVP  HASAAPVIT        0.1285      12445.6                 50.00     Sequence
   DRB1_0802    9  LAAASAAVEALTARL  AVEALTARL        0.1285      12447.9                 50.00     Sequence
   DRB1_0802   39  PPAADPVSLQTAAGF  PVSLQTAAG        0.1207      13540.4                 50.00     Sequence
   DRB1_0802   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.1190      13793.7                 50.00     Sequence
   DRB1_0802   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.1154      14348.2                 50.00     Sequence
   DRB1_0802   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.1152      14376.8                 50.00     Sequence
   DRB1_0802   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.1073      15664.0                 50.00     Sequence
   DRB1_0802   36  AVVPPAADPVSLQTA  AVVPPAADP        0.0792      21220.2                 50.00     Sequence
   DRB1_0802   37  VVPPAADPVSLQTAA  VPPAADPVS        0.0766      21829.0                 50.00     Sequence
   DRB1_0802   87  AGDAAAAATYGVVGG  AAATYGVVG        0.0743      22390.4                 50.00     Sequence
   DRB1_0802   86  LAGDAAAAATYGVVG  AAATYGVVG        0.0740      22457.1                 50.00     Sequence
   DRB1_0802   35  TAVVPPAADPVSLQT  AVVPPAADP        0.0656      24575.7                 50.00     Sequence
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Allele: DRB1_0802. Number of high binders 0. Number of weak binders 0. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.6435         47.3          SB     2.00     Sequence
   DRB1_0901   20  TARLAAAHASAAPVI  AHASAAPVI        0.6347         52.0          WB     2.00     Sequence
   DRB1_0901    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.6296         55.0          WB     4.00     Sequence
   DRB1_0901    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.6227         59.3          WB     4.00     Sequence
   DRB1_0901   21  ARLAAAHASAAPVIT  ARLAAAHAS        0.6217         59.9          WB     4.00     Sequence
   DRB1_0901   22  RLAAAHASAAPVITA  RLAAAHASA        0.6077         69.7          WB     4.00     Sequence
   DRB1_0901    4  VVPEGLAAASAAVEA  EGLAAASAA        0.5786         95.5          WB     8.00     Sequence
   DRB1_0901    7  EGLAAASAAVEALTA  EGLAAASAA        0.5747         99.7          WB     8.00     Sequence
   DRB1_0901    5  VPEGLAAASAAVEAL  EGLAAASAA        0.5712        103.5          WB     8.00     Sequence
   DRB1_0901    6  PEGLAAASAAVEALT  EGLAAASAA        0.5684        106.7          WB     8.00     Sequence
   DRB1_0901    3  RVVPEGLAAASAAVE  VPEGLAAAS        0.5668        108.6          WB     8.00     Sequence
   DRB1_0901   19  LTARLAAAHASAAPV  LAAAHASAA        0.5537        125.1          WB     8.00     Sequence
   DRB1_0901   32  PVITAVVPPAADPVS  VITAVVPPA        0.5473        134.0          WB    16.00     Sequence
   DRB1_0901   23  LAAAHASAAPVITAV  AHASAAPVI        0.5458        136.2          WB    16.00     Sequence
   DRB1_0901    9  LAAASAAVEALTARL  LAAASAAVE        0.5438        139.3          WB    16.00     Sequence
   DRB1_0901   13  SAAVEALTARLAAAH  AVEALTARL        0.5389        146.8          WB    16.00     Sequence
   DRB1_0901   10  AAASAAVEALTARLA  AAASAAVEA        0.5375        149.1          WB    16.00     Sequence
   DRB1_0901   33  VITAVVPPAADPVSL  VITAVVPPA        0.5355        152.3          WB    16.00     Sequence
   DRB1_0901    8  GLAAASAAVEALTAR  LAAASAAVE        0.5347        153.6          WB    16.00     Sequence
   DRB1_0901   12  ASAAVEALTARLAAA  AVEALTARL        0.5342        154.5          WB    16.00     Sequence
   DRB1_0901   31  APVITAVVPPAADPV  VITAVVPPA        0.5331        156.3          WB    16.00     Sequence
   DRB1_0901   24  AAAHASAAPVITAVV  AAHASAAPV        0.5329        156.7          WB    16.00     Sequence
   DRB1_0901   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.5285        164.3          WB    16.00     Sequence
   DRB1_0901   11  AASAAVEALTARLAA  AVEALTARL        0.5272        166.5          WB    16.00     Sequence
   DRB1_0901   25  AAHASAAPVITAVVP  AAHASAAPV        0.5265        167.9          WB    16.00     Sequence
   DRB1_0901   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.5236        173.2          WB    16.00     Sequence
   DRB1_0901   14  AAVEALTARLAAAHA  AVEALTARL        0.5234        173.6          WB    16.00     Sequence
   DRB1_0901   15  AVEALTARLAAAHAS  AVEALTARL        0.5215        177.1          WB    16.00     Sequence
   DRB1_0901   18  ALTARLAAAHASAAP  LAAAHASAA        0.5134        193.4          WB    16.00     Sequence
   DRB1_0901   30  AAPVITAVVPPAADP  VITAVVPPA        0.5115        197.5          WB    16.00     Sequence
   DRB1_0901   82  GASYLAGDAAAAATY  YLAGDAAAA        0.5113        197.8          WB    16.00     Sequence
   DRB1_0901   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.4991        225.8          WB    16.00     Sequence
   DRB1_0901   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.4925        242.5          WB    32.00     Sequence
   DRB1_0901   26  AHASAAPVITAVVPP  AHASAAPVI        0.4874        256.2          WB    32.00     Sequence
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   DRB1_0901   34  ITAVVPPAADPVSLQ  VVPPAADPV        0.4819        272.0          WB    32.00     Sequence
   DRB1_0901   51  AGFSAQGVEHAVVTA  AGFSAQGVE        0.4757        291.0          WB    32.00     Sequence
   DRB1_0901   17  EALTARLAAAHASAA  LAAAHASAA        0.4711        305.8          WB    32.00     Sequence
   DRB1_0901   80  ESGASYLAGDAAAAA  SYLAGDAAA        0.4672        318.9          WB    32.00     Sequence
   DRB1_0901   55  AQGVEHAVVTAEGVE  QGVEHAVVT        0.4590        348.3          WB    32.00     Sequence
   DRB1_0901   50  AAGFSAQGVEHAVVT  AGFSAQGVE        0.4559        360.4          WB    32.00     Sequence
   DRB1_0901   16  VEALTARLAAAHASA  TARLAAAHA        0.4472        396.1          WB    32.00     Sequence
   DRB1_0901   56  QGVEHAVVTAEGVEE  QGVEHAVVT        0.4445        407.6          WB    32.00     Sequence
   DRB1_0901   29  SAAPVITAVVPPAAD  VITAVVPPA        0.4429        415.0          WB    32.00     Sequence
   DRB1_0901   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.4324        464.6          WB    32.00     Sequence
   DRB1_0901   35  TAVVPPAADPVSLQT  VVPPAADPV        0.4313        470.2          WB    32.00     Sequence
   DRB1_0901   78  VGESGASYLAGDAAA  VGESGASYL        0.4254        501.1                50.00     Sequence
   DRB1_0901   57  GVEHAVVTAEGVEEL  GVEHAVVTA        0.4247        505.1                50.00     Sequence
   DRB1_0901   79  GESGASYLAGDAAAA  SYLAGDAAA        0.4233        512.6                50.00     Sequence
   DRB1_0901   49  TAAGFSAQGVEHAVV  AGFSAQGVE        0.4229        515.0                50.00     Sequence
   DRB1_0901   27  HASAAPVITAVVPPA  HASAAPVIT        0.4185        540.1                50.00     Sequence
   DRB1_0901   52  GFSAQGVEHAVVTAE  GFSAQGVEH        0.4174        546.3                50.00     Sequence
   DRB1_0901   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.4157        556.9                50.00     Sequence
   DRB1_0901   36  AVVPPAADPVSLQTA  VVPPAADPV        0.4128        574.5                50.00     Sequence
   DRB1_0901   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.4126        576.0                50.00     Sequence
   DRB1_0901   54  SAQGVEHAVVTAEGV  QGVEHAVVT        0.4094        595.7                50.00     Sequence
   DRB1_0901   86  LAGDAAAAATYGVVG  AGDAAAAAT        0.4071        611.0                50.00     Sequence
   DRB1_0901   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.4063        616.0                50.00     Sequence
   DRB1_0901   48  QTAAGFSAQGVEHAV  AGFSAQGVE        0.3932        709.9                50.00     Sequence
   DRB1_0901   28  ASAAPVITAVVPPAA  ASAAPVITA        0.3922        717.6                50.00     Sequence
   DRB1_0901   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.3922        718.1                50.00     Sequence
   DRB1_0901   77  GVGESGASYLAGDAA  VGESGASYL        0.3879        751.7                50.00     Sequence
   DRB1_0901   76  VGVGESGASYLAGDA  VGESGASYL        0.3846        779.8                50.00     Sequence
   DRB1_0901   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.3832        791.6                50.00     Sequence
   DRB1_0901   73  RAGVGVGESGASYLA  VGESGASYL        0.3761        854.0                50.00     Sequence
   DRB1_0901   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.3740        874.3                50.00     Sequence
   DRB1_0901   75  GVGVGESGASYLAGD  VGESGASYL        0.3654        958.9                50.00     Sequence
   DRB1_0901   72  GRAGVGVGESGASYL  VGESGASYL        0.3641        973.3                50.00     Sequence
   DRB1_0901   87  AGDAAAAATYGVVGG  AGDAAAAAT        0.3597       1019.9                50.00     Sequence
   DRB1_0901   37  VVPPAADPVSLQTAA  VVPPAADPV        0.3583       1036.0                50.00     Sequence
   DRB1_0901   74  AGVGVGESGASYLAG  VGESGASYL        0.3565       1055.9                50.00     Sequence
   DRB1_0901   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.3463       1180.2                50.00     Sequence
   DRB1_0901   71  LGRAGVGVGESGASY  LGRAGVGVG        0.3433       1217.9                50.00     Sequence
   DRB1_0901   70  ELGRAGVGVGESGAS  LGRAGVGVG        0.3341       1345.4                50.00     Sequence
   DRB1_0901   62  VVTAEGVEELGRAGV  VVTAEGVEE        0.3115       1719.0                50.00     Sequence
   DRB1_0901   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.3053       1838.1                50.00     Sequence
   DRB1_0901   66  EGVEELGRAGVGVGE  LGRAGVGVG        0.2937       2083.7                50.00     Sequence
   DRB1_0901   67  GVEELGRAGVGVGES  LGRAGVGVG        0.2887       2200.7                50.00     Sequence
   DRB1_0901   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.2852       2284.8                50.00     Sequence
   DRB1_0901   68  VEELGRAGVGVGESG  LGRAGVGVG        0.2850       2290.6                50.00     Sequence
   DRB1_0901   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.2786       2453.5                50.00     Sequence
   DRB1_0901   69  EELGRAGVGVGESGA  LGRAGVGVG        0.2745       2564.2                50.00     Sequence
   DRB1_0901   38  VPPAADPVSLQTAAG  VPPAADPVS        0.2694       2710.8                50.00     Sequence
   DRB1_0901   65  AEGVEELGRAGVGVG  LGRAGVGVG        0.2686       2734.8                50.00     Sequence
   DRB1_0901   63  VTAEGVEELGRAGVG  VTAEGVEEL        0.2573       3088.5                50.00     Sequence
   DRB1_0901   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.2555       3152.0                50.00     Sequence
   DRB1_0901   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.2429       3611.7                50.00     Sequence
   DRB1_0901   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.2247       4398.0                50.00     Sequence
   DRB1_0901   64  TAEGVEELGRAGVGV  EGVEELGRA        0.2152       4872.6                50.00     Sequence
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Allele: DRB1_0901. Number of high binders 1. Number of weak binders 44. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101   14  AAVEALTARLAAAHA  VEALTARLA        0.4888        252.5          WB    16.00     Sequence
   DRB1_1101   15  AVEALTARLAAAHAS  VEALTARLA        0.4856        261.3          WB    16.00     Sequence
   DRB1_1101   13  SAAVEALTARLAAAH  VEALTARLA        0.4737        297.2          WB    16.00     Sequence
   DRB1_1101   16  VEALTARLAAAHASA  VEALTARLA        0.4417        420.2          WB    32.00     Sequence
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DRB1_1101   12  ASAAVEALTARLAAA  VEALTARLA        0.4199       532.0                 32.00     Sequence
DRB1_1101    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.4171       548.1                 32.00     Sequence
DRB1_1101   17  EALTARLAAAHASAA  ALTARLAAA        0.3946       699.6                 32.00     Sequence
DRB1_1101    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.3830       792.7                 32.00     Sequence
DRB1_1101   11  AASAAVEALTARLAA  AVEALTARL        0.3482      1155.9                 50.00     Sequence
DRB1_1101   18  ALTARLAAAHASAAP  ALTARLAAA        0.3476      1163.7                 50.00     Sequence
DRB1_1101    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.3191      1583.9                 50.00     Sequence
DRB1_1101   19  LTARLAAAHASAAPV  RLAAAHASA        0.3114      1720.3                 50.00     Sequence
DRB1_1101   65  AEGVEELGRAGVGVG  VEELGRAGV        0.2936      2086.9                 50.00     Sequence
DRB1_1101   66  EGVEELGRAGVGVGE  VEELGRAGV        0.2801      2415.0                 50.00     Sequence
DRB1_1101   20  TARLAAAHASAAPVI  RLAAAHASA        0.2794      2433.2                 50.00     Sequence
DRB1_1101   67  GVEELGRAGVGVGES  VEELGRAGV        0.2785      2457.3                 50.00     Sequence
DRB1_1101   64  TAEGVEELGRAGVGV  VEELGRAGV        0.2616      2948.4                 50.00     Sequence
DRB1_1101   10  AAASAAVEALTARLA  VEALTARLA        0.2559      3137.7                 50.00     Sequence
DRB1_1101   44  PVSLQTAAGFSAQGV  SLQTAAGFS        0.2464      3476.3                 50.00     Sequence
DRB1_1101   43  DPVSLQTAAGFSAQG  SLQTAAGFS        0.2350      3933.4                 50.00     Sequence
DRB1_1101   45  VSLQTAAGFSAQGVE  SLQTAAGFS        0.2344      3957.6                 50.00     Sequence
DRB1_1101   68  VEELGRAGVGVGESG  VEELGRAGV        0.2098      5164.2                 50.00     Sequence
DRB1_1101   31  APVITAVVPPAADPV  ITAVVPPAA        0.2086      5233.7                 50.00     Sequence
DRB1_1101   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.2074      5299.0                 50.00     Sequence
DRB1_1101   42  ADPVSLQTAAGFSAQ  SLQTAAGFS        0.2010      5683.2                 50.00     Sequence
DRB1_1101   63  VTAEGVEELGRAGVG  VEELGRAGV        0.1982      5858.3                 50.00     Sequence
DRB1_1101   82  GASYLAGDAAAAATY  YLAGDAAAA        0.1978      5881.4                 50.00     Sequence
DRB1_1101   32  PVITAVVPPAADPVS  ITAVVPPAA        0.1970      5932.1                 50.00     Sequence
DRB1_1101   51  AGFSAQGVEHAVVTA  FSAQGVEHA        0.1884      6512.2                 50.00     Sequence
DRB1_1101   52  GFSAQGVEHAVVTAE  FSAQGVEHA        0.1874      6582.6                 50.00     Sequence
DRB1_1101   21  ARLAAAHASAAPVIT  RLAAAHASA        0.1825      6937.5                 50.00     Sequence
DRB1_1101   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.1818      6991.0                 50.00     Sequence
DRB1_1101   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.1794      7179.5                 50.00     Sequence
DRB1_1101   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.1789      7217.7                 50.00     Sequence
DRB1_1101   30  AAPVITAVVPPAADP  ITAVVPPAA        0.1781      7278.6                 50.00     Sequence
DRB1_1101   33  VITAVVPPAADPVSL  ITAVVPPAA        0.1754      7492.3                 50.00     Sequence
DRB1_1101    9  LAAASAAVEALTARL  SAAVEALTA        0.1696      7978.2                 50.00     Sequence
DRB1_1101   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.1679      8131.6                 50.00     Sequence
DRB1_1101   49  TAAGFSAQGVEHAVV  FSAQGVEHA        0.1627      8596.0                 50.00     Sequence
DRB1_1101   70  ELGRAGVGVGESGAS  RAGVGVGES        0.1626      8605.4                 50.00     Sequence
DRB1_1101   62  VVTAEGVEELGRAGV  VEELGRAGV        0.1614      8717.6                 50.00     Sequence
DRB1_1101   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.1604      8812.9                 50.00     Sequence
DRB1_1101   41  AADPVSLQTAAGFSA  SLQTAAGFS        0.1598      8874.1                 50.00     Sequence
DRB1_1101   71  LGRAGVGVGESGASY  RAGVGVGES        0.1559      9257.2                 50.00     Sequence
DRB1_1101   22  RLAAAHASAAPVITA  RLAAAHASA        0.1545      9397.0                 50.00     Sequence
DRB1_1101   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.1481     10069.2                 50.00     Sequence
DRB1_1101   29  SAAPVITAVVPPAAD  ITAVVPPAA        0.1439     10535.2                 50.00     Sequence
DRB1_1101   69  EELGRAGVGVGESGA  RAGVGVGES        0.1402     10964.0                 50.00     Sequence
DRB1_1101   72  GRAGVGVGESGASYL  RAGVGVGES        0.1380     11233.3                 50.00     Sequence
DRB1_1101   73  RAGVGVGESGASYLA  RAGVGVGES        0.1357     11513.7                 50.00     Sequence
DRB1_1101    5  VPEGLAAASAAVEAL  GLAAASAAV        0.1353     11571.6                 50.00     Sequence
DRB1_1101   79  GESGASYLAGDAAAA  YLAGDAAAA        0.1334     11807.4                 50.00     Sequence
DRB1_1101    8  GLAAASAAVEALTAR  SAAVEALTA        0.1332     11828.5                 50.00     Sequence
DRB1_1101    7  EGLAAASAAVEALTA  GLAAASAAV        0.1328     11877.7                 50.00     Sequence
DRB1_1101    6  PEGLAAASAAVEALT  GLAAASAAV        0.1292     12351.4                 50.00     Sequence
DRB1_1101   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1276     12569.0                 50.00     Sequence
DRB1_1101   25  AAHASAAPVITAVVP  ASAAPVITA        0.1271     12638.6                 50.00     Sequence
DRB1_1101    3  RVVPEGLAAASAAVE  VPEGLAAAS        0.1264     12742.2                 50.00     Sequence
DRB1_1101    4  VVPEGLAAASAAVEA  VPEGLAAAS        0.1258     12817.7                 50.00     Sequence
DRB1_1101   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.1258     12822.5                 50.00     Sequence
DRB1_1101   23  LAAAHASAAPVITAV  HASAAPVIT        0.1250     12936.7                 50.00     Sequence
DRB1_1101   48  QTAAGFSAQGVEHAV  FSAQGVEHA        0.1246     12980.5                 50.00     Sequence
DRB1_1101   28  ASAAPVITAVVPPAA  VITAVVPPA        0.1241     13057.2                 50.00     Sequence
DRB1_1101   24  AAAHASAAPVITAVV  ASAAPVITA        0.1219     13366.0                 50.00     Sequence
DRB1_1101   77  GVGESGASYLAGDAA  ESGASYLAG        0.1130     14721.1                 50.00     Sequence
DRB1_1101   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.1097     15258.7                 50.00     Sequence
DRB1_1101   26  AHASAAPVITAVVPP  ASAAPVITA        0.1095     15299.0                 50.00     Sequence
DRB1_1101   74  AGVGVGESGASYLAG  AGVGVGESG        0.1084     15481.3                 50.00     Sequence
DRB1_1101   40  PAADPVSLQTAAGFS  PVSLQTAAG        0.1063     15835.2                 50.00     Sequence
DRB1_1101   27  HASAAPVITAVVPPA  ASAAPVITA        0.1055     15959.4                 50.00     Sequence
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   DRB1_1101   78  VGESGASYLAGDAAA  GESGASYLA        0.1041      16214.6               50.00     Sequence
   DRB1_1101   76  VGVGESGASYLAGDA  GESGASYLA        0.1012      16725.6               50.00     Sequence
   DRB1_1101   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.0986      17211.0               50.00     Sequence
   DRB1_1101   54  SAQGVEHAVVTAEGV  GVEHAVVTA        0.0971      17480.9               50.00     Sequence
   DRB1_1101   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.0936      18169.5               50.00     Sequence
   DRB1_1101   75  GVGVGESGASYLAGD  VGVGESGAS        0.0916      18559.8               50.00     Sequence
   DRB1_1101   61  AVVTAEGVEELGRAG  VVTAEGVEE        0.0900      18882.2               50.00     Sequence
   DRB1_1101   56  QGVEHAVVTAEGVEE  GVEHAVVTA        0.0889      19102.9               50.00     Sequence
   DRB1_1101   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.0880      19300.5               50.00     Sequence
   DRB1_1101   55  AQGVEHAVVTAEGVE  GVEHAVVTA        0.0846      20009.4               50.00     Sequence
   DRB1_1101   60  HAVVTAEGVEELGRA  VVTAEGVEE        0.0746      22305.3               50.00     Sequence
   DRB1_1101   39  PPAADPVSLQTAAGF  PVSLQTAAG        0.0484      29627.5               50.00     Sequence
   DRB1_1101   35  TAVVPPAADPVSLQT  TAVVPPAAD        0.0319      35411.4               50.00     Sequence
   DRB1_1101   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.0299      36181.0               50.00     Sequence
   DRB1_1101   87  AGDAAAAATYGVVGG  AAAATYGVV        0.0263      37633.1               50.00     Sequence
   DRB1_1101   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.0233      38879.4               50.00     Sequence
   DRB1_1101   36  AVVPPAADPVSLQTA  AVVPPAADP        0.0199      40330.1               50.00     Sequence
   DRB1_1101   37  VVPPAADPVSLQTAA  AADPVSLQT        0.0163      41933.8               50.00     Sequence
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Allele: DRB1_1101. Number of high binders 0. Number of weak binders 4. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1302   12  ASAAVEALTARLAAA  AVEALTARL        0.6053         71.6         WB     8.00     Sequence
   DRB1_1302   19  LTARLAAAHASAAPV  AAHASAAPV        0.6044         72.2         WB     8.00     Sequence
   DRB1_1302   20  TARLAAAHASAAPVI  AAHASAAPV        0.6039         72.7         WB     8.00     Sequence
   DRB1_1302   21  ARLAAAHASAAPVIT  AAHASAAPV        0.5908         83.7         WB     8.00     Sequence
   DRB1_1302    9  LAAASAAVEALTARL  AVEALTARL        0.5886         85.7         WB     8.00     Sequence
   DRB1_1302   13  SAAVEALTARLAAAH  AVEALTARL        0.5880         86.3         WB     8.00     Sequence
   DRB1_1302   10  AAASAAVEALTARLA  AVEALTARL        0.5879         86.4         WB     8.00     Sequence
   DRB1_1302   14  AAVEALTARLAAAHA  AVEALTARL        0.5797         94.4         WB     8.00     Sequence
   DRB1_1302   11  AASAAVEALTARLAA  AVEALTARL        0.5756         98.6         WB     8.00     Sequence
   DRB1_1302    2  LRVVPEGLAAASAAV  GLAAASAAV        0.5677        107.5         WB     8.00     Sequence
   DRB1_1302   22  RLAAAHASAAPVITA  AAHASAAPV        0.5674        107.8         WB     8.00     Sequence
   DRB1_1302    3  RVVPEGLAAASAAVE  GLAAASAAV        0.5660        109.5         WB     8.00     Sequence
   DRB1_1302   15  AVEALTARLAAAHAS  AVEALTARL        0.5566        121.2         WB     8.00     Sequence
   DRB1_1302   23  LAAAHASAAPVITAV  AAHASAAPV        0.5556        122.5         WB     8.00     Sequence
   DRB1_1302   24  AAAHASAAPVITAVV  AAHASAAPV        0.5489        131.8         WB     8.00     Sequence
   DRB1_1302    4  VVPEGLAAASAAVEA  GLAAASAAV        0.5258        169.1         WB    16.00     Sequence
   DRB1_1302   25  AAHASAAPVITAVVP  AAHASAAPV        0.5237        173.0         WB    16.00     Sequence
   DRB1_1302    5  VPEGLAAASAAVEAL  GLAAASAAV        0.5124        195.6         WB    16.00     Sequence
   DRB1_1302    6  PEGLAAASAAVEALT  GLAAASAAV        0.4931        241.0         WB    16.00     Sequence
   DRB1_1302    7  EGLAAASAAVEALTA  GLAAASAAV        0.4764        288.6         WB    16.00     Sequence
   DRB1_1302    8  GLAAASAAVEALTAR  GLAAASAAV        0.4733        298.5         WB    16.00     Sequence
   DRB1_1302   17  EALTARLAAAHASAA  LAAAHASAA        0.4219        520.5               32.00     Sequence
   DRB1_1302   18  ALTARLAAAHASAAP  LAAAHASAA        0.4141        566.3               32.00     Sequence
   DRB1_1302   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.4081        604.6               32.00     Sequence
   DRB1_1302   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.4017        647.8               32.00     Sequence
   DRB1_1302   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.3810        810.7               32.00     Sequence
   DRB1_1302   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.3650        963.7               32.00     Sequence
   DRB1_1302   26  AHASAAPVITAVVPP  AAPVITAVV        0.3625        990.0               32.00     Sequence
   DRB1_1302    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.3582       1037.1               32.00     Sequence
   DRB1_1302    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.3545       1079.8               32.00     Sequence
   DRB1_1302   27  HASAAPVITAVVPPA  AAPVITAVV        0.3544       1080.1               32.00     Sequence
   DRB1_1302   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.3513       1117.4               32.00     Sequence
   DRB1_1302   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.3511       1120.2               32.00     Sequence
   DRB1_1302   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.3502       1130.7               32.00     Sequence
   DRB1_1302   16  VEALTARLAAAHASA  TARLAAAHA        0.3428       1224.8               32.00     Sequence
   DRB1_1302   28  ASAAPVITAVVPPAA  AAPVITAVV        0.3355       1325.8               32.00     Sequence
   DRB1_1302   85  YLAGDAAAAATYGVV  AAAAATYGV        0.3281       1435.8               50.00     Sequence
   DRB1_1302   29  SAAPVITAVVPPAAD  AAPVITAVV        0.3231       1516.9               50.00     Sequence
   DRB1_1302   84  SYLAGDAAAAATYGV  AAAAATYGV        0.3167       1624.9               50.00     Sequence
   DRB1_1302   86  LAGDAAAAATYGVVG  AAAAATYGV        0.3016       1913.2               50.00     Sequence
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   DRB1_1302    30  AAPVITAVVPPAADP  AAPVITAVV          0.2925        2112.0                50.00    Sequence
   DRB1_1302    31  APVITAVVPPAADPV  VVPPAADPV          0.2900        2168.2                50.00    Sequence
   DRB1_1302    82  GASYLAGDAAAAATY  LAGDAAAAA          0.2853        2283.3                50.00    Sequence
   DRB1_1302    73  RAGVGVGESGASYLA  VGESGASYL          0.2848        2293.6                50.00    Sequence
   DRB1_1302    72  GRAGVGVGESGASYL  VGESGASYL          0.2718        2640.0                50.00    Sequence
   DRB1_1302    74  AGVGVGESGASYLAG  VGESGASYL          0.2716        2646.5                50.00    Sequence
   DRB1_1302    56  QGVEHAVVTAEGVEE  VVTAEGVEE          0.2687        2732.6                50.00    Sequence
   DRB1_1302    83  ASYLAGDAAAAATYG  LAGDAAAAA          0.2681        2748.2                50.00    Sequence
   DRB1_1302    87  AGDAAAAATYGVVGG  AAAAATYGV          0.2671        2779.6                50.00    Sequence
   DRB1_1302    52  GFSAQGVEHAVVTAE  QGVEHAVVT          0.2559        3137.4                50.00    Sequence
   DRB1_1302    54  SAQGVEHAVVTAEGV  QGVEHAVVT          0.2516        3286.7                50.00    Sequence
   DRB1_1302    75  GVGVGESGASYLAGD  VGESGASYL          0.2513        3297.9                50.00    Sequence
   DRB1_1302    32  PVITAVVPPAADPVS  VVPPAADPV          0.2440        3568.3                50.00    Sequence
   DRB1_1302    53  FSAQGVEHAVVTAEG  QGVEHAVVT          0.2404        3707.8                50.00    Sequence
   DRB1_1302    55  AQGVEHAVVTAEGVE  QGVEHAVVT          0.2400        3726.0                50.00    Sequence
   DRB1_1302    81  SGASYLAGDAAAAAT  LAGDAAAAA          0.2378        3815.7                50.00    Sequence
   DRB1_1302    33  VITAVVPPAADPVSL  VVPPAADPV          0.2333        4007.0                50.00    Sequence
   DRB1_1302    76  VGVGESGASYLAGDA  VGESGASYL          0.2320        4060.8                50.00    Sequence
   DRB1_1302    51  AGFSAQGVEHAVVTA  QGVEHAVVT          0.2266        4309.0                50.00    Sequence
   DRB1_1302    80  ESGASYLAGDAAAAA  LAGDAAAAA          0.2245        4406.8                50.00    Sequence
   DRB1_1302    57  GVEHAVVTAEGVEEL  VVTAEGVEE          0.2241        4423.5                50.00    Sequence
   DRB1_1302    77  GVGESGASYLAGDAA  VGESGASYL          0.2129        4997.8                50.00    Sequence
   DRB1_1302    34  ITAVVPPAADPVSLQ  VVPPAADPV          0.2074        5298.7                50.00    Sequence
   DRB1_1302    58  VEHAVVTAEGVEELG  VVTAEGVEE          0.1914        6300.4                50.00    Sequence
   DRB1_1302    50  AAGFSAQGVEHAVVT  QGVEHAVVT          0.1887        6490.4                50.00    Sequence
   DRB1_1302    35  TAVVPPAADPVSLQT  VVPPAADPV          0.1880        6541.7                50.00    Sequence
   DRB1_1302    46  SLQTAAGFSAQGVEH  LQTAAGFSA          0.1786        7243.8                50.00    Sequence
   DRB1_1302    78  VGESGASYLAGDAAA  VGESGASYL          0.1761        7440.8                50.00    Sequence
   DRB1_1302    36  AVVPPAADPVSLQTA  VVPPAADPV          0.1716        7812.4                50.00    Sequence
   DRB1_1302    47  LQTAAGFSAQGVEHA  LQTAAGFSA          0.1696        7977.2                50.00    Sequence
   DRB1_1302    59  EHAVVTAEGVEELGR  VVTAEGVEE          0.1642        8462.4                50.00    Sequence
   DRB1_1302    37  VVPPAADPVSLQTAA  VVPPAADPV          0.1605        8806.1                50.00    Sequence
   DRB1_1302    62  VVTAEGVEELGRAGV  VVTAEGVEE          0.1564        9202.2                50.00    Sequence
   DRB1_1302    60  HAVVTAEGVEELGRA  VVTAEGVEE          0.1540        9443.3                50.00    Sequence
   DRB1_1302    71  LGRAGVGVGESGASY  GVGESGASY          0.1501        9856.6                50.00    Sequence
   DRB1_1302    65  AEGVEELGRAGVGVG  LGRAGVGVG          0.1427       10679.8                50.00    Sequence
   DRB1_1302    66  EGVEELGRAGVGVGE  LGRAGVGVG          0.1425       10696.6                50.00    Sequence
   DRB1_1302    70  ELGRAGVGVGESGAS  VGVGESGAS          0.1319       11997.6                50.00    Sequence
   DRB1_1302    79  GESGASYLAGDAAAA  YLAGDAAAA          0.1316       12033.5                50.00    Sequence
   DRB1_1302    67  GVEELGRAGVGVGES  LGRAGVGVG          0.1292       12360.3                50.00    Sequence
   DRB1_1302    64  TAEGVEELGRAGVGV  VEELGRAGV          0.1209       13518.1                50.00    Sequence
   DRB1_1302    61  AVVTAEGVEELGRAG  VVTAEGVEE          0.1198       13676.3                50.00    Sequence
   DRB1_1302    68  VEELGRAGVGVGESG  VEELGRAGV          0.1151       14391.6                50.00    Sequence
   DRB1_1302    49  TAAGFSAQGVEHAVV  GFSAQGVEH          0.1144       14508.7                50.00    Sequence
   DRB1_1302    63  VTAEGVEELGRAGVG  VEELGRAGV          0.1115       14970.0                50.00    Sequence
   DRB1_1302    48  QTAAGFSAQGVEHAV  GFSAQGVEH          0.1083       15496.8                50.00    Sequence
   DRB1_1302    38  VPPAADPVSLQTAAG  PVSLQTAAG          0.0938       18126.7                50.00    Sequence
   DRB1_1302    69  EELGRAGVGVGESGA  LGRAGVGVG          0.0860       19724.8                50.00    Sequence
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Allele: DRB1_1302. Number of high binders 0. Number of weak binders 21. Number of peptides 88

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1501    13  SAAVEALTARLAAAH  AVEALTARL          0.7910           9.6         SB      0.30    Sequence
   DRB1_1501    12  ASAAVEALTARLAAA  AVEALTARL          0.7838          10.4         SB      0.30    Sequence
   DRB1_1501    14  AAVEALTARLAAAHA  AVEALTARL          0.7751          11.4         SB      0.30    Sequence
   DRB1_1501    11  AASAAVEALTARLAA  AVEALTARL          0.7478          15.3         SB      0.80    Sequence
   DRB1_1501    10  AAASAAVEALTARLA  AVEALTARL          0.7144          22.0         SB      2.00    Sequence
   DRB1_1501    15  AVEALTARLAAAHAS  AVEALTARL          0.6996          25.8         SB      2.00    Sequence
   DRB1_1501     9  LAAASAAVEALTARL  AVEALTARL          0.6035          72.9         WB      8.00    Sequence
   DRB1_1501    16  VEALTARLAAAHASA  ALTARLAAA          0.5973          78.0         WB      8.00    Sequence
   DRB1_1501    17  EALTARLAAAHASAA  LTARLAAAH          0.5417         142.4         WB     16.00    Sequence
   DRB1_1501    18  ALTARLAAAHASAAP  LTARLAAAH          0.5252         170.3         WB     16.00    Sequence
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DRB1_1501   19  LTARLAAAHASAAPV  LTARLAAAH        0.3893        740.9                 32.00      Sequence
DRB1_1501   44  PVSLQTAAGFSAQGV  TAAGFSAQG        0.3390       1277.2                 50.00      Sequence
DRB1_1501   46  SLQTAAGFSAQGVEH  TAAGFSAQG        0.3369       1305.5                 50.00      Sequence
DRB1_1501   45  VSLQTAAGFSAQGVE  TAAGFSAQG        0.3352       1329.7                 50.00      Sequence
DRB1_1501   47  LQTAAGFSAQGVEHA  TAAGFSAQG        0.3335       1354.7                 50.00      Sequence
DRB1_1501   48  QTAAGFSAQGVEHAV  TAAGFSAQG        0.3296       1413.2                 50.00      Sequence
DRB1_1501   66  EGVEELGRAGVGVGE  ELGRAGVGV        0.3259       1471.7                 50.00      Sequence
DRB1_1501   65  AEGVEELGRAGVGVG  ELGRAGVGV        0.3256       1475.0                 50.00      Sequence
DRB1_1501    8  GLAAASAAVEALTAR  AAVEALTAR        0.3226       1523.7                 50.00      Sequence
DRB1_1501   67  GVEELGRAGVGVGES  ELGRAGVGV        0.3198       1571.0                 50.00      Sequence
DRB1_1501   49  TAAGFSAQGVEHAVV  TAAGFSAQG        0.3045       1853.6                 50.00      Sequence
DRB1_1501   30  AAPVITAVVPPAADP  PVITAVVPP        0.2929       2102.1                 50.00      Sequence
DRB1_1501   64  TAEGVEELGRAGVGV  ELGRAGVGV        0.2891       2189.6                 50.00      Sequence
DRB1_1501   43  DPVSLQTAAGFSAQG  TAAGFSAQG        0.2887       2200.2                 50.00      Sequence
DRB1_1501   68  VEELGRAGVGVGESG  ELGRAGVGV        0.2871       2239.3                 50.00      Sequence
DRB1_1501   29  SAAPVITAVVPPAAD  PVITAVVPP        0.2832       2334.5                 50.00      Sequence
DRB1_1501   28  ASAAPVITAVVPPAA  PVITAVVPP        0.2831       2336.0                 50.00      Sequence
DRB1_1501   27  HASAAPVITAVVPPA  AAPVITAVV        0.2663       2801.7                 50.00      Sequence
DRB1_1501    0  MTLRVVPEGLAAASA  VVPEGLAAA        0.2526       3251.9                 50.00      Sequence
DRB1_1501   31  APVITAVVPPAADPV  VITAVVPPA        0.2499       3348.5                 50.00      Sequence
DRB1_1501   75  GVGVGESGASYLAGD  VGVGESGAS        0.2494       3364.9                 50.00      Sequence
DRB1_1501    2  LRVVPEGLAAASAAV  VVPEGLAAA        0.2489       3383.8                 50.00      Sequence
DRB1_1501   21  ARLAAAHASAAPVIT  LAAAHASAA        0.2478       3426.1                 50.00      Sequence
DRB1_1501    3  RVVPEGLAAASAAVE  VVPEGLAAA        0.2452       3521.9                 50.00      Sequence
DRB1_1501   32  PVITAVVPPAADPVS  VITAVVPPA        0.2445       3549.1                 50.00      Sequence
DRB1_1501   22  RLAAAHASAAPVITA  RLAAAHASA        0.2421       3643.9                 50.00      Sequence
DRB1_1501    1  TLRVVPEGLAAASAA  VVPEGLAAA        0.2418       3652.5                 50.00      Sequence
DRB1_1501   20  TARLAAAHASAAPVI  LAAAHASAA        0.2417       3657.3                 50.00      Sequence
DRB1_1501   74  AGVGVGESGASYLAG  VGVGESGAS        0.2415       3666.6                 50.00      Sequence
DRB1_1501   70  ELGRAGVGVGESGAS  ELGRAGVGV        0.2414       3669.7                 50.00      Sequence
DRB1_1501   69  EELGRAGVGVGESGA  ELGRAGVGV        0.2406       3703.0                 50.00      Sequence
DRB1_1501   73  RAGVGVGESGASYLA  VGVGESGAS        0.2309       4112.5                 50.00      Sequence
DRB1_1501   76  VGVGESGASYLAGDA  GVGESGASY        0.2286       4214.1                 50.00      Sequence
DRB1_1501   42  ADPVSLQTAAGFSAQ  PVSLQTAAG        0.2285       4220.1                 50.00      Sequence
DRB1_1501   72  GRAGVGVGESGASYL  VGVGESGAS        0.2136       4957.5                 50.00      Sequence
DRB1_1501   81  SGASYLAGDAAAAAT  YLAGDAAAA        0.2128       5003.0                 50.00      Sequence
DRB1_1501   41  AADPVSLQTAAGFSA  PVSLQTAAG        0.2112       5085.6                 50.00      Sequence
DRB1_1501   82  GASYLAGDAAAAATY  SYLAGDAAA        0.2088       5219.3                 50.00      Sequence
DRB1_1501   71  LGRAGVGVGESGASY  LGRAGVGVG        0.2078       5278.6                 50.00      Sequence
DRB1_1501   50  AAGFSAQGVEHAVVT  AAGFSAQGV        0.2074       5299.6                 50.00      Sequence
DRB1_1501   77  GVGESGASYLAGDAA  GVGESGASY        0.2038       5511.3                 50.00      Sequence
DRB1_1501   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.2018       5635.3                 50.00      Sequence
DRB1_1501   26  AHASAAPVITAVVPP  PVITAVVPP        0.2009       5685.1                 50.00      Sequence
DRB1_1501   40  PAADPVSLQTAAGFS  DPVSLQTAA        0.1992       5792.9                 50.00      Sequence
DRB1_1501   33  VITAVVPPAADPVSL  VITAVVPPA        0.1975       5902.4                 50.00      Sequence
DRB1_1501    4  VVPEGLAAASAAVEA  VVPEGLAAA        0.1973       5915.2                 50.00      Sequence
DRB1_1501   63  VTAEGVEELGRAGVG  VEELGRAGV        0.1961       5988.1                 50.00      Sequence
DRB1_1501   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.1896       6424.6                 50.00      Sequence
DRB1_1501   51  AGFSAQGVEHAVVTA  AQGVEHAVV        0.1866       6643.2                 50.00      Sequence
DRB1_1501   23  LAAAHASAAPVITAV  LAAAHASAA        0.1861       6674.5                 50.00      Sequence
DRB1_1501   52  GFSAQGVEHAVVTAE  GVEHAVVTA        0.1850       6758.2                 50.00      Sequence
DRB1_1501   79  GESGASYLAGDAAAA  YLAGDAAAA        0.1800       7130.9                 50.00      Sequence
DRB1_1501   39  PPAADPVSLQTAAGF  PVSLQTAAG        0.1797       7150.9                 50.00      Sequence
DRB1_1501   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.1717       7798.2                 50.00      Sequence
DRB1_1501    7  EGLAAASAAVEALTA  GLAAASAAV        0.1619       8673.0                 50.00      Sequence
DRB1_1501   78  VGESGASYLAGDAAA  VGESGASYL        0.1613       8726.2                 50.00      Sequence
DRB1_1501   62  VVTAEGVEELGRAGV  VEELGRAGV        0.1575       9098.3                 50.00      Sequence
DRB1_1501   54  SAQGVEHAVVTAEGV  GVEHAVVTA        0.1548       9361.5                 50.00      Sequence
DRB1_1501   55  AQGVEHAVVTAEGVE  GVEHAVVTA        0.1544       9410.7                 50.00      Sequence
DRB1_1501   25  AAHASAAPVITAVVP  AAPVITAVV        0.1526       9587.6                 50.00      Sequence
DRB1_1501   24  AAAHASAAPVITAVV  AAPVITAVV        0.1505       9817.0                 50.00      Sequence
DRB1_1501   87  AGDAAAAATYGVVGG  AAATYGVVG        0.1461      10293.2                 50.00      Sequence
DRB1_1501    5  VPEGLAAASAAVEAL  GLAAASAAV        0.1460      10298.2                 50.00      Sequence
DRB1_1501   37  VVPPAADPVSLQTAA  VVPPAADPV        0.1455      10359.5                 50.00      Sequence
DRB1_1501   36  AVVPPAADPVSLQTA  AVVPPAADP        0.1444      10486.2                 50.00      Sequence
DRB1_1501   53  FSAQGVEHAVVTAEG  GVEHAVVTA        0.1440      10524.8                 50.00      Sequence
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   DRB1_1501   56  QGVEHAVVTAEGVEE  GVEHAVVTA        0.1405      10932.0                  50.00     Sequence
   DRB1_1501    6  PEGLAAASAAVEALT  GLAAASAAV        0.1398      11012.9                  50.00     Sequence
   DRB1_1501   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.1395      11057.8                  50.00     Sequence
   DRB1_1501   57  GVEHAVVTAEGVEEL  GVEHAVVTA        0.1366      11403.2                  50.00     Sequence
   DRB1_1501   34  ITAVVPPAADPVSLQ  AVVPPAADP        0.1325      11924.5                  50.00     Sequence
   DRB1_1501   35  TAVVPPAADPVSLQT  VVPPAADPV        0.1267      12693.9                  50.00     Sequence
   DRB1_1501   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.1219      13364.8                  50.00     Sequence
   DRB1_1501   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.1177      13994.2                  50.00     Sequence
   DRB1_1501   61  AVVTAEGVEELGRAG  GVEELGRAG        0.1168      14129.2                  50.00     Sequence
   DRB1_1501   58  VEHAVVTAEGVEELG  AVVTAEGVE        0.0893      19030.5                  50.00     Sequence
   DRB1_1501   60  HAVVTAEGVEELGRA  AVVTAEGVE        0.0876      19381.3                  50.00     Sequence
   DRB1_1501   59  EHAVVTAEGVEELGR  AVVTAEGVE        0.0854      19848.4                  50.00     Sequence
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Allele: DRB1_1501. Number of high binders 6. Number of weak binders 4. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB3_0101   80  ESGASYLAGDAAAAA  LAGDAAAAA        0.2417       3658.7                  32.00     Sequence
   DRB3_0101   81  SGASYLAGDAAAAAT  LAGDAAAAA        0.2387       3777.7                  32.00     Sequence
   DRB3_0101   82  GASYLAGDAAAAATY  LAGDAAAAA        0.2328       4025.6                  32.00     Sequence
   DRB3_0101   83  ASYLAGDAAAAATYG  LAGDAAAAA        0.2181       4724.3                  32.00     Sequence
   DRB3_0101   84  SYLAGDAAAAATYGV  LAGDAAAAA        0.1953       6042.3                  50.00     Sequence
   DRB3_0101   85  YLAGDAAAAATYGVV  LAGDAAAAA        0.1810       7052.1                  50.00     Sequence
   DRB3_0101   79  GESGASYLAGDAAAA  YLAGDAAAA        0.1619       8672.9                  50.00     Sequence
   DRB3_0101   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.1574       9107.5                  50.00     Sequence
   DRB3_0101   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.1516       9691.3                  50.00     Sequence
   DRB3_0101   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.1513       9725.8                  50.00     Sequence
   DRB3_0101   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.1469      10197.1                  50.00     Sequence
   DRB3_0101   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.1383      11196.7                  50.00     Sequence
   DRB3_0101   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.1261      12779.1                  50.00     Sequence
   DRB3_0101   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.1211      13483.2                  50.00     Sequence
   DRB3_0101   50  AAGFSAQGVEHAVVT  SAQGVEHAV        0.1206      13567.6                  50.00     Sequence
   DRB3_0101   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.1119      14905.4                  50.00     Sequence
   DRB3_0101   73  RAGVGVGESGASYLA  VGESGASYL        0.1063      15834.0                  50.00     Sequence
   DRB3_0101    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.1042      16185.1                  50.00     Sequence
   DRB3_0101   21  ARLAAAHASAAPVIT  HASAAPVIT        0.1034      16339.4                  50.00     Sequence
   DRB3_0101   75  GVGVGESGASYLAGD  VGESGASYL        0.1028      16448.9                  50.00     Sequence
   DRB3_0101   54  SAQGVEHAVVTAEGV  HAVVTAEGV        0.1021      16557.6                  50.00     Sequence
   DRB3_0101   72  GRAGVGVGESGASYL  VGESGASYL        0.1021      16559.3                  50.00     Sequence
   DRB3_0101   51  AGFSAQGVEHAVVTA  SAQGVEHAV        0.1018      16621.4                  50.00     Sequence
   DRB3_0101   48  QTAAGFSAQGVEHAV  SAQGVEHAV        0.1013      16700.7                  50.00     Sequence
   DRB3_0101   76  VGVGESGASYLAGDA  VGESGASYL        0.1005      16857.2                  50.00     Sequence
   DRB3_0101   49  TAAGFSAQGVEHAVV  SAQGVEHAV        0.1003      16886.4                  50.00     Sequence
   DRB3_0101   78  VGESGASYLAGDAAA  VGESGASYL        0.0991      17116.7                  50.00     Sequence
   DRB3_0101   77  GVGESGASYLAGDAA  VGESGASYL        0.0990      17137.4                  50.00     Sequence
   DRB3_0101   74  AGVGVGESGASYLAG  VGESGASYL        0.0987      17183.5                  50.00     Sequence
   DRB3_0101    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.0981      17288.8                  50.00     Sequence
   DRB3_0101    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.0973      17448.4                  50.00     Sequence
   DRB3_0101   22  RLAAAHASAAPVITA  HASAAPVIT        0.0971      17490.5                  50.00     Sequence
   DRB3_0101   52  GFSAQGVEHAVVTAE  SAQGVEHAV        0.0967      17560.5                  50.00     Sequence
   DRB3_0101   34  ITAVVPPAADPVSLQ  PAADPVSLQ        0.0964      17624.3                  50.00     Sequence
   DRB3_0101   20  TARLAAAHASAAPVI  LAAAHASAA        0.0958      17730.2                  50.00     Sequence
   DRB3_0101   23  LAAAHASAAPVITAV  LAAAHASAA        0.0911      18665.3                  50.00     Sequence
   DRB3_0101   17  EALTARLAAAHASAA  LAAAHASAA        0.0887      19150.3                  50.00     Sequence
   DRB3_0101   53  FSAQGVEHAVVTAEG  SAQGVEHAV        0.0885      19183.1                  50.00     Sequence
   DRB3_0101   35  TAVVPPAADPVSLQT  VVPPAADPV        0.0882      19261.3                  50.00     Sequence
   DRB3_0101   71  LGRAGVGVGESGASY  GVGESGASY        0.0868      19550.2                  50.00     Sequence
   DRB3_0101   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.0865      19602.7                  50.00     Sequence
   DRB3_0101   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.0827      20427.9                  50.00     Sequence
   DRB3_0101   24  AAAHASAAPVITAVV  HASAAPVIT        0.0823      20529.0                  50.00     Sequence
   DRB3_0101   18  ALTARLAAAHASAAP  LAAAHASAA        0.0818      20633.2                  50.00     Sequence
   DRB3_0101   19  LTARLAAAHASAAPV  LAAAHASAA        0.0802      20985.8                  50.00     Sequence
   DRB3_0101   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.0795      21157.7                  50.00     Sequence
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   DRB3_0101   25  AAHASAAPVITAVVP  HASAAPVIT        0.0790      21265.3               50.00     Sequence
   DRB3_0101   36  AVVPPAADPVSLQTA  PAADPVSLQ        0.0784      21409.6               50.00     Sequence
   DRB3_0101   56  QGVEHAVVTAEGVEE  HAVVTAEGV        0.0765      21848.1               50.00     Sequence
   DRB3_0101   33  VITAVVPPAADPVSL  VVPPAADPV        0.0750      22211.6               50.00     Sequence
   DRB3_0101   31  APVITAVVPPAADPV  VVPPAADPV        0.0741      22436.5               50.00     Sequence
   DRB3_0101   26  AHASAAPVITAVVPP  HASAAPVIT        0.0738      22503.1               50.00     Sequence
   DRB3_0101   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.0715      23077.1               50.00     Sequence
   DRB3_0101   29  SAAPVITAVVPPAAD  VITAVVPPA        0.0714      23101.9               50.00     Sequence
   DRB3_0101   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.0711      23157.7               50.00     Sequence
   DRB3_0101   27  HASAAPVITAVVPPA  VITAVVPPA        0.0698      23505.0               50.00     Sequence
   DRB3_0101   32  PVITAVVPPAADPVS  VVPPAADPV        0.0680      23955.1               50.00     Sequence
   DRB3_0101   28  ASAAPVITAVVPPAA  VITAVVPPA        0.0678      24010.4               50.00     Sequence
   DRB3_0101   15  AVEALTARLAAAHAS  ARLAAAHAS        0.0666      24330.2               50.00     Sequence
   DRB3_0101   37  VVPPAADPVSLQTAA  VVPPAADPV        0.0649      24772.2               50.00     Sequence
   DRB3_0101   70  ELGRAGVGVGESGAS  VGVGESGAS        0.0641      25003.2               50.00     Sequence
   DRB3_0101   30  AAPVITAVVPPAADP  VITAVVPPA        0.0639      25034.9               50.00     Sequence
   DRB3_0101   47  LQTAAGFSAQGVEHA  FSAQGVEHA        0.0626      25410.4               50.00     Sequence
   DRB3_0101   87  AGDAAAAATYGVVGG  AAAAATYGV        0.0618      25633.3               50.00     Sequence
   DRB3_0101   16  VEALTARLAAAHASA  ARLAAAHAS        0.0599      26146.7               50.00     Sequence
   DRB3_0101   38  VPPAADPVSLQTAAG  PAADPVSLQ        0.0546      27690.8               50.00     Sequence
   DRB3_0101    3  RVVPEGLAAASAAVE  GLAAASAAV        0.0522      28427.0               50.00     Sequence
   DRB3_0101   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.0514      28663.9               50.00     Sequence
   DRB3_0101    4  VVPEGLAAASAAVEA  GLAAASAAV        0.0498      29179.9               50.00     Sequence
   DRB3_0101   10  AAASAAVEALTARLA  VEALTARLA        0.0495      29257.3               50.00     Sequence
   DRB3_0101   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.0456      30535.5               50.00     Sequence
   DRB3_0101   11  AASAAVEALTARLAA  VEALTARLA        0.0451      30695.2               50.00     Sequence
   DRB3_0101    5  VPEGLAAASAAVEAL  GLAAASAAV        0.0444      30920.5               50.00     Sequence
   DRB3_0101    6  PEGLAAASAAVEALT  GLAAASAAV        0.0438      31122.9               50.00     Sequence
   DRB3_0101   14  AAVEALTARLAAAHA  LTARLAAAH        0.0438      31131.7               50.00     Sequence
   DRB3_0101   13  SAAVEALTARLAAAH  LTARLAAAH        0.0430      31411.1               50.00     Sequence
   DRB3_0101    8  GLAAASAAVEALTAR  GLAAASAAV        0.0425      31560.0               50.00     Sequence
   DRB3_0101   62  VVTAEGVEELGRAGV  VTAEGVEEL        0.0420      31730.5               50.00     Sequence
   DRB3_0101    7  EGLAAASAAVEALTA  GLAAASAAV        0.0418      31808.5               50.00     Sequence
   DRB3_0101   12  ASAAVEALTARLAAA  VEALTARLA        0.0406      32241.0               50.00     Sequence
   DRB3_0101   66  EGVEELGRAGVGVGE  LGRAGVGVG        0.0403      32328.3               50.00     Sequence
   DRB3_0101   65  AEGVEELGRAGVGVG  LGRAGVGVG        0.0399      32467.5               50.00     Sequence
   DRB3_0101   63  VTAEGVEELGRAGVG  VTAEGVEEL        0.0397      32531.1               50.00     Sequence
   DRB3_0101    9  LAAASAAVEALTARL  AVEALTARL        0.0391      32766.0               50.00     Sequence
   DRB3_0101   67  GVEELGRAGVGVGES  LGRAGVGVG        0.0379      33191.0               50.00     Sequence
   DRB3_0101   68  VEELGRAGVGVGESG  LGRAGVGVG        0.0331      34964.5               50.00     Sequence
   DRB3_0101   69  EELGRAGVGVGESGA  LGRAGVGVG        0.0309      35773.4               50.00     Sequence
   DRB3_0101   64  TAEGVEELGRAGVGV  EGVEELGRA        0.0263      37618.1               50.00     Sequence
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Allele: DRB3_0101. Number of high binders 0. Number of weak binders 0. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB4_0101   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.5799         94.2         WB     8.00     Sequence
   DRB4_0101   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.5737        100.7         WB     8.00     Sequence
   DRB4_0101   42  ADPVSLQTAAGFSAQ  DPVSLQTAA        0.5656        110.0         WB    16.00     Sequence
   DRB4_0101   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.5587        118.5         WB    16.00     Sequence
   DRB4_0101   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.4806        275.7         WB    32.00     Sequence
   DRB4_0101    0  MTLRVVPEGLAAASA  LRVVPEGLA        0.4602        343.9         WB    32.00     Sequence
   DRB4_0101   38  VPPAADPVSLQTAAG  ADPVSLQTA        0.4337        458.1         WB    32.00     Sequence
   DRB4_0101    1  TLRVVPEGLAAASAA  LRVVPEGLA        0.4281        486.7         WB    32.00     Sequence
   DRB4_0101   37  VVPPAADPVSLQTAA  ADPVSLQTA        0.3854        772.6               50.00     Sequence
   DRB4_0101    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.3776        841.1               50.00     Sequence
   DRB4_0101   15  AVEALTARLAAAHAS  VEALTARLA        0.3476       1163.0               50.00     Sequence
   DRB4_0101   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.3471       1169.0               50.00     Sequence
   DRB4_0101   14  AAVEALTARLAAAHA  VEALTARLA        0.3304       1401.3               50.00     Sequence
   DRB4_0101   16  VEALTARLAAAHASA  VEALTARLA        0.3258       1471.9               50.00     Sequence
   DRB4_0101   31  APVITAVVPPAADPV  APVITAVVP        0.3234       1511.7               50.00     Sequence
   DRB4_0101   13  SAAVEALTARLAAAH  VEALTARLA        0.3136       1681.0               50.00     Sequence
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DRB4_0101   17  EALTARLAAAHASAA  LTARLAAAH        0.3120       1710.5                   50.00      Sequence
DRB4_0101   30  AAPVITAVVPPAADP  APVITAVVP        0.3088       1769.7                   50.00      Sequence
DRB4_0101   18  ALTARLAAAHASAAP  LTARLAAAH        0.3054       1837.1                   50.00      Sequence
DRB4_0101   29  SAAPVITAVVPPAAD  APVITAVVP        0.3041       1862.9                   50.00      Sequence
DRB4_0101   81  SGASYLAGDAAAAAT  ASYLAGDAA        0.2969       2013.4                   50.00      Sequence
DRB4_0101   28  ASAAPVITAVVPPAA  APVITAVVP        0.2959       2036.0                   50.00      Sequence
DRB4_0101   78  VGESGASYLAGDAAA  ASYLAGDAA        0.2942       2072.0                   50.00      Sequence
DRB4_0101   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.2938       2082.7                   50.00      Sequence
DRB4_0101   80  ESGASYLAGDAAAAA  ASYLAGDAA        0.2914       2136.4                   50.00      Sequence
DRB4_0101   77  GVGESGASYLAGDAA  ASYLAGDAA        0.2860       2264.6                   50.00      Sequence
DRB4_0101   79  GESGASYLAGDAAAA  ASYLAGDAA        0.2832       2334.3                   50.00      Sequence
DRB4_0101   82  GASYLAGDAAAAATY  ASYLAGDAA        0.2826       2351.1                   50.00      Sequence
DRB4_0101   19  LTARLAAAHASAAPV  LTARLAAAH        0.2779       2472.1                   50.00      Sequence
DRB4_0101   36  AVVPPAADPVSLQTA  ADPVSLQTA        0.2686       2733.9                   50.00      Sequence
DRB4_0101   12  ASAAVEALTARLAAA  VEALTARLA        0.2618       2942.4                   50.00      Sequence
DRB4_0101   32  PVITAVVPPAADPVS  ITAVVPPAA        0.2618       2943.9                   50.00      Sequence
DRB4_0101   27  HASAAPVITAVVPPA  APVITAVVP        0.2566       3111.6                   50.00      Sequence
DRB4_0101   50  AAGFSAQGVEHAVVT  AAGFSAQGV        0.2498       3349.3                   50.00      Sequence
DRB4_0101   49  TAAGFSAQGVEHAVV  AAGFSAQGV        0.2466       3467.4                   50.00      Sequence
DRB4_0101   54  SAQGVEHAVVTAEGV  HAVVTAEGV        0.2434       3591.2                   50.00      Sequence
DRB4_0101   83  ASYLAGDAAAAATYG  ASYLAGDAA        0.2352       3922.9                   50.00      Sequence
DRB4_0101   11  AASAAVEALTARLAA  VEALTARLA        0.2324       4044.4                   50.00      Sequence
DRB4_0101   48  QTAAGFSAQGVEHAV  AAGFSAQGV        0.2310       4105.3                   50.00      Sequence
DRB4_0101   26  AHASAAPVITAVVPP  APVITAVVP        0.2216       4545.9                   50.00      Sequence
DRB4_0101   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.2191       4669.6                   50.00      Sequence
DRB4_0101   53  FSAQGVEHAVVTAEG  SAQGVEHAV        0.2175       4750.7                   50.00      Sequence
DRB4_0101   47  LQTAAGFSAQGVEHA  AAGFSAQGV        0.2141       4933.4                   50.00      Sequence
DRB4_0101   52  GFSAQGVEHAVVTAE  AQGVEHAVV        0.2051       5434.1                   50.00      Sequence
DRB4_0101   51  AGFSAQGVEHAVVTA  AQGVEHAVV        0.2031       5556.4                   50.00      Sequence
DRB4_0101   33  VITAVVPPAADPVSL  ITAVVPPAA        0.2030       5560.5                   50.00      Sequence
DRB4_0101   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.2029       5567.1                   50.00      Sequence
DRB4_0101   10  AAASAAVEALTARLA  VEALTARLA        0.2024       5593.3                   50.00      Sequence
DRB4_0101   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.1946       6088.6                   50.00      Sequence
DRB4_0101   57  GVEHAVVTAEGVEEL  HAVVTAEGV        0.1900       6401.4                   50.00      Sequence
DRB4_0101   20  TARLAAAHASAAPVI  ARLAAAHAS        0.1892       6455.0                   50.00      Sequence
DRB4_0101   56  QGVEHAVVTAEGVEE  HAVVTAEGV        0.1884       6514.1                   50.00      Sequence
DRB4_0101   66  EGVEELGRAGVGVGE  VEELGRAGV        0.1838       6846.0                   50.00      Sequence
DRB4_0101   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.1838       6846.2                   50.00      Sequence
DRB4_0101    3  RVVPEGLAAASAAVE  VPEGLAAAS        0.1801       7119.7                   50.00      Sequence
DRB4_0101   64  TAEGVEELGRAGVGV  VEELGRAGV        0.1790       7212.2                   50.00      Sequence
DRB4_0101   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1761       7439.6                   50.00      Sequence
DRB4_0101   67  GVEELGRAGVGVGES  VEELGRAGV        0.1759       7458.0                   50.00      Sequence
DRB4_0101   65  AEGVEELGRAGVGVG  VEELGRAGV        0.1750       7529.3                   50.00      Sequence
DRB4_0101    4  VVPEGLAAASAAVEA  VPEGLAAAS        0.1749       7533.8                   50.00      Sequence
DRB4_0101   63  VTAEGVEELGRAGVG  VEELGRAGV        0.1728       7710.9                   50.00      Sequence
DRB4_0101   76  VGVGESGASYLAGDA  GASYLAGDA        0.1727       7715.1                   50.00      Sequence
DRB4_0101    5  VPEGLAAASAAVEAL  VPEGLAAAS        0.1678       8135.1                   50.00      Sequence
DRB4_0101   62  VVTAEGVEELGRAGV  VEELGRAGV        0.1634       8537.4                   50.00      Sequence
DRB4_0101   46  SLQTAAGFSAQGVEH  AAGFSAQGV        0.1622       8649.5                   50.00      Sequence
DRB4_0101   21  ARLAAAHASAAPVIT  ARLAAAHAS        0.1597       8885.8                   50.00      Sequence
DRB4_0101   35  TAVVPPAADPVSLQT  TAVVPPAAD        0.1590       8946.4                   50.00      Sequence
DRB4_0101   75  GVGVGESGASYLAGD  GVGVGESGA        0.1564       9203.8                   50.00      Sequence
DRB4_0101   73  RAGVGVGESGASYLA  AGVGVGESG        0.1559       9254.0                   50.00      Sequence
DRB4_0101   68  VEELGRAGVGVGESG  VEELGRAGV        0.1557       9280.0                   50.00      Sequence
DRB4_0101   74  AGVGVGESGASYLAG  AGVGVGESG        0.1546       9382.5                   50.00      Sequence
DRB4_0101   25  AAHASAAPVITAVVP  APVITAVVP        0.1443      10497.6                   50.00      Sequence
DRB4_0101   72  GRAGVGVGESGASYL  AGVGVGESG        0.1427      10675.1                   50.00      Sequence
DRB4_0101    6  PEGLAAASAAVEALT  EGLAAASAA        0.1329      11873.8                   50.00      Sequence
DRB4_0101   61  AVVTAEGVEELGRAG  VTAEGVEEL        0.1291      12373.6                   50.00      Sequence
DRB4_0101   71  LGRAGVGVGESGASY  LGRAGVGVG        0.1246      12979.2                   50.00      Sequence
DRB4_0101    9  LAAASAAVEALTARL  AVEALTARL        0.1241      13055.4                   50.00      Sequence
DRB4_0101   70  ELGRAGVGVGESGAS  LGRAGVGVG        0.1211      13482.9                   50.00      Sequence
DRB4_0101    7  EGLAAASAAVEALTA  EGLAAASAA        0.1172      14073.8                   50.00      Sequence
DRB4_0101   69  EELGRAGVGVGESGA  AGVGVGESG        0.1167      14145.7                   50.00      Sequence
DRB4_0101   22  RLAAAHASAAPVITA  RLAAAHASA        0.1081      15520.4                   50.00      Sequence
DRB4_0101    8  GLAAASAAVEALTAR  GLAAASAAV        0.1072      15676.4                   50.00      Sequence
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   DRB4_0101   84  SYLAGDAAAAATYGV  SYLAGDAAA        0.0882     19250.9                 50.00     Sequence
   DRB4_0101   24  AAAHASAAPVITAVV  AAPVITAVV        0.0826     20465.3                 50.00     Sequence
   DRB4_0101   23  LAAAHASAAPVITAV  AAHASAAPV        0.0739     22476.8                 50.00     Sequence
   DRB4_0101   85  YLAGDAAAAATYGVV  LAGDAAAAA        0.0626     25402.7                 50.00     Sequence
   DRB4_0101   86  LAGDAAAAATYGVVG  LAGDAAAAA        0.0599     26152.7                 50.00     Sequence
   DRB4_0101   87  AGDAAAAATYGVVGG  AATYGVVGG        0.0503     29023.1                 50.00     Sequence
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Allele: DRB4_0101. Number of high binders 0. Number of weak binders 8. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB5_0101   13  SAAVEALTARLAAAH  AVEALTARL        0.5477       133.4          WB   16.00     Sequence
   DRB5_0101   12  ASAAVEALTARLAAA  AVEALTARL        0.5434       139.8          WB   16.00     Sequence
   DRB5_0101   11  AASAAVEALTARLAA  AVEALTARL        0.5255       169.7          WB   16.00     Sequence
   DRB5_0101   14  AAVEALTARLAAAHA  AVEALTARL        0.5091       202.7          WB   32.00     Sequence
   DRB5_0101   10  AAASAAVEALTARLA  AVEALTARL        0.4850       262.9          WB   32.00     Sequence
   DRB5_0101   15  AVEALTARLAAAHAS  AVEALTARL        0.4576       353.9          WB   32.00     Sequence
   DRB5_0101    9  LAAASAAVEALTARL  AVEALTARL        0.4399       428.6          WB   32.00     Sequence
   DRB5_0101   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.3865       763.4               50.00     Sequence
   DRB5_0101   57  GVEHAVVTAEGVEEL  VVTAEGVEE        0.3765       850.7               50.00     Sequence
   DRB5_0101   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.3737       876.7               50.00     Sequence
   DRB5_0101   59  EHAVVTAEGVEELGR  VVTAEGVEE        0.3734       879.6               50.00     Sequence
   DRB5_0101   58  VEHAVVTAEGVEELG  VVTAEGVEE        0.3645       968.8               50.00     Sequence
   DRB5_0101   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.3620       995.5               50.00     Sequence
   DRB5_0101   60  HAVVTAEGVEELGRA  VVTAEGVEE        0.3569      1052.0               50.00     Sequence
   DRB5_0101   45  VSLQTAAGFSAQGVE  VSLQTAAGF        0.3445      1203.2               50.00     Sequence
   DRB5_0101    0  MTLRVVPEGLAAASA  RVVPEGLAA        0.3356      1324.6               50.00     Sequence
   DRB5_0101   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.3351      1331.1               50.00     Sequence
   DRB5_0101   17  EALTARLAAAHASAA  LTARLAAAH        0.3327      1366.8               50.00     Sequence
   DRB5_0101   56  QGVEHAVVTAEGVEE  VVTAEGVEE        0.3302      1404.1               50.00     Sequence
   DRB5_0101   16  VEALTARLAAAHASA  LTARLAAAH        0.3301      1405.8               50.00     Sequence
   DRB5_0101   19  LTARLAAAHASAAPV  ARLAAAHAS        0.3271      1452.1               50.00     Sequence
   DRB5_0101    2  LRVVPEGLAAASAAV  LRVVPEGLA        0.3231      1516.2               50.00     Sequence
   DRB5_0101   20  TARLAAAHASAAPVI  ARLAAAHAS        0.3220      1533.5               50.00     Sequence
   DRB5_0101   18  ALTARLAAAHASAAP  ARLAAAHAS        0.3200      1568.2               50.00     Sequence
   DRB5_0101    8  GLAAASAAVEALTAR  GLAAASAAV        0.3164      1630.3               50.00     Sequence
   DRB5_0101   50  AAGFSAQGVEHAVVT  GFSAQGVEH        0.3147      1661.0               50.00     Sequence
   DRB5_0101    1  TLRVVPEGLAAASAA  RVVPEGLAA        0.3138      1676.8               50.00     Sequence
   DRB5_0101   61  AVVTAEGVEELGRAG  VVTAEGVEE        0.3111      1726.8               50.00     Sequence
   DRB5_0101   51  AGFSAQGVEHAVVTA  GFSAQGVEH        0.3086      1772.7               50.00     Sequence
   DRB5_0101   21  ARLAAAHASAAPVIT  ARLAAAHAS        0.3080      1785.7               50.00     Sequence
   DRB5_0101   49  TAAGFSAQGVEHAVV  GFSAQGVEH        0.3064      1816.3               50.00     Sequence
   DRB5_0101   52  GFSAQGVEHAVVTAE  GFSAQGVEH        0.3013      1920.1               50.00     Sequence
   DRB5_0101    3  RVVPEGLAAASAAVE  GLAAASAAV        0.2817      2374.0               50.00     Sequence
   DRB5_0101   62  VVTAEGVEELGRAGV  VVTAEGVEE        0.2801      2413.7               50.00     Sequence
   DRB5_0101   48  QTAAGFSAQGVEHAV  GFSAQGVEH        0.2725      2620.7               50.00     Sequence
   DRB5_0101   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.2716      2648.2               50.00     Sequence
   DRB5_0101   22  RLAAAHASAAPVITA  AAHASAAPV        0.2617      2947.1               50.00     Sequence
   DRB5_0101   47  LQTAAGFSAQGVEHA  GFSAQGVEH        0.2609      2972.0               50.00     Sequence
   DRB5_0101   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.2569      3102.3               50.00     Sequence
   DRB5_0101    7  EGLAAASAAVEALTA  GLAAASAAV        0.2554      3154.9               50.00     Sequence
   DRB5_0101   74  AGVGVGESGASYLAG  GVGESGASY        0.2520      3271.9               50.00     Sequence
   DRB5_0101   75  GVGVGESGASYLAGD  GVGESGASY        0.2494      3364.2               50.00     Sequence
   DRB5_0101    5  VPEGLAAASAAVEAL  GLAAASAAV        0.2483      3405.3               50.00     Sequence
   DRB5_0101   76  VGVGESGASYLAGDA  GVGESGASY        0.2375      3829.7               50.00     Sequence
   DRB5_0101    4  VVPEGLAAASAAVEA  GLAAASAAV        0.2355      3912.0               50.00     Sequence
   DRB5_0101   73  RAGVGVGESGASYLA  GVGESGASY        0.2292      4189.7               50.00     Sequence
   DRB5_0101    6  PEGLAAASAAVEALT  GLAAASAAV        0.2261      4328.7               50.00     Sequence
   DRB5_0101   23  LAAAHASAAPVITAV  AAHASAAPV        0.2245      4405.6               50.00     Sequence
   DRB5_0101   24  AAAHASAAPVITAVV  HASAAPVIT        0.2240      4429.6               50.00     Sequence
   DRB5_0101   64  TAEGVEELGRAGVGV  AEGVEELGR        0.2220      4528.2               50.00     Sequence
   DRB5_0101   65  AEGVEELGRAGVGVG  GVEELGRAG        0.2169      4784.1               50.00     Sequence
   DRB5_0101   25  AAHASAAPVITAVVP  HASAAPVIT        0.2156      4851.4               50.00     Sequence
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   DRB5_0101   63  VTAEGVEELGRAGVG  AEGVEELGR        0.2146       4906.7                   50.00     Sequence
   DRB5_0101   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.2091       5204.3                   50.00     Sequence
   DRB5_0101   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.2073       5305.5                   50.00     Sequence
   DRB5_0101   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.2053       5423.8                   50.00     Sequence
   DRB5_0101   72  GRAGVGVGESGASYL  GVGESGASY        0.2046       5465.4                   50.00     Sequence
   DRB5_0101   32  PVITAVVPPAADPVS  ITAVVPPAA        0.1961       5993.2                   50.00     Sequence
   DRB5_0101   31  APVITAVVPPAADPV  ITAVVPPAA        0.1937       6150.2                   50.00     Sequence
   DRB5_0101   26  AHASAAPVITAVVPP  HASAAPVIT        0.1936       6153.2                   50.00     Sequence
   DRB5_0101   77  GVGESGASYLAGDAA  GVGESGASY        0.1814       7021.4                   50.00     Sequence
   DRB5_0101   33  VITAVVPPAADPVSL  VITAVVPPA        0.1715       7819.8                   50.00     Sequence
   DRB5_0101   66  EGVEELGRAGVGVGE  GVEELGRAG        0.1666       8239.4                   50.00     Sequence
   DRB5_0101   30  AAPVITAVVPPAADP  ITAVVPPAA        0.1664       8257.8                   50.00     Sequence
   DRB5_0101   71  LGRAGVGVGESGASY  GVGESGASY        0.1613       8726.3                   50.00     Sequence
   DRB5_0101   27  HASAAPVITAVVPPA  HASAAPVIT        0.1536       9490.6                   50.00     Sequence
   DRB5_0101   54  SAQGVEHAVVTAEGV  HAVVTAEGV        0.1522       9631.7                   50.00     Sequence
   DRB5_0101   29  SAAPVITAVVPPAAD  VITAVVPPA        0.1490       9975.6                   50.00     Sequence
   DRB5_0101   34  ITAVVPPAADPVSLQ  TAVVPPAAD        0.1471      10177.2                   50.00     Sequence
   DRB5_0101   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.1428      10664.2                   50.00     Sequence
   DRB5_0101   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.1418      10782.0                   50.00     Sequence
   DRB5_0101   82  GASYLAGDAAAAATY  YLAGDAAAA        0.1403      10952.8                   50.00     Sequence
   DRB5_0101   67  GVEELGRAGVGVGES  GVEELGRAG        0.1381      11217.6                   50.00     Sequence
   DRB5_0101   28  ASAAPVITAVVPPAA  VITAVVPPA        0.1356      11528.6                   50.00     Sequence
   DRB5_0101   85  YLAGDAAAAATYGVV  YLAGDAAAA        0.1245      13006.5                   50.00     Sequence
   DRB5_0101   81  SGASYLAGDAAAAAT  SYLAGDAAA        0.1151      14389.1                   50.00     Sequence
   DRB5_0101   35  TAVVPPAADPVSLQT  VVPPAADPV        0.1051      16042.5                   50.00     Sequence
   DRB5_0101   38  VPPAADPVSLQTAAG  PVSLQTAAG        0.1040      16225.5                   50.00     Sequence
   DRB5_0101   80  ESGASYLAGDAAAAA  SYLAGDAAA        0.1039      16248.8                   50.00     Sequence
   DRB5_0101   70  ELGRAGVGVGESGAS  ELGRAGVGV        0.1018      16625.3                   50.00     Sequence
   DRB5_0101   86  LAGDAAAAATYGVVG  GDAAAAATY        0.0992      17095.4                   50.00     Sequence
   DRB5_0101   87  AGDAAAAATYGVVGG  GDAAAAATY        0.0965      17595.9                   50.00     Sequence
   DRB5_0101   79  GESGASYLAGDAAAA  YLAGDAAAA        0.0958      17728.1                   50.00     Sequence
   DRB5_0101   78  VGESGASYLAGDAAA  VGESGASYL        0.0905      18781.0                   50.00     Sequence
   DRB5_0101   37  VVPPAADPVSLQTAA  VVPPAADPV        0.0887      19143.7                   50.00     Sequence
   DRB5_0101   69  EELGRAGVGVGESGA  ELGRAGVGV        0.0813      20757.4                   50.00     Sequence
   DRB5_0101   68  VEELGRAGVGVGESG  ELGRAGVGV        0.0756      22062.4                   50.00     Sequence
   DRB5_0101   36  AVVPPAADPVSLQTA  VVPPAADPV        0.0703      23360.2                   50.00     Sequence
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Allele: DRB5_0101. Number of high binders 0. Number of weak binders 7. Number of peptides 88

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAb   23  LAAAHASAAPVITAV  LAAAHASAA        0.7849         10.3           SB     0.05     Sequence
         IAb   21  ARLAAAHASAAPVIT  LAAAHASAA        0.7813         10.7           SB     0.10     Sequence
         IAb   22  RLAAAHASAAPVITA  LAAAHASAA        0.7749         11.4           SB     0.10     Sequence
         IAb   20  TARLAAAHASAAPVI  LAAAHASAA        0.7633         13.0           SB     0.10     Sequence
         IAb   19  LTARLAAAHASAAPV  LAAAHASAA        0.7330         18.0           SB     0.20     Sequence
         IAb   24  AAAHASAAPVITAVV  HASAAPVIT        0.7223         20.2           SB     0.30     Sequence
         IAb   34  ITAVVPPAADPVSLQ  TAVVPPAAD        0.7010         25.4           SB     0.40     Sequence
         IAb   32  PVITAVVPPAADPVS  TAVVPPAAD        0.6984         26.1           SB     0.40     Sequence
         IAb   33  VITAVVPPAADPVSL  TAVVPPAAD        0.6966         26.6           SB     0.40     Sequence
         IAb   25  AAHASAAPVITAVVP  HASAAPVIT        0.6861         29.8           SB     0.80     Sequence
         IAb   18  ALTARLAAAHASAAP  LAAAHASAA        0.6847         30.3           SB     0.80     Sequence
         IAb   31  APVITAVVPPAADPV  TAVVPPAAD        0.6678         36.4           SB     0.80     Sequence
         IAb    7  EGLAAASAAVEALTA  LAAASAAVE        0.6671         36.7           SB     0.80     Sequence
         IAb    6  PEGLAAASAAVEALT  LAAASAAVE        0.6625         38.6           SB     0.80     Sequence
         IAb   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.6527         42.9           SB     0.80     Sequence
         IAb   17  EALTARLAAAHASAA  LAAAHASAA        0.6488         44.7           SB     0.80     Sequence
         IAb   82  GASYLAGDAAAAATY  ASYLAGDAA        0.6487         44.8           SB     0.80     Sequence
         IAb    5  VPEGLAAASAAVEAL  LAAASAAVE        0.6469         45.6           SB     0.80     Sequence
         IAb   26  AHASAAPVITAVVPP  HASAAPVIT        0.6380         50.2           WB     1.00     Sequence
         IAb   30  AAPVITAVVPPAADP  TAVVPPAAD        0.6267         56.8           WB     2.00     Sequence
         IAb   81  SGASYLAGDAAAAAT  ASYLAGDAA        0.6229         59.2           WB     2.00     Sequence
         IAb    8  GLAAASAAVEALTAR  LAAASAAVE        0.6221         59.7           WB     2.00     Sequence
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IAb    4  VVPEGLAAASAAVEA  LAAASAAVE      0.6189      61.8      WB    2.00    Sequence
IAb   35  TAVVPPAADPVSLQT  TAVVPPAAD      0.6051      71.7      WB    2.00    Sequence
IAb   80  ESGASYLAGDAAAAA  ASYLAGDAA      0.5914      83.2      WB    2.00    Sequence
IAb   27  HASAAPVITAVVPPA  HASAAPVIT      0.5902      84.3      WB    2.00    Sequence
IAb   29  SAAPVITAVVPPAAD  TAVVPPAAD      0.5872      87.1      WB    2.00    Sequence
IAb    3  RVVPEGLAAASAAVE  EGLAAASAA      0.5783      95.8      WB    2.00    Sequence
IAb    9  LAAASAAVEALTARL  LAAASAAVE      0.5717     102.9      WB    4.00    Sequence
IAb   84  SYLAGDAAAAATYGV  YLAGDAAAA      0.5655     110.0      WB    4.00    Sequence
IAb   16  VEALTARLAAAHASA  ARLAAAHAS      0.5598     117.1      WB    4.00    Sequence
IAb   79  GESGASYLAGDAAAA  ASYLAGDAA      0.5402     144.8      WB    4.00    Sequence
IAb   85  YLAGDAAAAATYGVV  YLAGDAAAA      0.5323     157.6      WB    4.00    Sequence
IAb   28  ASAAPVITAVVPPAA  ITAVVPPAA      0.5305     160.8      WB    4.00    Sequence
IAb    2  LRVVPEGLAAASAAV  EGLAAASAA      0.5142     191.8      WB    4.00    Sequence
IAb   15  AVEALTARLAAAHAS  ARLAAAHAS      0.5084     204.2      WB    8.00    Sequence
IAb   50  AAGFSAQGVEHAVVT  AAGFSAQGV      0.4849     263.4      WB    8.00    Sequence
IAb   48  QTAAGFSAQGVEHAV  FSAQGVEHA      0.4774     285.6      WB    8.00    Sequence
IAb   49  TAAGFSAQGVEHAVV  AGFSAQGVE      0.4749     293.2      WB    8.00    Sequence
IAb   47  LQTAAGFSAQGVEHA  LQTAAGFSA      0.4673     318.6      WB    8.00    Sequence
IAb    1  TLRVVPEGLAAASAA  EGLAAASAA      0.4544     366.1      WB    8.00    Sequence
IAb   10  AAASAAVEALTARLA  AAASAAVEA      0.4480     392.5      WB    8.00    Sequence
IAb   14  AAVEALTARLAAAHA  VEALTARLA      0.4419     419.3      WB    8.00    Sequence
IAb   44  PVSLQTAAGFSAQGV  LQTAAGFSA      0.4101     591.3           16.00    Sequence
IAb   46  SLQTAAGFSAQGVEH  LQTAAGFSA      0.4094     596.1           16.00    Sequence
IAb   13  SAAVEALTARLAAAH  VEALTARLA      0.4079     605.6           16.00    Sequence
IAb   36  AVVPPAADPVSLQTA  VPPAADPVS      0.4029     639.2           16.00    Sequence
IAb   45  VSLQTAAGFSAQGVE  LQTAAGFSA      0.4010     652.7           16.00    Sequence
IAb   11  AASAAVEALTARLAA  AASAAVEAL      0.3843     781.7           16.00    Sequence
IAb   78  VGESGASYLAGDAAA  ASYLAGDAA      0.3840     784.6           16.00    Sequence
IAb   37  VVPPAADPVSLQTAA  VPPAADPVS      0.3822     799.9           16.00    Sequence
IAb   86  LAGDAAAAATYGVVG  LAGDAAAAA      0.3792     826.4           16.00    Sequence
IAb   51  AGFSAQGVEHAVVTA  FSAQGVEHA      0.3736     878.1           16.00    Sequence
IAb   12  ASAAVEALTARLAAA  VEALTARLA      0.3718     894.7           16.00    Sequence
IAb    0  MTLRVVPEGLAAASA  VVPEGLAAA      0.3583    1036.3           16.00    Sequence
IAb   43  DPVSLQTAAGFSAQG  LQTAAGFSA      0.3363    1313.7           32.00    Sequence
IAb   38  VPPAADPVSLQTAAG  VPPAADPVS      0.3291    1420.6           32.00    Sequence
IAb   42  ADPVSLQTAAGFSAQ  LQTAAGFSA      0.3217    1540.1           32.00    Sequence
IAb   53  FSAQGVEHAVVTAEG  FSAQGVEHA      0.3098    1751.0           32.00    Sequence
IAb   52  GFSAQGVEHAVVTAE  FSAQGVEHA      0.3083    1780.2           32.00    Sequence
IAb   77  GVGESGASYLAGDAA  ASYLAGDAA      0.3080    1784.6           32.00    Sequence
IAb   87  AGDAAAAATYGVVGG  AGDAAAAAT      0.3018    1908.1           32.00    Sequence
IAb   41  AADPVSLQTAAGFSA  LQTAAGFSA      0.2798    2420.9           32.00    Sequence
IAb   55  AQGVEHAVVTAEGVE  VEHAVVTAE      0.2458    3498.8           32.00    Sequence
IAb   39  PPAADPVSLQTAAGF  PPAADPVSL      0.2430    3605.3           50.00    Sequence
IAb   56  QGVEHAVVTAEGVEE  VEHAVVTAE      0.2426    3623.2           50.00    Sequence
IAb   54  SAQGVEHAVVTAEGV  VEHAVVTAE      0.2410    3686.6           50.00    Sequence
IAb   76  VGVGESGASYLAGDA  VGVGESGAS      0.2114    5079.2           50.00    Sequence
IAb   57  GVEHAVVTAEGVEEL  VEHAVVTAE      0.2101    5147.4           50.00    Sequence
IAb   40  PAADPVSLQTAAGFS  ADPVSLQTA      0.2009    5686.2           50.00    Sequence
IAb   58  VEHAVVTAEGVEELG  VEHAVVTAE      0.1922    6249.7           50.00    Sequence
IAb   73  RAGVGVGESGASYLA  VGVGESGAS      0.1888    6482.7           50.00    Sequence
IAb   74  AGVGVGESGASYLAG  VGVGESGAS      0.1857    6702.5           50.00    Sequence
IAb   75  GVGVGESGASYLAGD  VGVGESGAS      0.1857    6705.7           50.00    Sequence
IAb   72  GRAGVGVGESGASYL  RAGVGVGES      0.1614    8716.2           50.00    Sequence
IAb   71  LGRAGVGVGESGASY  RAGVGVGES      0.1441   10515.9           50.00    Sequence
IAb   70  ELGRAGVGVGESGAS  RAGVGVGES      0.1346   11652.7           50.00    Sequence
IAb   60  HAVVTAEGVEELGRA  HAVVTAEGV      0.1294   12322.9           50.00    Sequence
IAb   59  EHAVVTAEGVEELGR  HAVVTAEGV      0.1278   12538.7           50.00    Sequence
IAb   69  EELGRAGVGVGESGA  RAGVGVGES      0.1223   13313.4           50.00    Sequence
IAb   61  AVVTAEGVEELGRAG  AVVTAEGVE      0.1104   15139.4           50.00    Sequence
IAb   68  VEELGRAGVGVGESG  RAGVGVGES      0.1097   15252.1           50.00    Sequence
IAb   67  GVEELGRAGVGVGES  RAGVGVGES      0.0968   17550.3           50.00    Sequence
IAb   62  VVTAEGVEELGRAGV  VVTAEGVEE      0.0871   19478.4           50.00    Sequence
IAb   66  EGVEELGRAGVGVGE  LGRAGVGVG      0.0601   26103.8           50.00    Sequence
IAb   63  VTAEGVEELGRAGVG  VTAEGVEEL      0.0596   26248.5           50.00    Sequence
IAb   65  AEGVEELGRAGVGVG  LGRAGVGVG      0.0519   28506.1           50.00    Sequence
IAb   64  TAEGVEELGRAGVGV  EELGRAGVG      0.0344   34464.9           50.00    Sequence
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Allele: IAb. Number of high binders 18. Number of weak binders 25. Number of peptides 88

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAd   15  AVEALTARLAAAHAS  ARLAAAHAS        0.5756         98.7         WB     0.15     Sequence
         IAd   10  AAASAAVEALTARLA  AASAAVEAL        0.5710        103.7         WB     0.15     Sequence
         IAd   16  VEALTARLAAAHASA  ARLAAAHAS        0.5452        137.1         WB     0.20     Sequence
         IAd   11  AASAAVEALTARLAA  VEALTARLA        0.5309        160.0         WB     0.30     Sequence
         IAd    9  LAAASAAVEALTARL  AASAAVEAL        0.5182        183.6         WB     0.40     Sequence
         IAd    7  EGLAAASAAVEALTA  AAASAAVEA        0.4924        242.9         WB     0.80     Sequence
         IAd    8  GLAAASAAVEALTAR  AASAAVEAL        0.4809        274.8         WB     0.80     Sequence
         IAd   12  ASAAVEALTARLAAA  VEALTARLA        0.4778        284.4         WB     0.80     Sequence
         IAd   14  AAVEALTARLAAAHA  VEALTARLA        0.4749        293.5         WB     0.80     Sequence
         IAd   13  SAAVEALTARLAAAH  VEALTARLA        0.4612        340.2         WB     1.00     Sequence
         IAd   17  EALTARLAAAHASAA  ARLAAAHAS        0.4595        346.6         WB     1.00     Sequence
         IAd   19  LTARLAAAHASAAPV  ARLAAAHAS        0.4400        428.0         WB     2.00     Sequence
         IAd   20  TARLAAAHASAAPVI  ARLAAAHAS        0.4359        447.5         WB     2.00     Sequence
         IAd   18  ALTARLAAAHASAAP  ARLAAAHAS        0.4343        455.1         WB     2.00     Sequence
         IAd    6  PEGLAAASAAVEALT  AASAAVEAL        0.4246        505.8                2.00     Sequence
         IAd   28  ASAAPVITAVVPPAA  ASAAPVITA        0.4104        589.5                2.00     Sequence
         IAd   42  ADPVSLQTAAGFSAQ  LQTAAGFSA        0.4083        603.1                2.00     Sequence
         IAd   24  AAAHASAAPVITAVV  ASAAPVITA        0.4041        631.2                2.00     Sequence
         IAd   27  HASAAPVITAVVPPA  ASAAPVITA        0.3982        672.9                4.00     Sequence
         IAd    5  VPEGLAAASAAVEAL  AAASAAVEA        0.3981        673.2                4.00     Sequence
         IAd   21  ARLAAAHASAAPVIT  ARLAAAHAS        0.3972        680.1                4.00     Sequence
         IAd   25  AAHASAAPVITAVVP  ASAAPVITA        0.3968        683.2                4.00     Sequence
         IAd   41  AADPVSLQTAAGFSA  LQTAAGFSA        0.3891        742.1                4.00     Sequence
         IAd   26  AHASAAPVITAVVPP  ASAAPVITA        0.3824        798.3                4.00     Sequence
         IAd   22  RLAAAHASAAPVITA  ASAAPVITA        0.3795        823.6                4.00     Sequence
         IAd   23  LAAAHASAAPVITAV  ASAAPVITA        0.3752        863.2                4.00     Sequence
         IAd   53  FSAQGVEHAVVTAEG  FSAQGVEHA        0.3394       1271.0                8.00     Sequence
         IAd   56  QGVEHAVVTAEGVEE  HAVVTAEGV        0.3248       1488.2                8.00     Sequence
         IAd   29  SAAPVITAVVPPAAD  VITAVVPPA        0.3202       1564.6                8.00     Sequence
         IAd   57  GVEHAVVTAEGVEEL  GVEHAVVTA        0.3183       1597.3                8.00     Sequence
         IAd   54  SAQGVEHAVVTAEGV  HAVVTAEGV        0.3123       1704.9                8.00     Sequence
         IAd    4  VVPEGLAAASAAVEA  AAASAAVEA        0.2990       1967.9               16.00     Sequence
         IAd   43  DPVSLQTAAGFSAQG  LQTAAGFSA        0.2940       2077.9               16.00     Sequence
         IAd   55  AQGVEHAVVTAEGVE  HAVVTAEGV        0.2905       2156.6               16.00     Sequence
         IAd   52  GFSAQGVEHAVVTAE  FSAQGVEHA        0.2904       2158.7               16.00     Sequence
         IAd   44  PVSLQTAAGFSAQGV  LQTAAGFSA        0.2883       2210.1               16.00     Sequence
         IAd   58  VEHAVVTAEGVEELG  HAVVTAEGV        0.2855       2277.9               16.00     Sequence
         IAd   45  VSLQTAAGFSAQGVE  LQTAAGFSA        0.2757       2530.9               16.00     Sequence
         IAd   30  AAPVITAVVPPAADP  VITAVVPPA        0.2674       2771.2               16.00     Sequence
         IAd   47  LQTAAGFSAQGVEHA  LQTAAGFSA        0.2628       2912.1               16.00     Sequence
         IAd   80  ESGASYLAGDAAAAA  YLAGDAAAA        0.2515       3289.8               16.00     Sequence
         IAd   85  YLAGDAAAAATYGVV  AAAATYGVV        0.2504       3329.4               16.00     Sequence
         IAd   81  SGASYLAGDAAAAAT  ASYLAGDAA        0.2455       3512.2               16.00     Sequence
         IAd   51  AGFSAQGVEHAVVTA  FSAQGVEHA        0.2413       3675.6               32.00     Sequence
         IAd   82  GASYLAGDAAAAATY  ASYLAGDAA        0.2378       3815.0               32.00     Sequence
         IAd   87  AGDAAAAATYGVVGG  AAAATYGVV        0.2359       3895.6               32.00     Sequence
         IAd   86  LAGDAAAAATYGVVG  AAAAATYGV        0.2340       3977.7               32.00     Sequence
         IAd   79  GESGASYLAGDAAAA  YLAGDAAAA        0.2335       3999.3               32.00     Sequence
         IAd   50  AAGFSAQGVEHAVVT  FSAQGVEHA        0.2329       4022.4               32.00     Sequence
         IAd   48  QTAAGFSAQGVEHAV  FSAQGVEHA        0.2309       4111.6               32.00     Sequence
         IAd   59  EHAVVTAEGVEELGR  HAVVTAEGV        0.2291       4194.1               32.00     Sequence
         IAd   49  TAAGFSAQGVEHAVV  FSAQGVEHA        0.2273       4274.8               32.00     Sequence
         IAd   39  PPAADPVSLQTAAGF  ADPVSLQTA        0.2263       4321.2               32.00     Sequence
         IAd   84  SYLAGDAAAAATYGV  YLAGDAAAA        0.2259       4339.4               32.00     Sequence
         IAd   46  SLQTAAGFSAQGVEH  LQTAAGFSA        0.2240       4429.7               32.00     Sequence
         IAd   38  VPPAADPVSLQTAAG  ADPVSLQTA        0.2206       4598.0               32.00     Sequence
         IAd   37  VVPPAADPVSLQTAA  ADPVSLQTA        0.2196       4648.2               32.00     Sequence
         IAd   40  PAADPVSLQTAAGFS  ADPVSLQTA        0.2194       4653.9               32.00     Sequence
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         IAd   33  VITAVVPPAADPVSL  VITAVVPPA        0.2090       5209.6                   32.00     Sequence
         IAd   60  HAVVTAEGVEELGRA  HAVVTAEGV        0.2086       5234.1                   32.00     Sequence
         IAd   31  APVITAVVPPAADPV  VITAVVPPA        0.2080       5267.5                   32.00     Sequence
         IAd   36  AVVPPAADPVSLQTA  PPAADPVSL        0.2079       5273.2                   32.00     Sequence
         IAd   83  ASYLAGDAAAAATYG  YLAGDAAAA        0.2054       5418.6                   32.00     Sequence
         IAd   32  PVITAVVPPAADPVS  VITAVVPPA        0.2016       5643.1                   32.00     Sequence
         IAd   78  VGESGASYLAGDAAA  ASYLAGDAA        0.1960       5995.7                   32.00     Sequence
         IAd   77  GVGESGASYLAGDAA  GESGASYLA        0.1787       7231.5                   50.00     Sequence
         IAd    3  RVVPEGLAAASAAVE  PEGLAAASA        0.1730       7688.7                   50.00     Sequence
         IAd    0  MTLRVVPEGLAAASA  VPEGLAAAS        0.1573       9114.3                   50.00     Sequence
         IAd    2  LRVVPEGLAAASAAV  PEGLAAASA        0.1566       9185.3                   50.00     Sequence
         IAd    1  TLRVVPEGLAAASAA  PEGLAAASA        0.1548       9368.2                   50.00     Sequence
         IAd   76  VGVGESGASYLAGDA  GESGASYLA        0.1429      10655.7                   50.00     Sequence
         IAd   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1375      11297.5                   50.00     Sequence
         IAd   62  VVTAEGVEELGRAGV  EGVEELGRA        0.1048      16091.2                   50.00     Sequence
         IAd   73  RAGVGVGESGASYLA  GESGASYLA        0.1046      16117.3                   50.00     Sequence
         IAd   67  GVEELGRAGVGVGES  RAGVGVGES        0.1025      16487.6                   50.00     Sequence
         IAd   66  EGVEELGRAGVGVGE  EGVEELGRA        0.1014      16685.3                   50.00     Sequence
         IAd   35  TAVVPPAADPVSLQT  PPAADPVSL        0.0986      17198.9                   50.00     Sequence
         IAd   61  AVVTAEGVEELGRAG  EGVEELGRA        0.0984      17238.2                   50.00     Sequence
         IAd   75  GVGVGESGASYLAGD  GESGASYLA        0.0950      17885.2                   50.00     Sequence
         IAd   68  VEELGRAGVGVGESG  RAGVGVGES        0.0932      18243.0                   50.00     Sequence
         IAd   74  AGVGVGESGASYLAG  GESGASYLA        0.0922      18439.7                   50.00     Sequence
         IAd   63  VTAEGVEELGRAGVG  EGVEELGRA        0.0878      19335.0                   50.00     Sequence
         IAd   69  EELGRAGVGVGESGA  RAGVGVGES        0.0859      19739.6                   50.00     Sequence
         IAd   65  AEGVEELGRAGVGVG  EGVEELGRA        0.0812      20757.7                   50.00     Sequence
         IAd   64  TAEGVEELGRAGVGV  EGVEELGRA        0.0770      21726.0                   50.00     Sequence
         IAd   70  ELGRAGVGVGESGAS  RAGVGVGES        0.0717      23017.8                   50.00     Sequence
         IAd   71  LGRAGVGVGESGASY  RAGVGVGES        0.0703      23360.2                   50.00     Sequence
         IAd   72  GRAGVGVGESGASYL  RAGVGVGES        0.0693      23632.3                   50.00     Sequence
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Allele: IAd. Number of high binders 0. Number of weak binders 14. Number of peptides 88

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAs   25  AAHASAAPVITAVVP  APVITAVVP        0.2974       2001.3                    4.00     Sequence
         IAs   31  APVITAVVPPAADPV  APVITAVVP        0.2778       2474.2                    4.00     Sequence
         IAs   27  HASAAPVITAVVPPA  APVITAVVP        0.2698       2698.1                    4.00     Sequence
         IAs   29  SAAPVITAVVPPAAD  VITAVVPPA        0.2683       2743.5                    4.00     Sequence
         IAs   30  AAPVITAVVPPAADP  VITAVVPPA        0.2636       2887.4                    8.00     Sequence
         IAs   28  ASAAPVITAVVPPAA  VITAVVPPA        0.2602       2994.5                    8.00     Sequence
         IAs   20  TARLAAAHASAAPVI  AHASAAPVI        0.2553       3157.9                    8.00     Sequence
         IAs   32  PVITAVVPPAADPVS  VITAVVPPA        0.2464       3476.4                    8.00     Sequence
         IAs   21  ARLAAAHASAAPVIT  AHASAAPVI        0.2462       3483.1                    8.00     Sequence
         IAs   22  RLAAAHASAAPVITA  AHASAAPVI        0.2348       3941.7                    8.00     Sequence
         IAs   24  AAAHASAAPVITAVV  AHASAAPVI        0.2336       3992.3                    8.00     Sequence
         IAs   23  LAAAHASAAPVITAV  AHASAAPVI        0.2313       4093.0                    8.00     Sequence
         IAs   33  VITAVVPPAADPVSL  VITAVVPPA        0.2291       4193.0                    8.00     Sequence
         IAs   26  AHASAAPVITAVVPP  APVITAVVP        0.2210       4577.9                    8.00     Sequence
         IAs   19  LTARLAAAHASAAPV  AAHASAAPV        0.1891       6462.0                   16.00     Sequence
         IAs   50  AAGFSAQGVEHAVVT  AGFSAQGVE        0.1654       8347.3                   16.00     Sequence
         IAs   45  VSLQTAAGFSAQGVE  AGFSAQGVE        0.1567       9177.6                   32.00     Sequence
         IAs   55  AQGVEHAVVTAEGVE  AVVTAEGVE        0.1542       9426.4                   32.00     Sequence
         IAs   49  TAAGFSAQGVEHAVV  AGFSAQGVE        0.1469      10205.2                   32.00     Sequence
         IAs   46  SLQTAAGFSAQGVEH  AGFSAQGVE        0.1458      10324.6                   32.00     Sequence
         IAs   47  LQTAAGFSAQGVEHA  AGFSAQGVE        0.1396      11035.1                   32.00     Sequence
         IAs   51  AGFSAQGVEHAVVTA  AGFSAQGVE        0.1389      11124.2                   32.00     Sequence
         IAs   56  QGVEHAVVTAEGVEE  AVVTAEGVE        0.1375      11290.3                   32.00     Sequence
         IAs   48  QTAAGFSAQGVEHAV  AGFSAQGVE        0.1367      11388.0                   32.00     Sequence
         IAs   57  GVEHAVVTAEGVEEL  AVVTAEGVE        0.1312      12097.4                   32.00     Sequence
         IAs   58  VEHAVVTAEGVEELG  AVVTAEGVE        0.1304      12199.0                   32.00     Sequence
         IAs   73  RAGVGVGESGASYLA  RAGVGVGES        0.1180      13952.8                   32.00     Sequence
         IAs   72  GRAGVGVGESGASYL  RAGVGVGES        0.1116      14949.3                   32.00     Sequence
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          IAs   34  ITAVVPPAADPVSLQ  ITAVVPPAA        0.1104      15148.0                 50.00     Sequence
          IAs   53  FSAQGVEHAVVTAEG  QGVEHAVVT        0.1089      15388.7                 50.00     Sequence
          IAs   54  SAQGVEHAVVTAEGV  QGVEHAVVT        0.1088      15402.3                 50.00     Sequence
          IAs    5  VPEGLAAASAAVEAL  EGLAAASAA        0.1057      15929.8                 50.00     Sequence
          IAs    6  PEGLAAASAAVEALT  EGLAAASAA        0.1048      16092.1                 50.00     Sequence
          IAs    9  LAAASAAVEALTARL  AAVEALTAR        0.1047      16102.9                 50.00     Sequence
          IAs   69  EELGRAGVGVGESGA  AGVGVGESG        0.1047      16113.8                 50.00     Sequence
          IAs   52  GFSAQGVEHAVVTAE  QGVEHAVVT        0.1030      16397.4                 50.00     Sequence
          IAs   35  TAVVPPAADPVSLQT  TAVVPPAAD        0.1023      16521.9                 50.00     Sequence
          IAs   70  ELGRAGVGVGESGAS  AGVGVGESG        0.1022      16547.3                 50.00     Sequence
          IAs   68  VEELGRAGVGVGESG  RAGVGVGES        0.1008      16803.1                 50.00     Sequence
          IAs    4  VVPEGLAAASAAVEA  EGLAAASAA        0.1007      16824.9                 50.00     Sequence
          IAs    8  GLAAASAAVEALTAR  AAVEALTAR        0.1006      16833.8                 50.00     Sequence
          IAs   60  HAVVTAEGVEELGRA  AVVTAEGVE        0.1006      16842.8                 50.00     Sequence
          IAs    3  RVVPEGLAAASAAVE  EGLAAASAA        0.1004      16871.8                 50.00     Sequence
          IAs   71  LGRAGVGVGESGASY  AGVGVGESG        0.1003      16899.5                 50.00     Sequence
          IAs   59  EHAVVTAEGVEELGR  AVVTAEGVE        0.0979      17334.4                 50.00     Sequence
          IAs   36  AVVPPAADPVSLQTA  AVVPPAADP        0.0958      17728.1                 50.00     Sequence
          IAs   10  AAASAAVEALTARLA  AASAAVEAL        0.0939      18106.3                 50.00     Sequence
          IAs   44  PVSLQTAAGFSAQGV  VSLQTAAGF        0.0931      18267.1                 50.00     Sequence
          IAs    7  EGLAAASAAVEALTA  EGLAAASAA        0.0925      18375.3                 50.00     Sequence
          IAs   18  ALTARLAAAHASAAP  AAAHASAAP        0.0923      18426.3                 50.00     Sequence
          IAs   61  AVVTAEGVEELGRAG  AVVTAEGVE        0.0909      18704.7                 50.00     Sequence
          IAs   11  AASAAVEALTARLAA  AASAAVEAL        0.0899      18898.8                 50.00     Sequence
          IAs   16  VEALTARLAAAHASA  ARLAAAHAS        0.0849      19953.7                 50.00     Sequence
          IAs    2  LRVVPEGLAAASAAV  EGLAAASAA        0.0822      20535.2                 50.00     Sequence
          IAs   15  AVEALTARLAAAHAS  ARLAAAHAS        0.0810      20822.7                 50.00     Sequence
          IAs   74  AGVGVGESGASYLAG  AGVGVGESG        0.0790      21271.7                 50.00     Sequence
          IAs   85  YLAGDAAAAATYGVV  AAAATYGVV        0.0790      21272.4                 50.00     Sequence
          IAs   86  LAGDAAAAATYGVVG  AAAATYGVV        0.0776      21592.2                 50.00     Sequence
          IAs   17  EALTARLAAAHASAA  ARLAAAHAS        0.0772      21691.0                 50.00     Sequence
          IAs   39  PPAADPVSLQTAAGF  VSLQTAAGF        0.0761      21952.1                 50.00     Sequence
          IAs   37  VVPPAADPVSLQTAA  VVPPAADPV        0.0747      22282.9                 50.00     Sequence
          IAs   42  ADPVSLQTAAGFSAQ  VSLQTAAGF        0.0746      22314.0                 50.00     Sequence
          IAs   63  VTAEGVEELGRAGVG  EELGRAGVG        0.0742      22398.7                 50.00     Sequence
          IAs   67  GVEELGRAGVGVGES  RAGVGVGES        0.0714      23101.6                 50.00     Sequence
          IAs    1  TLRVVPEGLAAASAA  EGLAAASAA        0.0711      23157.4                 50.00     Sequence
          IAs   40  PAADPVSLQTAAGFS  VSLQTAAGF        0.0703      23358.5                 50.00     Sequence
          IAs   41  AADPVSLQTAAGFSA  VSLQTAAGF        0.0694      23599.8                 50.00     Sequence
          IAs   14  AAVEALTARLAAAHA  VEALTARLA        0.0682      23897.9                 50.00     Sequence
          IAs    0  MTLRVVPEGLAAASA  MTLRVVPEG        0.0669      24234.0                 50.00     Sequence
          IAs   62  VVTAEGVEELGRAGV  EGVEELGRA        0.0639      25039.8                 50.00     Sequence
          IAs   12  ASAAVEALTARLAAA  VEALTARLA        0.0632      25236.7                 50.00     Sequence
          IAs   77  GVGESGASYLAGDAA  ASYLAGDAA        0.0625      25421.1                 50.00     Sequence
          IAs   75  GVGVGESGASYLAGD  GVGVGESGA        0.0612      25777.3                 50.00     Sequence
          IAs   78  VGESGASYLAGDAAA  ASYLAGDAA        0.0604      26018.0                 50.00     Sequence
          IAs   13  SAAVEALTARLAAAH  VEALTARLA        0.0604      26020.3                 50.00     Sequence
          IAs   87  AGDAAAAATYGVVGG  AAAATYGVV        0.0602      26071.3                 50.00     Sequence
          IAs   64  TAEGVEELGRAGVGV  EELGRAGVG        0.0587      26481.8                 50.00     Sequence
          IAs   81  SGASYLAGDAAAAAT  ASYLAGDAA        0.0570      26986.3                 50.00     Sequence
          IAs   65  AEGVEELGRAGVGVG  EGVEELGRA        0.0566      27092.5                 50.00     Sequence
          IAs   82  GASYLAGDAAAAATY  GDAAAAATY        0.0563      27195.3                 50.00     Sequence
          IAs   84  SYLAGDAAAAATYGV  GDAAAAATY        0.0558      27329.5                 50.00     Sequence
          IAs   80  ESGASYLAGDAAAAA  ASYLAGDAA        0.0538      27934.0                 50.00     Sequence
          IAs   38  VPPAADPVSLQTAAG  PPAADPVSL        0.0519      28506.7                 50.00     Sequence
          IAs   83  ASYLAGDAAAAATYG  GDAAAAATY        0.0518      28545.3                 50.00     Sequence
          IAs   76  VGVGESGASYLAGDA  VGVGESGAS        0.0513      28714.2                 50.00     Sequence
          IAs   79  GESGASYLAGDAAAA  ASYLAGDAA        0.0504      28986.4                 50.00     Sequence
          IAs   43  DPVSLQTAAGFSAQG  VSLQTAAGF        0.0441      31026.1                 50.00     Sequence
          IAs   66  EGVEELGRAGVGVGE  EGVEELGRA        0.0415      31898.8                 50.00     Sequence
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Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 88

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Explain the output. Go **back**.