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  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.9056        2.8       SB    0.01     Sequence
  DRB1_0101  108  IGWRRLEAQAVLSRL  WRRLEAQAV      0.9020        2.9       SB    0.05     Sequence
  DRB1_0101  106  PKIGWRRLEAQAVLS  WRRLEAQAV      0.9008        2.9       SB    0.05     Sequence
  DRB1_0101  109  GWRRLEAQAVLSRLL  WRRLEAQAV      0.8958        3.1       SB    0.10     Sequence
  DRB1_0101  105  RPKIGWRRLEAQAVL  WRRLEAQAV      0.8942        3.1       SB    0.10     Sequence
  DRB1_0101  110  WRRLEAQAVLSRLLN  WRRLEAQAV      0.8887        3.3       SB    0.30     Sequence
  DRB1_0101  116  QAVLSRLLNAPVSVS  LSRLLNAPV      0.8793        3.7       SB    0.80     Sequence
  DRB1_0101  104  NRPKIGWRRLEAQAV  WRRLEAQAV      0.8703        4.1       SB    1.00     Sequence
  DRB1_0101  117  AVLSRLLNAPVSVSA  LSRLLNAPV      0.8647        4.3       SB    2.00     Sequence
  DRB1_0101  115  AQAVLSRLLNAPVSV  LSRLLNAPV      0.8640        4.4       SB    2.00     Sequence
  DRB1_0101  118  VLSRLLNAPVSVSAT  LSRLLNAPV      0.8469        5.2       SB    4.00     Sequence
  DRB1_0101   83  VVVLITQHGYRVGNA  LITQHGYRV      0.8336        6.0       SB    4.00     Sequence
  DRB1_0101   80  LRHVVVLITQHGYRV  VVVLITQHG      0.8254        6.6       SB    4.00     Sequence
  DRB1_0101  114  EAQAVLSRLLNAPVS  LSRLLNAPV      0.8241        6.7       SB    4.00     Sequence
  DRB1_0101   81  RHVVVLITQHGYRVG  LITQHGYRV      0.8195        7.1       SB    8.00     Sequence
  DRB1_0101   82  HVVVLITQHGYRVGN  LITQHGYRV      0.8193        7.1       SB    8.00     Sequence
  DRB1_0101  119  LSRLLNAPVSVSATT  LSRLLNAPV      0.8175        7.2       SB    8.00     Sequence
  DRB1_0101  143  GEGLAAIATALVVSL  LAAIATALV      0.8079        8.0       SB    8.00     Sequence
  DRB1_0101   84  VVLITQHGYRVGNAV  LITQHGYRV      0.8044        8.3       SB    8.00     Sequence
  DRB1_0101  142  RGEGLAAIATALVVS  LAAIATALV      0.8023        8.5       SB    8.00     Sequence
  DRB1_0101   89  QHGYRVGNAVVQVIG  YRVGNAVVQ      0.7996        8.7       SB    8.00     Sequence
  DRB1_0101   88  TQHGYRVGNAVVQVI  YRVGNAVVQ      0.7917        9.5       SB    8.00     Sequence
  DRB1_0101   68  DPRWQGVSGADMLRH  WQGVSGADM      0.7901        9.7       SB    8.00     Sequence
  DRB1_0101  141  GRGEGLAAIATALVV  LAAIATALV      0.7887        9.8       SB    8.00     Sequence
  DRB1_0101  113  LEAQAVLSRLLNAPV  LSRLLNAPV      0.7831       10.4       SB    8.00     Sequence
  DRB1_0101   69  PRWQGVSGADMLRHV  WQGVSGADM      0.7793       10.9       SB   16.00     Sequence
  DRB1_0101  144  EGLAAIATALVVSLR  LAAIATALV      0.7755       11.3       SB   16.00     Sequence
  DRB1_0101   85  VLITQHGYRVGNAVV  LITQHGYRV      0.7685       12.2       SB   16.00     Sequence
  DRB1_0101  140  TGRGEGLAAIATALV  LAAIATALV      0.7665       12.5       SB   16.00     Sequence
  DRB1_0101   90  HGYRVGNAVVQVIGN  YRVGNAVVQ      0.7575       13.8       SB   16.00     Sequence
  DRB1_0101  120  SRLLNAPVSVSATTT  LNAPVSVSA      0.7559       14.0       SB   16.00     Sequence
  DRB1_0101   46  ALCDAVLSAAGLGDI  DAVLSAAGL      0.7547       14.2       SB   16.00     Sequence
  DRB1_0101   41  DVAVHALCDAVLSAA  VHALCDAVL      0.7515       14.7       SB   16.00     Sequence
  DRB1_0101   70  RWQGVSGADMLRHVV  WQGVSGADM      0.7515       14.7       SB   16.00     Sequence
  DRB1_0101   79  MLRHVVVLITQHGYR  VVVLITQHG      0.7433       16.1       SB   16.00     Sequence
  DRB1_0101   86  LITQHGYRVGNAVVQ  LITQHGYRV      0.7397       16.7       SB   16.00     Sequence
  DRB1_0101   95  GNAVVQVIGNRPKIG  VVQVIGNRP      0.7379       17.0       SB   16.00     Sequence
  DRB1_0101   42  VAVHALCDAVLSAAG  VHALCDAVL      0.7330       18.0       SB   16.00     Sequence
  DRB1_0101   67  DDPRWQGVSGADMLR  WQGVSGADM      0.7284       18.9       SB   16.00     Sequence
  DRB1_0101   87  ITQHGYRVGNAVVQV  YRVGNAVVQ      0.7269       19.2       SB   16.00     Sequence
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DRB1_0101  44  VHALCDAVLSAAGLG  DAVLSAAGL     0.7262    19.3    SB   16.00   Sequence
DRB1_0101  45  HALCDAVLSAAGLGD  DAVLSAAGL     0.7199    20.7    SB   16.00   Sequence
DRB1_0101  91  GYRVGNAVVQVIGNR  YRVGNAVVQ     0.7059    24.1    SB   32.00   Sequence
DRB1_0101  43  AVHALCDAVLSAAGL  VHALCDAVL     0.7050    24.3    SB   32.00   Sequence
DRB1_0101  47  LCDAVLSAAGLGDIG  DAVLSAAGL     0.6989    26.0    SB   32.00   Sequence
DRB1_0101  40  GDVAVHALCDAVLSA  VHALCDAVL     0.6948    27.2    SB   32.00   Sequence
DRB1_0101  94  VGNAVVQVIGNRPKI  VVQVIGNRP     0.6904    28.5    SB   32.00   Sequence
DRB1_0101  96  NAVVQVIGNRPKIGW  VVQVIGNRP     0.6862    29.8    SB   32.00   Sequence
DRB1_0101  78  DMLRHVVVLITQHGY  VVVLITQHG     0.6847    30.3    SB   32.00   Sequence
DRB1_0101 121  RLLNAPVSVSATTTD  LNAPVSVSA     0.6841    30.5    SB   32.00   Sequence
DRB1_0101  71  WQGVSGADMLRHVVV  WQGVSGADM     0.6716    34.9    SB   32.00   Sequence
DRB1_0101 111  RRLEAQAVLSRLLNA  AQAVLSRLL     0.6687    36.0    SB   32.00   Sequence
DRB1_0101 139  LTGRGEGLAAIATAL  GEGLAAIAT     0.6588    40.1    SB   32.00   Sequence
DRB1_0101  98  VVQVIGNRPKIGWRR  VIGNRPKIG     0.6568    41.0    SB   32.00   Sequence
DRB1_0101 112  RLEAQAVLSRLLNAP  AQAVLSRLL     0.6518    43.3    SB   32.00   Sequence
DRB1_0101  92  YRVGNAVVQVIGNRP  YRVGNAVVQ     0.6491    44.5    SB   32.00   Sequence
DRB1_0101  97  AVVQVIGNRPKIGWR  VVQVIGNRP     0.6472    45.5    SB   32.00   Sequence
DRB1_0101  74  VSGADMLRHVVVLIT  ADMLRHVVV     0.6430    47.6    SB   32.00   Sequence
DRB1_0101  66  VDDPRWQGVSGADML  WQGVSGADM     0.6406    48.9    SB   32.00   Sequence
DRB1_0101  77  ADMLRHVVVLITQHG  VVVLITQHG     0.6344    52.2    WB   32.00   Sequence
DRB1_0101  39  DGDVAVHALCDAVLS  VHALCDAVL     0.6304    54.6    WB   32.00   Sequence
DRB1_0101  73  GVSGADMLRHVVVLI  ADMLRHVVV     0.6215    60.1    WB   32.00   Sequence
DRB1_0101  48  CDAVLSAAGLGDIGE  DAVLSAAGL     0.6182    62.3    WB   32.00   Sequence
DRB1_0101  75  SGADMLRHVVVLITQ  ADMLRHVVV     0.6163    63.5    WB   32.00   Sequence
DRB1_0101  19  RPCWLVGLLFPSADG  WLVGLLFPS     0.6133    65.6    WB   32.00   Sequence
DRB1_0101  76  GADMLRHVVVLITQH  MLRHVVVLI     0.5999    75.9    WB   50.00   Sequence
DRB1_0101 137  LGLTGRGEGLAAIAT  TGRGEGLAA     0.5929    81.8    WB   50.00   Sequence
DRB1_0101  21  CWLVGLLFPSADGCA  VGLLFPSAD     0.5924    82.3    WB   50.00   Sequence
DRB1_0101  17  PGRPCWLVGLLFPSA  WLVGLLFPS     0.5882    86.1    WB   50.00   Sequence
DRB1_0101 122  LLNAPVSVSATTTDG  LNAPVSVSA     0.5870    87.2    WB   50.00   Sequence
DRB1_0101  18  GRPCWLVGLLFPSAD  WLVGLLFPS     0.5847    89.4    WB   50.00   Sequence
DRB1_0101 138  GLTGRGEGLAAIATA  GEGLAAIAT     0.5814    92.7    WB   50.00   Sequence
DRB1_0101  38  SDGDVAVHALCDAVL  VHALCDAVL     0.5765    97.8    WB   50.00   Sequence
DRB1_0101  20  PCWLVGLLFPSADGC  LVGLLFPSA     0.5765    97.8    WB   50.00   Sequence
DRB1_0101  93  RVGNAVVQVIGNRPK  VVQVIGNRP     0.5757    98.5    WB   50.00   Sequence
DRB1_0101  72  QGVSGADMLRHVVVL  ADMLRHVVV     0.5720   102.6    WB   50.00   Sequence
DRB1_0101 123  LNAPVSVSATTTDGL  PVSVSATTT     0.5650   110.7    WB   50.00   Sequence
DRB1_0101 136  GLGLTGRGEGLAAIA  GLTGRGEGL     0.5589   118.2    WB   50.00   Sequence
DRB1_0101 135  DGLGLTGRGEGLAAI  GLTGRGEGL     0.5579   119.5    WB   50.00   Sequence
DRB1_0101  22  WLVGLLFPSADGCAG  LVGLLFPSA     0.5551   123.2    WB   50.00   Sequence
DRB1_0101  23  LVGLLFPSADGCAGH  LLFPSADGC     0.5399   145.3    WB   50.00   Sequence
DRB1_0101  99  VQVIGNRPKIGWRRL  VIGNRPKIG     0.5397   145.5    WB   50.00   Sequence
DRB1_0101  49  DAVLSAAGLGDIGEV  DAVLSAAGL     0.5393   146.2    WB   50.00   Sequence
DRB1_0101  16  EPGRPCWLVGLLFPS  WLVGLLFPS     0.5390   146.6    WB   50.00   Sequence
DRB1_0101  12  VHPIEPGRPCWLVGL  IEPGRPCWL     0.5360   151.4    WB   50.00   Sequence
DRB1_0101  14  PIEPGRPCWLVGLLF  PCWLVGLLF     0.5127   194.9    WB   50.00   Sequence
DRB1_0101  13  HPIEPGRPCWLVGLL  IEPGRPCWL     0.5054   210.8    WB   50.00   Sequence
DRB1_0101  65  GVDDPRWQGVSGADM  WQGVSGADM     0.5011   220.9    WB   50.00   Sequence
DRB1_0101  15  IEPGRPCWLVGLLFP  PCWLVGLLF     0.4966   232.1    WB   50.00   Sequence
DRB1_0101  24  VGLLFPSADGCAGHS  FPSADGCAG     0.4746   294.3    WB   50.00   Sequence
DRB1_0101  11  DVHPIEPGRPCWLVG  IEPGRPCWL     0.4603   343.7    WB   50.00   Sequence
DRB1_0101 134  TDGLGLTGRGEGLAA  GLTGRGEGL     0.4596   346.1    WB   50.00   Sequence
DRB1_0101   1  NQLPRVGLGTDVHPI  PRVGLGTDV     0.4567   357.1    WB   50.00   Sequence
DRB1_0101  10  TDVHPIEPGRPCWLV  IEPGRPCWL     0.4419   419.1    WB   50.00   Sequence
DRB1_0101 100  QVIGNRPKIGWRRLE  VIGNRPKIG     0.4395   430.3    WB   50.00   Sequence
DRB1_0101  25  GLLFPSADGCAGHSD  FPSADGCAG     0.4369   442.8    WB   50.00   Sequence
DRB1_0101 124  NAPVSVSATTTDGLG  PVSVSATTT     0.4334   459.8    WB   50.00   Sequence
DRB1_0101 133  TTDGLGLTGRGEGLA  GLGLTGRGE     0.4329   462.3    WB   50.00   Sequence
DRB1_0101 128  SVSATTTDGLGLTGR  ATTTDGLGL     0.4306   473.8    WB   50.00   Sequence
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  DRB1_0101   2  QLPRVGLGTDVHPIE  GLGTDVHPI     0.4271     491.9     WB   50.00   Sequence
  DRB1_0101  37  HSDGDVAVHALCDAV  DGDVAVHAL     0.4198     532.3          50.00   Sequence
  DRB1_0101  50  AVLSAAGLGDIGEVF  VLSAAGLGD     0.4198     532.8          50.00   Sequence
  DRB1_0101   9  GTDVHPIEPGRPCWL  VHPIEPGRP     0.4154     558.4          50.00   Sequence
  DRB1_0101   3  LPRVGLGTDVHPIEP  GLGTDVHPI     0.4041     631.2          50.00   Sequence
  DRB1_0101   4  PRVGLGTDVHPIEPG  GLGTDVHPI     0.4009     653.4          50.00   Sequence
  DRB1_0101  36  GHSDGDVAVHALCDA  DGDVAVHAL     0.3991     666.1          50.00   Sequence
  DRB1_0101 126  PVSVSATTTDGLGLT  VSATTTDGL     0.3890     743.0          50.00   Sequence
  DRB1_0101 125  APVSVSATTTDGLGL  PVSVSATTT     0.3780     837.3          50.00   Sequence
  DRB1_0101   0  VNQLPRVGLGTDVHP  PRVGLGTDV     0.3722     891.2          50.00   Sequence
  DRB1_0101 101  VIGNRPKIGWRRLEA  VIGNRPKIG     0.3721     892.6          50.00   Sequence
  DRB1_0101  26  LLFPSADGCAGHSDG  FPSADGCAG     0.3692     920.4          50.00   Sequence
  DRB1_0101 132  TTTDGLGLTGRGEGL  GLGLTGRGE     0.3683     929.9          50.00   Sequence
  DRB1_0101   5  RVGLGTDVHPIEPGR  GLGTDVHPI     0.3627     987.8          50.00   Sequence
  DRB1_0101 129  VSATTTDGLGLTGRG  ATTTDGLGL     0.3626     988.6          50.00   Sequence
  DRB1_0101  35  AGHSDGDVAVHALCD  DGDVAVHAL     0.3612    1003.8          50.00   Sequence
  DRB1_0101 127  VSVSATTTDGLGLTG  VSATTTDGL     0.3598    1018.9          50.00   Sequence
  DRB1_0101  34  CAGHSDGDVAVHALC  DGDVAVHAL     0.3546    1078.4          50.00   Sequence
  DRB1_0101   6  VGLGTDVHPIEPGRP  GLGTDVHPI     0.3432    1219.3          50.00   Sequence
  DRB1_0101  51  VLSAAGLGDIGEVFG  VLSAAGLGD     0.3274    1447.6          50.00   Sequence
  DRB1_0101   7  GLGTDVHPIEPGRPC  VHPIEPGRP     0.3246    1491.5          50.00   Sequence
  DRB1_0101 130  SATTTDGLGLTGRGE  ATTTDGLGL     0.3246    1492.4          50.00   Sequence
  DRB1_0101 102  IGNRPKIGWRRLEAQ  NRPKIGWRR     0.3066    1813.4          50.00   Sequence
  DRB1_0101 131  ATTTDGLGLTGRGEG  GLGLTGRGE     0.3016    1913.2          50.00   Sequence
  DRB1_0101 103  GNRPKIGWRRLEAQA  KIGWRRLEA     0.3013    1919.7          50.00   Sequence
  DRB1_0101   8  LGTDVHPIEPGRPCW  VHPIEPGRP     0.2983    1983.0          50.00   Sequence
  DRB1_0101  52  LSAAGLGDIGEVFGV  GLGDIGEVF     0.2925    2112.1          50.00   Sequence
  DRB1_0101  33  GCAGHSDGDVAVHAL  DGDVAVHAL     0.2907    2152.4          50.00   Sequence
  DRB1_0101  27  LFPSADGCAGHSDGD  FPSADGCAG     0.2727    2614.5          50.00   Sequence
  DRB1_0101  53  SAAGLGDIGEVFGVD  GLGDIGEVF     0.2719    2639.0          50.00   Sequence
  DRB1_0101  61  GEVFGVDDPRWQGVS  FGVDDPRWQ     0.2550    3166.6          50.00   Sequence
  DRB1_0101  60  IGEVFGVDDPRWQGV  FGVDDPRWQ     0.2524    3256.4          50.00   Sequence
  DRB1_0101  54  AAGLGDIGEVFGVDD  GDIGEVFGV     0.2500    3344.0          50.00   Sequence
  DRB1_0101  55  AGLGDIGEVFGVDDP  GDIGEVFGV     0.2427    3620.3          50.00   Sequence
  DRB1_0101  56  GLGDIGEVFGVDDPR  DIGEVFGVD     0.2373    3837.0          50.00   Sequence
  DRB1_0101  28  FPSADGCAGHSDGDV  FPSADGCAG     0.2232    4468.1          50.00   Sequence
  DRB1_0101  62  EVFGVDDPRWQGVSG  FGVDDPRWQ     0.2215    4551.1          50.00   Sequence
  DRB1_0101  32  DGCAGHSDGDVAVHA  AGHSDGDVA     0.2165    4805.0          50.00   Sequence
  DRB1_0101  57  LGDIGEVFGVDDPRW  GDIGEVFGV     0.2160    4829.3          50.00   Sequence
  DRB1_0101  59  DIGEVFGVDDPRWQG  FGVDDPRWQ     0.2142    4925.7          50.00   Sequence
  DRB1_0101  58  GDIGEVFGVDDPRWQ  FGVDDPRWQ     0.2091    5207.5          50.00   Sequence
  DRB1_0101  31  ADGCAGHSDGDVAVH  CAGHSDGDV     0.2059    5389.0          50.00   Sequence
  DRB1_0101  63  VFGVDDPRWQGVSGA  FGVDDPRWQ     0.2001    5738.7          50.00   Sequence
  DRB1_0101  30  SADGCAGHSDGDVAV  CAGHSDGDV     0.1969    5939.7          50.00   Sequence
  DRB1_0101  29  PSADGCAGHSDGDVA  ADGCAGHSD     0.1801    7126.5          50.00   Sequence
  DRB1_0101  64  FGVDDPRWQGVSGAD  FGVDDPRWQ     0.1689    8043.9          50.00   Sequence
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Allele: DRB1_0101. Number of high binders 59. Number of weak binders 41. Number of peptides 145

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     Allele  pos        peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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  DRB1_0301  98  VVQVIGNRPKIGWRR  VVQVIGNRP     0.5758      98.5     WB    4.00   Sequence
  DRB1_0301  97  AVVQVIGNRPKIGWR  VVQVIGNRP     0.5530     126.0     WB    4.00   Sequence
  DRB1_0301   5  RVGLGTDVHPIEPGR  RVGLGTDVH     0.5098     201.0     WB    8.00   Sequence
  DRB1_0301   3  LPRVGLGTDVHPIEP  RVGLGTDVH     0.5028     216.9     WB    8.00   Sequence
  DRB1_0301  96  NAVVQVIGNRPKIGW  VVQVIGNRP     0.5017     219.4     WB    8.00   Sequence
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DRB1_0301   4  PRVGLGTDVHPIEPG  RVGLGTDVH      0.5007     221.9     WB    8.00    Sequence
DRB1_0301  83  VVVLITQHGYRVGNA  VVVLITQHG      0.4816     272.9     WB    8.00    Sequence
DRB1_0301  82  HVVVLITQHGYRVGN  VVVLITQHG      0.4696     310.5     WB   16.00    Sequence
DRB1_0301   2  QLPRVGLGTDVHPIE  RVGLGTDVH      0.4660     322.9     WB   16.00    Sequence
DRB1_0301  43  AVHALCDAVLSAAGL  AVHALCDAV      0.4540     367.9     WB   16.00    Sequence
DRB1_0301  61  GEVFGVDDPRWQGVS  EVFGVDDPR      0.4480     392.4     WB   16.00    Sequence
DRB1_0301  60  IGEVFGVDDPRWQGV  EVFGVDDPR      0.4358     448.1     WB   16.00    Sequence
DRB1_0301  95  GNAVVQVIGNRPKIG  VVQVIGNRP      0.4317     468.4     WB   16.00    Sequence
DRB1_0301  72  QGVSGADMLRHVVVL  GVSGADMLR      0.4313     470.1     WB   16.00    Sequence
DRB1_0301  81  RHVVVLITQHGYRVG  VVVLITQHG      0.4286     483.9     WB   16.00    Sequence
DRB1_0301  42  VAVHALCDAVLSAAG  AVHALCDAV      0.4196     533.6          16.00    Sequence
DRB1_0301 116  QAVLSRLLNAPVSVS  AVLSRLLNA      0.4179     543.8          16.00    Sequence
DRB1_0301  71  WQGVSGADMLRHVVV  QGVSGADML      0.4166     551.6          16.00    Sequence
DRB1_0301 117  AVLSRLLNAPVSVSA  AVLSRLLNA      0.4150     560.6          16.00    Sequence
DRB1_0301  70  RWQGVSGADMLRHVV  QGVSGADML      0.4026     641.4          16.00    Sequence
DRB1_0301 112  RLEAQAVLSRLLNAP  RLEAQAVLS      0.4026     641.8          16.00    Sequence
DRB1_0301 113  LEAQAVLSRLLNAPV  LEAQAVLSR      0.3995     663.4          16.00    Sequence
DRB1_0301 115  AQAVLSRLLNAPVSV  AVLSRLLNA      0.3983     672.3          16.00    Sequence
DRB1_0301  84  VVLITQHGYRVGNAV  VLITQHGYR      0.3954     693.5          32.00    Sequence
DRB1_0301 114  EAQAVLSRLLNAPVS  AVLSRLLNA      0.3942     702.7          32.00    Sequence
DRB1_0301  73  GVSGADMLRHVVVLI  GVSGADMLR      0.3910     727.5          32.00    Sequence
DRB1_0301  80  LRHVVVLITQHGYRV  VVVLITQHG      0.3908     728.8          32.00    Sequence
DRB1_0301  41  DVAVHALCDAVLSAA  AVHALCDAV      0.3889     744.0          32.00    Sequence
DRB1_0301  59  DIGEVFGVDDPRWQG  EVFGVDDPR      0.3880     750.9          32.00    Sequence
DRB1_0301   6  VGLGTDVHPIEPGRP  LGTDVHPIE      0.3859     768.3          32.00    Sequence
DRB1_0301  45  HALCDAVLSAAGLGD  ALCDAVLSA      0.3769     847.0          32.00    Sequence
DRB1_0301  99  VQVIGNRPKIGWRRL  VQVIGNRPK      0.3697     915.6          32.00    Sequence
DRB1_0301 118  VLSRLLNAPVSVSAT  SRLLNAPVS      0.3687     926.1          32.00    Sequence
DRB1_0301  69  PRWQGVSGADMLRHV  QGVSGADML      0.3672     941.2          32.00    Sequence
DRB1_0301  62  EVFGVDDPRWQGVSG  EVFGVDDPR      0.3613    1002.9          32.00    Sequence
DRB1_0301  94  VGNAVVQVIGNRPKI  VVQVIGNRP      0.3580    1039.2          32.00    Sequence
DRB1_0301  44  VHALCDAVLSAAGLG  HALCDAVLS      0.3580    1039.3          32.00    Sequence
DRB1_0301  76  GADMLRHVVVLITQH  GADMLRHVV      0.3575    1044.4          32.00    Sequence
DRB1_0301 119  LSRLLNAPVSVSATT  LSRLLNAPV      0.3553    1070.7          32.00    Sequence
DRB1_0301  74  VSGADMLRHVVVLIT  GADMLRHVV      0.3503    1129.6          32.00    Sequence
DRB1_0301 111  RRLEAQAVLSRLLNA  RLEAQAVLS      0.3492    1143.5          32.00    Sequence
DRB1_0301  75  SGADMLRHVVVLITQ  GADMLRHVV      0.3429    1224.0          32.00    Sequence
DRB1_0301   7  GLGTDVHPIEPGRPC  LGTDVHPIE      0.3408    1252.1          32.00    Sequence
DRB1_0301  40  GDVAVHALCDAVLSA  AVHALCDAV      0.3402    1259.8          32.00    Sequence
DRB1_0301  58  GDIGEVFGVDDPRWQ  EVFGVDDPR      0.3397    1266.7          32.00    Sequence
DRB1_0301 129  VSATTTDGLGLTGRG  VSATTTDGL      0.3339    1349.3          32.00    Sequence
DRB1_0301 126  PVSVSATTTDGLGLT  VSATTTDGL      0.3308    1395.1          32.00    Sequence
DRB1_0301  85  VLITQHGYRVGNAVV  VLITQHGYR      0.3290    1422.2          32.00    Sequence
DRB1_0301 128  SVSATTTDGLGLTGR  VSATTTDGL      0.3183    1597.1          32.00    Sequence
DRB1_0301  77  ADMLRHVVVLITQHG  ADMLRHVVV      0.3181    1601.1          32.00    Sequence
DRB1_0301  24  VGLLFPSADGCAGHS  VGLLFPSAD      0.3172    1615.9          32.00    Sequence
DRB1_0301 127  VSVSATTTDGLGLTG  VSATTTDGL      0.3159    1638.8          32.00    Sequence
DRB1_0301  46  ALCDAVLSAAGLGDI  ALCDAVLSA      0.3104    1740.3          32.00    Sequence
DRB1_0301 110  WRRLEAQAVLSRLLN  RLEAQAVLS      0.3084    1777.7          32.00    Sequence
DRB1_0301  35  AGHSDGDVAVHALCD  AGHSDGDVA      0.3082    1781.2          32.00    Sequence
DRB1_0301 120  SRLLNAPVSVSATTT  SRLLNAPVS      0.3056    1832.4          32.00    Sequence
DRB1_0301  79  MLRHVVVLITQHGYR  LRHVVVLIT      0.3043    1858.4          32.00    Sequence
DRB1_0301   1  NQLPRVGLGTDVHPI  RVGLGTDVH      0.3040    1864.2          32.00    Sequence
DRB1_0301  26  LLFPSADGCAGHSDG  LLFPSADGC      0.2986    1975.4          50.00    Sequence
DRB1_0301  78  DMLRHVVVLITQHGY  LRHVVVLIT      0.2982    1985.3          50.00    Sequence
DRB1_0301  68  DPRWQGVSGADMLRH  GVSGADMLR      0.2936    2087.0          50.00    Sequence
DRB1_0301  23  LVGLLFPSADGCAGH  VGLLFPSAD      0.2932    2094.3          50.00    Sequence
DRB1_0301  34  CAGHSDGDVAVHALC  AGHSDGDVA      0.2932    2095.1          50.00    Sequence
DRB1_0301 100  QVIGNRPKIGWRRLE  QVIGNRPKI      0.2821    2363.5          50.00    Sequence
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DRB1_0301  105  RPKIGWRRLEAQAVL  RPKIGWRRL       0.2781       2466.9             50.00     Sequence
DRB1_0301  25  GLLFPSADGCAGHSD  LLFPSADGC       0.2755       2538.1             50.00     Sequence
DRB1_0301  33  GCAGHSDGDVAVHAL  AGHSDGDVA       0.2709       2667.6             50.00     Sequence
DRB1_0301  125  APVSVSATTTDGLGL  VSATTTDGL      0.2650       2844.3             50.00     Sequence
DRB1_0301  109  GWRRLEAQAVLSRLL  RRLEAQAVL      0.2569       3101.9             50.00     Sequence
DRB1_0301  57  LGDIGEVFGVDDPRW  EVFGVDDPR       0.2568       3107.8             50.00     Sequence
DRB1_0301   8  LGTDVHPIEPGRPCW  LGTDVHPIE       0.2516       3287.9             50.00     Sequence
DRB1_0301  104  NRPKIGWRRLEAQAV  RPKIGWRRL      0.2492       3374.3             50.00     Sequence
DRB1_0301  22  WLVGLLFPSADGCAG  VGLLFPSAD       0.2477       3428.8             50.00     Sequence
DRB1_0301  93  RVGNAVVQVIGNRPK  VVQVIGNRP       0.2447       3539.7             50.00     Sequence
DRB1_0301  36  GHSDGDVAVHALCDA  SDGDVAVHA       0.2425       3626.5             50.00     Sequence
DRB1_0301  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.2350       3931.9             50.00     Sequence
DRB1_0301  37  HSDGDVAVHALCDAV  SDGDVAVHA       0.2337       3990.5             50.00     Sequence
DRB1_0301  32  DGCAGHSDGDVAVHA  AGHSDGDVA       0.2304       4133.3             50.00     Sequence
DRB1_0301  108  IGWRRLEAQAVLSRL  RRLEAQAVL      0.2284       4225.5             50.00     Sequence
DRB1_0301  39  DGDVAVHALCDAVLS  AVHALCDAV       0.2278       4249.8             50.00     Sequence
DRB1_0301  38  SDGDVAVHALCDAVL  SDGDVAVHA       0.2276       4262.5             50.00     Sequence
DRB1_0301  90  HGYRVGNAVVQVIGN  HGYRVGNAV       0.2249       4384.7             50.00     Sequence
DRB1_0301   0  VNQLPRVGLGTDVHP  RVGLGTDVH       0.2227       4491.7             50.00     Sequence
DRB1_0301  56  GLGDIGEVFGVDDPR  GEVFGVDDP       0.2210       4576.2             50.00     Sequence
DRB1_0301  63  VFGVDDPRWQGVSGA  VFGVDDPRW       0.2193       4662.9             50.00     Sequence
DRB1_0301  47  LCDAVLSAAGLGDIG  CDAVLSAAG       0.2188       4684.3             50.00     Sequence
DRB1_0301  67  DDPRWQGVSGADMLR  GVSGADMLR       0.2186       4695.6             50.00     Sequence
DRB1_0301  92  YRVGNAVVQVIGNRP  VVQVIGNRP       0.2121       5036.0             50.00     Sequence
DRB1_0301  103  GNRPKIGWRRLEAQA  RPKIGWRRL      0.2092       5197.3             50.00     Sequence
DRB1_0301  107  KIGWRRLEAQAVLSR  IGWRRLEAQ      0.2070       5325.8             50.00     Sequence
DRB1_0301  21  CWLVGLLFPSADGCA  VGLLFPSAD       0.2060       5381.8             50.00     Sequence
DRB1_0301  89  QHGYRVGNAVVQVIG  HGYRVGNAV       0.2051       5436.6             50.00     Sequence
DRB1_0301  86  LITQHGYRVGNAVVQ  LITQHGYRV       0.1968       5948.5             50.00     Sequence
DRB1_0301  91  GYRVGNAVVQVIGNR  GYRVGNAVV       0.1963       5981.2             50.00     Sequence
DRB1_0301  124  NAPVSVSATTTDGLG  VSATTTDGL      0.1930       6196.8             50.00     Sequence
DRB1_0301  122  LLNAPVSVSATTTDG  LNAPVSVSA      0.1927       6213.7             50.00     Sequence
DRB1_0301  123  LNAPVSVSATTTDGL  LNAPVSVSA      0.1883       6518.2             50.00     Sequence
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DRB1_0301  88  TQHGYRVGNAVVQVI  HGYRVGNAV       0.1851       6747.4             50.00     Sequence
DRB1_0301  144  EGLAAIATALVVSLR  LAAIATALV      0.1847       6775.5             50.00     Sequence
DRB1_0301  102  IGNRPKIGWRRLEAQ  RPKIGWRRL      0.1808       7072.8             50.00     Sequence
DRB1_0301  31  ADGCAGHSDGDVAVH  AGHSDGDVA       0.1796       7160.3             50.00     Sequence
DRB1_0301  48  CDAVLSAAGLGDIGE  CDAVLSAAG       0.1702       7927.1             50.00     Sequence
DRB1_0301  106  PKIGWRRLEAQAVLS  IGWRRLEAQ      0.1680       8119.8             50.00     Sequence
DRB1_0301  142  RGEGLAAIATALVVS  GLAAIATAL      0.1667       8230.7             50.00     Sequence
DRB1_0301  53  SAAGLGDIGEVFGVD  GLGDIGEVF       0.1636       8514.0             50.00     Sequence
DRB1_0301  55  AGLGDIGEVFGVDDP  GLGDIGEVF       0.1625       8613.3             50.00     Sequence
DRB1_0301  52  LSAAGLGDIGEVFGV  GLGDIGEVF       0.1615       8715.8             50.00     Sequence
DRB1_0301  143  GEGLAAIATALVVSL  LAAIATALV      0.1608       8774.3             50.00     Sequence
DRB1_0301  27  LFPSADGCAGHSDGD  LFPSADGCA       0.1565       9198.9             50.00     Sequence
DRB1_0301  87  ITQHGYRVGNAVVQV  HGYRVGNAV       0.1537       9474.7             50.00     Sequence
DRB1_0301  51  VLSAAGLGDIGEVFG  LSAAGLGDI       0.1465      10243.7             50.00     Sequence
DRB1_0301  54  AAGLGDIGEVFGVDD  GLGDIGEVF       0.1393      11072.5             50.00     Sequence
DRB1_0301  141  GRGEGLAAIATALVV  RGEGLAAIA      0.1383      11193.5             50.00     Sequence
DRB1_0301  30  SADGCAGHSDGDVAV  AGHSDGDVA       0.1365      11414.9             50.00     Sequence
DRB1_0301  50  AVLSAAGLGDIGEVF  LSAAGLGDI       0.1350      11603.9             50.00     Sequence
DRB1_0301  134  TDGLGLTGRGEGLAA  TDGLGLTGR      0.1297      12291.2             50.00     Sequence
DRB1_0301  135  DGLGLTGRGEGLAAI  LTGRGEGLA      0.1265      12720.1             50.00     Sequence
DRB1_0301  136  GLGLTGRGEGLAAIA  LGLTGRGEG      0.1245      13003.2             50.00     Sequence
DRB1_0301  20  PCWLVGLLFPSADGC  LVGLLFPSA       0.1226      13275.8             50.00     Sequence
DRB1_0301  49  DAVLSAAGLGDIGEV  DAVLSAAGL       0.1212      13471.0             50.00     Sequence
DRB1_0301  139  LTGRGEGLAAIATAL  LTGRGEGLA      0.1194      13736.2             50.00     Sequence
DRB1_0301   9  GTDVHPIEPGRPCWL  DVHPIEPGR       0.1186      13862.2             50.00     Sequence
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  DRB1_0301  11  DVHPIEPGRPCWLVG  VHPIEPGRP      0.1180     13943.3           50.00    Sequence
  DRB1_0301  140  TGRGEGLAAIATALV  RGEGLAAIA      0.1167     14147.7           50.00    Sequence
  DRB1_0301  137  LGLTGRGEGLAAIAT  LGLTGRGEG      0.1148     14433.2           50.00    Sequence
  DRB1_0301  133  TTDGLGLTGRGEGLA  TDGLGLTGR      0.1112     15017.7           50.00    Sequence
  DRB1_0301  10  TDVHPIEPGRPCWLV  VHPIEPGRP      0.1077     15591.9           50.00    Sequence
  DRB1_0301  138  GLTGRGEGLAAIATA  GLTGRGEGL      0.1072     15668.4           50.00    Sequence
  DRB1_0301  64  FGVDDPRWQGVSGAD  FGVDDPRWQ      0.1055     15965.6           50.00    Sequence
  DRB1_0301  29  PSADGCAGHSDGDVA  CAGHSDGDV      0.1026     16484.3           50.00    Sequence
  DRB1_0301  12  VHPIEPGRPCWLVGL  VHPIEPGRP      0.1019     16608.6           50.00    Sequence
  DRB1_0301  66  VDDPRWQGVSGADML  QGVSGADML      0.1015     16671.8           50.00    Sequence
  DRB1_0301  132  TTTDGLGLTGRGEGL  TDGLGLTGR      0.0998     16975.2           50.00    Sequence
  DRB1_0301  28  FPSADGCAGHSDGDV  FPSADGCAG      0.0881     19270.9           50.00    Sequence
  DRB1_0301  131  ATTTDGLGLTGRGEG  TDGLGLTGR      0.0881     19275.7           50.00    Sequence
  DRB1_0301  19  RPCWLVGLLFPSADG  LVGLLFPSA      0.0872     19469.8           50.00    Sequence
  DRB1_0301  130  SATTTDGLGLTGRGE  SATTTDGLG      0.0831     20344.3           50.00    Sequence
  DRB1_0301  18  GRPCWLVGLLFPSAD  RPCWLVGLL      0.0785     21393.6           50.00    Sequence
  DRB1_0301  17  PGRPCWLVGLLFPSA  RPCWLVGLL      0.0713     23125.6           50.00    Sequence
  DRB1_0301  65  GVDDPRWQGVSGADM  VDDPRWQGV      0.0663     24390.5           50.00    Sequence
  DRB1_0301  16  EPGRPCWLVGLLFPS  RPCWLVGLL      0.0558     27349.3           50.00    Sequence
  DRB1_0301  15  IEPGRPCWLVGLLFP  RPCWLVGLL      0.0455     30553.4           50.00    Sequence
  DRB1_0301  14  PIEPGRPCWLVGLLF  RPCWLVGLL      0.0389     32837.7           50.00    Sequence
  DRB1_0301  13  HPIEPGRPCWLVGLL  HPIEPGRPC      0.0354     34094.4           50.00    Sequence
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Allele: DRB1_0301. Number of high binders 0. Number of weak binders 15. Number of peptides 145

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    Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_0401  118  VLSRLLNAPVSVSAT  RLLNAPVSV      0.6603        39.5       SB    4.00    Sequence
  DRB1_0401  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.6436        47.3       SB    4.00    Sequence
  DRB1_0401  119  LSRLLNAPVSVSATT  RLLNAPVSV      0.6390        49.7       SB    4.00    Sequence
  DRB1_0401  117  AVLSRLLNAPVSVSA  RLLNAPVSV      0.6283        55.8       WB    8.00    Sequence
  DRB1_0401  79  MLRHVVVLITQHGYR  RHVVVLITQ      0.6183        62.2       WB    8.00    Sequence
  DRB1_0401  78  DMLRHVVVLITQHGY  RHVVVLITQ      0.6151        64.4       WB    8.00    Sequence
  DRB1_0401  120  SRLLNAPVSVSATTT  RLLNAPVSV      0.6135        65.5       WB    8.00    Sequence
  DRB1_0401  80  LRHVVVLITQHGYRV  RHVVVLITQ      0.6095        68.4       WB    8.00    Sequence
  DRB1_0401  108  IGWRRLEAQAVLSRL  WRRLEAQAV      0.6076        69.8       WB    8.00    Sequence
  DRB1_0401  106  PKIGWRRLEAQAVLS  WRRLEAQAV      0.6029        73.5       WB    8.00    Sequence
  DRB1_0401  77  ADMLRHVVVLITQHG  RHVVVLITQ      0.5803        93.8       WB    8.00    Sequence
  DRB1_0401  116  QAVLSRLLNAPVSVS  RLLNAPVSV      0.5802        93.9       WB    8.00    Sequence
  DRB1_0401  109  GWRRLEAQAVLSRLL  WRRLEAQAV      0.5718       102.8       WB    8.00    Sequence
  DRB1_0401  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.5673       107.9       WB   16.00    Sequence
  DRB1_0401  89  QHGYRVGNAVVQVIG  YRVGNAVVQ      0.5643       111.5       WB   16.00    Sequence
  DRB1_0401  81  RHVVVLITQHGYRVG  RHVVVLITQ      0.5594       117.6       WB   16.00    Sequence
  DRB1_0401  88  TQHGYRVGNAVVQVI  QHGYRVGNA      0.5568       121.0       WB   16.00    Sequence
  DRB1_0401  110  WRRLEAQAVLSRLLN  WRRLEAQAV      0.5538       125.0       WB   16.00    Sequence
  DRB1_0401  105  RPKIGWRRLEAQAVL  WRRLEAQAV      0.5347       153.6       WB   16.00    Sequence
  DRB1_0401  115  AQAVLSRLLNAPVSV  VLSRLLNAP      0.5305       160.8       WB   16.00    Sequence
  DRB1_0401  76  GADMLRHVVVLITQH  RHVVVLITQ      0.5283       164.5       WB   16.00    Sequence
  DRB1_0401  87  ITQHGYRVGNAVVQV  QHGYRVGNA      0.5200       180.1       WB   16.00    Sequence
  DRB1_0401  90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.5063       209.0       WB   16.00    Sequence
  DRB1_0401  111  RRLEAQAVLSRLLNA  RLEAQAVLS      0.5045       212.9       WB   16.00    Sequence
  DRB1_0401  104  NRPKIGWRRLEAQAV  WRRLEAQAV      0.4990       226.0       WB   16.00    Sequence
  DRB1_0401  112  RLEAQAVLSRLLNAP  RLEAQAVLS      0.4914       245.5       WB   16.00    Sequence
  DRB1_0401  22  WLVGLLFPSADGCAG  WLVGLLFPS      0.4822       271.2       WB   32.00    Sequence
  DRB1_0401  86  LITQHGYRVGNAVVQ  QHGYRVGNA      0.4743       295.2       WB   32.00    Sequence
  DRB1_0401  75  SGADMLRHVVVLITQ  RHVVVLITQ      0.4635       331.8       WB   32.00    Sequence
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DRB1_0401  20  PCWLVGLLFPSADGC  WLVGLLFPS     0.4616   338.7    WB   32.00   Sequence
DRB1_0401  91  GYRVGNAVVQVIGNR  YRVGNAVVQ     0.4609   341.4    WB   32.00   Sequence
DRB1_0401  21  CWLVGLLFPSADGCA  WLVGLLFPS     0.4599   345.1    WB   32.00   Sequence
DRB1_0401  43  AVHALCDAVLSAAGL  HALCDAVLS     0.4564   358.2    WB   32.00   Sequence
DRB1_0401  44  VHALCDAVLSAAGLG  HALCDAVLS     0.4465   398.7    WB   32.00   Sequence
DRB1_0401  19  RPCWLVGLLFPSADG  WLVGLLFPS     0.4376   439.5    WB   32.00   Sequence
DRB1_0401 114  EAQAVLSRLLNAPVS  VLSRLLNAP     0.4373   440.5    WB   32.00   Sequence
DRB1_0401  42  VAVHALCDAVLSAAG  HALCDAVLS     0.4273   491.2    WB   32.00   Sequence
DRB1_0401  45  HALCDAVLSAAGLGD  HALCDAVLS     0.4114   583.4         32.00   Sequence
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DRB1_0401 142  RGEGLAAIATALVVS  GEGLAAIAT     0.4052   623.6         32.00   Sequence
DRB1_0401 143  GEGLAAIATALVVSL  GEGLAAIAT     0.4039   632.6         32.00   Sequence
DRB1_0401  92  YRVGNAVVQVIGNRP  YRVGNAVVQ     0.3969   682.4         32.00   Sequence
DRB1_0401 140  TGRGEGLAAIATALV  GEGLAAIAT     0.3937   706.3         32.00   Sequence
DRB1_0401  85  VLITQHGYRVGNAVV  QHGYRVGNA     0.3916   722.3         32.00   Sequence
DRB1_0401 113  LEAQAVLSRLLNAPV  LEAQAVLSR     0.3914   724.0         32.00   Sequence
DRB1_0401  83  VVVLITQHGYRVGNA  VVVLITQHG     0.3846   779.4         50.00   Sequence
DRB1_0401  41  DVAVHALCDAVLSAA  HALCDAVLS     0.3830   793.3         50.00   Sequence
DRB1_0401   2  QLPRVGLGTDVHPIE  RVGLGTDVH     0.3711   901.9         50.00   Sequence
DRB1_0401   4  PRVGLGTDVHPIEPG  RVGLGTDVH     0.3647   966.5         50.00   Sequence
DRB1_0401  69  PRWQGVSGADMLRHV  WQGVSGADM     0.3636   977.8         50.00   Sequence
DRB1_0401  68  DPRWQGVSGADMLRH  WQGVSGADM     0.3614   1001.8        50.00   Sequence
DRB1_0401  82  HVVVLITQHGYRVGN  VVVLITQHG     0.3577   1042.5        50.00   Sequence
DRB1_0401   3  LPRVGLGTDVHPIEP  RVGLGTDVH     0.3568   1053.0        50.00   Sequence
DRB1_0401   5  RVGLGTDVHPIEPGR  RVGLGTDVH     0.3563   1058.7        50.00   Sequence
DRB1_0401  18  GRPCWLVGLLFPSAD  WLVGLLFPS     0.3554   1069.2        50.00   Sequence
DRB1_0401 144  EGLAAIATALVVSLR  LAAIATALV     0.3547   1077.6        50.00   Sequence
DRB1_0401 139  LTGRGEGLAAIATAL  GEGLAAIAT     0.3523   1105.6        50.00   Sequence
DRB1_0401  74  VSGADMLRHVVVLIT  DMLRHVVVL     0.3507   1124.8        50.00   Sequence
DRB1_0401  61  GEVFGVDDPRWQGVS  EVFGVDDPR     0.3480   1158.0        50.00   Sequence
DRB1_0401  23  LVGLLFPSADGCAGH  GLLFPSADG     0.3453   1191.9        50.00   Sequence
DRB1_0401  62  EVFGVDDPRWQGVSG  EVFGVDDPR     0.3416   1240.5        50.00   Sequence
DRB1_0401  60  IGEVFGVDDPRWQGV  EVFGVDDPR     0.3341   1345.5        50.00   Sequence
DRB1_0401   1  NQLPRVGLGTDVHPI  RVGLGTDVH     0.3331   1360.1        50.00   Sequence
DRB1_0401  73  GVSGADMLRHVVVLI  DMLRHVVVL     0.3321   1376.1        50.00   Sequence
DRB1_0401  70  RWQGVSGADMLRHVV  WQGVSGADM     0.3318   1380.6        50.00   Sequence
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DRB1_0401  40  GDVAVHALCDAVLSA  HALCDAVLS     0.3159   1639.7        50.00   Sequence
DRB1_0401  17  PGRPCWLVGLLFPSA  WLVGLLFPS     0.3154   1648.6        50.00   Sequence
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DRB1_0401  59  DIGEVFGVDDPRWQG  EVFGVDDPR     0.3061   1822.9        50.00   Sequence
DRB1_0401   0  VNQLPRVGLGTDVHP  RVGLGTDVH     0.3053   1838.2        50.00   Sequence
DRB1_0401  84  VVLITQHGYRVGNAV  QHGYRVGNA     0.3033   1878.4        50.00   Sequence
DRB1_0401  95  GNAVVQVIGNRPKIG  NAVVQVIGN     0.2960   2031.9        50.00   Sequence
DRB1_0401  93  RVGNAVVQVIGNRPK  RVGNAVVQV     0.2932   2094.3        50.00   Sequence
DRB1_0401  24  VGLLFPSADGCAGHS  GLLFPSADG     0.2847   2297.2        50.00   Sequence
DRB1_0401  66  VDDPRWQGVSGADML  WQGVSGADM     0.2800   2417.3        50.00   Sequence
DRB1_0401 122  LLNAPVSVSATTTDG  LLNAPVSVS     0.2679   2755.5        50.00   Sequence
DRB1_0401  94  VGNAVVQVIGNRPKI  NAVVQVIGN     0.2674   2770.3        50.00   Sequence
DRB1_0401  58  GDIGEVFGVDDPRWQ  EVFGVDDPR     0.2610   2969.6        50.00   Sequence
DRB1_0401   6  VGLGTDVHPIEPGRP  VGLGTDVHP     0.2604   2988.8        50.00   Sequence
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DRB1_0401  72  QGVSGADMLRHVVVL  VSGADMLRH     0.2552   3159.6        50.00   Sequence
DRB1_0401 102  IGNRPKIGWRRLEAQ  KIGWRRLEA     0.2526   3250.5        50.00   Sequence
DRB1_0401  63  VFGVDDPRWQGVSGA  VFGVDDPRW     0.2500   3343.6        50.00   Sequence
DRB1_0401  25  GLLFPSADGCAGHSD  GLLFPSADG     0.2481   3414.4        50.00   Sequence
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DRB1_0401   97  AVVQVIGNRPKIGWR  VVQVIGNRP       0.2451       3525.0              50.00     Sequence
DRB1_0401   16  EPGRPCWLVGLLFPS  WLVGLLFPS       0.2390       3765.8              50.00     Sequence
DRB1_0401   46  ALCDAVLSAAGLGDI  ALCDAVLSA       0.2388       3775.9              50.00     Sequence
DRB1_0401  137  LGLTGRGEGLAAIAT  GRGEGLAAI       0.2383       3793.1              50.00     Sequence
DRB1_0401   65  GVDDPRWQGVSGADM  WQGVSGADM       0.2375       3826.9              50.00     Sequence
DRB1_0401  125  APVSVSATTTDGLGL  PVSVSATTT       0.2370       3846.8              50.00     Sequence
DRB1_0401   39  DGDVAVHALCDAVLS  HALCDAVLS       0.2365       3870.5              50.00     Sequence
DRB1_0401  124  NAPVSVSATTTDGLG  PVSVSATTT       0.2326       4037.4              50.00     Sequence
DRB1_0401  126  PVSVSATTTDGLGLT  PVSVSATTT       0.2283       4230.0              50.00     Sequence
DRB1_0401   98  VVQVIGNRPKIGWRR  VQVIGNRPK       0.2190       4676.5              50.00     Sequence
DRB1_0401   57  LGDIGEVFGVDDPRW  EVFGVDDPR       0.2063       5367.2              50.00     Sequence
DRB1_0401   99  VQVIGNRPKIGWRRL  VQVIGNRPK       0.1773       7342.6              50.00     Sequence
DRB1_0401   35  AGHSDGDVAVHALCD  GHSDGDVAV       0.1694       7997.0              50.00     Sequence
DRB1_0401  136  GLGLTGRGEGLAAIA  LTGRGEGLA       0.1661       8290.4              50.00     Sequence
DRB1_0401   34  CAGHSDGDVAVHALC  GHSDGDVAV       0.1649       8394.5              50.00     Sequence
DRB1_0401   36  GHSDGDVAVHALCDA  GHSDGDVAV       0.1639       8492.6              50.00     Sequence
DRB1_0401  127  VSVSATTTDGLGLTG  VSVSATTTD       0.1547       9380.8              50.00     Sequence
DRB1_0401  101  VIGNRPKIGWRRLEA  KIGWRRLEA       0.1544       9408.4              50.00     Sequence
DRB1_0401   33  GCAGHSDGDVAVHAL  GHSDGDVAV       0.1484      10035.3              50.00     Sequence
DRB1_0401   38  SDGDVAVHALCDAVL  VHALCDAVL       0.1466      10240.6              50.00     Sequence
DRB1_0401   51  VLSAAGLGDIGEVFG  LSAAGLGDI       0.1383      11191.1              50.00     Sequence
DRB1_0401   52  LSAAGLGDIGEVFGV  GLGDIGEVF       0.1341      11718.0              50.00     Sequence
DRB1_0401   49  DAVLSAAGLGDIGEV  DAVLSAAGL       0.1333      11813.8              50.00     Sequence
DRB1_0401   56  GLGDIGEVFGVDDPR  GEVFGVDDP       0.1322      11955.4              50.00     Sequence
DRB1_0401   26  LLFPSADGCAGHSDG  LLFPSADGC       0.1317      12019.6              50.00     Sequence
DRB1_0401  100  QVIGNRPKIGWRRLE  QVIGNRPKI       0.1290      12386.0              50.00     Sequence
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DRB1_0401   64  FGVDDPRWQGVSGAD  FGVDDPRWQ       0.1280      12517.6              50.00     Sequence
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DRB1_0401   48  CDAVLSAAGLGDIGE  DAVLSAAGL       0.1172      14065.9              50.00     Sequence
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DRB1_0401   27  LFPSADGCAGHSDGD  LFPSADGCA       0.1135      14647.5              50.00     Sequence
DRB1_0401   53  SAAGLGDIGEVFGVD  GLGDIGEVF       0.1116      14949.8              50.00     Sequence
DRB1_0401   55  AGLGDIGEVFGVDDP  GLGDIGEVF       0.1095      15291.4              50.00     Sequence
DRB1_0401   54  AAGLGDIGEVFGVDD  GLGDIGEVF       0.1063      15829.9              50.00     Sequence
DRB1_0401  134  TDGLGLTGRGEGLAA  LTGRGEGLA       0.1054      15986.6              50.00     Sequence
DRB1_0401  128  SVSATTTDGLGLTGR  VSATTTDGL       0.1016      16650.0              50.00     Sequence
DRB1_0401   15  IEPGRPCWLVGLLFP  RPCWLVGLL       0.1011      16737.9              50.00     Sequence
DRB1_0401  129  VSATTTDGLGLTGRG  VSATTTDGL       0.0974      17432.9              50.00     Sequence
DRB1_0401  130  SATTTDGLGLTGRGE  ATTTDGLGL       0.0946      17962.5              50.00     Sequence
DRB1_0401  131  ATTTDGLGLTGRGEG  ATTTDGLGL       0.0945      17977.1              50.00     Sequence
DRB1_0401   31  ADGCAGHSDGDVAVH  GHSDGDVAV       0.0895      18983.6              50.00     Sequence
DRB1_0401   30  SADGCAGHSDGDVAV  GHSDGDVAV       0.0889      19117.8              50.00     Sequence
DRB1_0401   29  PSADGCAGHSDGDVA  PSADGCAGH       0.0887      19141.8              50.00     Sequence
DRB1_0401  133  TTDGLGLTGRGEGLA  TDGLGLTGR       0.0885      19185.0              50.00     Sequence
DRB1_0401  132  TTTDGLGLTGRGEGL  TTTDGLGLT       0.0860      19722.7              50.00     Sequence
DRB1_0401   14  PIEPGRPCWLVGLLF  RPCWLVGLL       0.0784      21398.5              50.00     Sequence
DRB1_0401   28  FPSADGCAGHSDGDV  PSADGCAGH       0.0733      22633.3              50.00     Sequence
DRB1_0401    8  LGTDVHPIEPGRPCW  TDVHPIEPG       0.0625      25437.7              50.00     Sequence
DRB1_0401    9  GTDVHPIEPGRPCWL  VHPIEPGRP       0.0602      26053.0              50.00     Sequence
DRB1_0401   10  TDVHPIEPGRPCWLV  VHPIEPGRP       0.0564      27167.9              50.00     Sequence
DRB1_0401   13  HPIEPGRPCWLVGLL  RPCWLVGLL       0.0550      27565.9              50.00     Sequence
DRB1_0401   11  DVHPIEPGRPCWLVG  VHPIEPGRP       0.0511      28751.2              50.00     Sequence
DRB1_0401   12  VHPIEPGRPCWLVGL  VHPIEPGRP       0.0489      29456.8              50.00     Sequence
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Allele: DRB1_0401. Number of high binders 3. Number of weak binders 34. Number of peptides 145

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    Allele  pos        peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_0404  82  HVVVLITQHGYRVGN  HVVVLITQH      0.8062       8.1       SB    0.30    Sequence
  DRB1_0404  81  RHVVVLITQHGYRVG  HVVVLITQH      0.8058       8.2       SB    0.30    Sequence
  DRB1_0404  80  LRHVVVLITQHGYRV  HVVVLITQH      0.7965       9.0       SB    0.40    Sequence
  DRB1_0404  79  MLRHVVVLITQHGYR  HVVVLITQH      0.7806       10.7      SB    0.80    Sequence
  DRB1_0404  78  DMLRHVVVLITQHGY  HVVVLITQH      0.7474       15.4      SB    2.00    Sequence
  DRB1_0404  117  AVLSRLLNAPVSVSA  VLSRLLNAP     0.7251       19.6      SB    2.00    Sequence
  DRB1_0404  116  QAVLSRLLNAPVSVS  VLSRLLNAP     0.7244       19.7      SB    2.00    Sequence
  DRB1_0404  115  AQAVLSRLLNAPVSV  VLSRLLNAP     0.7130       22.3      SB    4.00    Sequence
  DRB1_0404  77  ADMLRHVVVLITQHG  HVVVLITQH      0.7115       22.7      SB    4.00    Sequence
  DRB1_0404  118  VLSRLLNAPVSVSAT  VLSRLLNAP     0.7047       24.4      SB    4.00    Sequence
  DRB1_0404  114  EAQAVLSRLLNAPVS  VLSRLLNAP     0.6642       37.8      SB    8.00    Sequence
  DRB1_0404  95  GNAVVQVIGNRPKIG  AVVQVIGNR      0.6546       42.0      SB    8.00    Sequence
  DRB1_0404  96  NAVVQVIGNRPKIGW  AVVQVIGNR      0.6524       43.0      SB    8.00    Sequence
  DRB1_0404  94  VGNAVVQVIGNRPKI  AVVQVIGNR      0.6325       53.3      WB    8.00    Sequence
  DRB1_0404  76  GADMLRHVVVLITQH  HVVVLITQH      0.6275       56.3      WB    8.00    Sequence
  DRB1_0404  119  LSRLLNAPVSVSATT  RLLNAPVSV     0.6144       64.8      WB    8.00    Sequence
  DRB1_0404  113  LEAQAVLSRLLNAPV  VLSRLLNAP     0.6055       71.4      WB    16.00    Sequence
  DRB1_0404  93  RVGNAVVQVIGNRPK  AVVQVIGNR      0.5841       90.0      WB    16.00    Sequence
  DRB1_0404  97  AVVQVIGNRPKIGWR  AVVQVIGNR      0.5829       91.2      WB    16.00    Sequence
  DRB1_0404  22  WLVGLLFPSADGCAG  LVGLLFPSA      0.5814       92.7      WB    16.00    Sequence
  DRB1_0404  21  CWLVGLLFPSADGCA  LVGLLFPSA      0.5809       93.2      WB    16.00    Sequence
  DRB1_0404  19  RPCWLVGLLFPSADG  LVGLLFPSA      0.5790       95.2      WB    16.00    Sequence
  DRB1_0404  20  PCWLVGLLFPSADGC  LVGLLFPSA      0.5777       96.4      WB    16.00    Sequence
  DRB1_0404  120  SRLLNAPVSVSATTT  RLLNAPVSV     0.5674       107.9     WB    16.00    Sequence
  DRB1_0404  43  AVHALCDAVLSAAGL  AVHALCDAV      0.5616       114.8     WB    16.00    Sequence
  DRB1_0404  42  VAVHALCDAVLSAAG  AVHALCDAV      0.5545       124.0     WB    16.00    Sequence
  DRB1_0404  18  GRPCWLVGLLFPSAD  LVGLLFPSA      0.5479       133.1     WB    16.00    Sequence
  DRB1_0404  41  DVAVHALCDAVLSAA  AVHALCDAV      0.5405       144.2     WB    16.00    Sequence
  DRB1_0404  23  LVGLLFPSADGCAGH  LVGLLFPSA      0.5362       151.1     WB    16.00    Sequence
  DRB1_0404  143  GEGLAAIATALVVSL  GLAAIATAL     0.5216       177.0     WB    32.00    Sequence
  DRB1_0404  40  GDVAVHALCDAVLSA  AVHALCDAV      0.5186       182.8     WB    32.00    Sequence
  DRB1_0404  144  EGLAAIATALVVSLR  GLAAIATAL     0.5159       188.3     WB    32.00    Sequence
  DRB1_0404  142  RGEGLAAIATALVVS  GLAAIATAL     0.5093       202.1     WB    32.00    Sequence
  DRB1_0404  83  VVVLITQHGYRVGNA  VVVLITQHG      0.5088       203.3     WB    32.00    Sequence
  DRB1_0404  112  RLEAQAVLSRLLNAP  AVLSRLLNA     0.5068       207.6     WB    32.00    Sequence
  DRB1_0404  75  SGADMLRHVVVLITQ  DMLRHVVVL      0.5045       213.1     WB    32.00    Sequence
  DRB1_0404  92  YRVGNAVVQVIGNRP  AVVQVIGNR      0.5023       218.1     WB    32.00    Sequence
  DRB1_0404  121  RLLNAPVSVSATTTD  RLLNAPVSV     0.5006       222.1     WB    32.00    Sequence
  DRB1_0404  141  GRGEGLAAIATALVV  GLAAIATAL     0.4749       293.3     WB    32.00    Sequence
  DRB1_0404  17  PGRPCWLVGLLFPSA  LVGLLFPSA      0.4718       303.3     WB    32.00    Sequence
  DRB1_0404  74  VSGADMLRHVVVLIT  DMLRHVVVL      0.4645       328.4     WB    32.00    Sequence
  DRB1_0404  44  VHALCDAVLSAAGLG  ALCDAVLSA      0.4534       370.1     WB    32.00    Sequence
  DRB1_0404  39  DGDVAVHALCDAVLS  AVHALCDAV      0.4519       376.3     WB    32.00    Sequence
  DRB1_0404  140  TGRGEGLAAIATALV  GLAAIATAL     0.4282       486.3     WB    32.00    Sequence
  DRB1_0404  45  HALCDAVLSAAGLGD  ALCDAVLSA      0.4245       506.3           32.00    Sequence
  DRB1_0404  98  VVQVIGNRPKIGWRR  QVIGNRPKI      0.4244       506.7           32.00    Sequence
  DRB1_0404  91  GYRVGNAVVQVIGNR  RVGNAVVQV      0.4046       627.7           50.00    Sequence
  DRB1_0404  111  RRLEAQAVLSRLLNA  AVLSRLLNA     0.4045       628.3           50.00    Sequence
  DRB1_0404  73  GVSGADMLRHVVVLI  DMLRHVVVL      0.4044       629.1           50.00    Sequence
  DRB1_0404  24  VGLLFPSADGCAGHS  VGLLFPSAD      0.3945       700.3           50.00    Sequence
  DRB1_0404  46  ALCDAVLSAAGLGDI  DAVLSAAGL      0.3902       733.4           50.00    Sequence
  DRB1_0404  90  HGYRVGNAVVQVIGN  RVGNAVVQV      0.3732       882.0           50.00    Sequence
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DRB1_0404  47  LCDAVLSAAGLGDIG  LCDAVLSAA      0.3630      984.3          50.00    Sequence
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DRB1_0404   2  QLPRVGLGTDVHPIE  RVGLGTDVH      0.3523      1105.8         50.00    Sequence
DRB1_0404  109  GWRRLEAQAVLSRLL  RLEAQAVLS      0.3522      1107.1         50.00    Sequence
DRB1_0404   1  NQLPRVGLGTDVHPI  RVGLGTDVH      0.3398      1265.4         50.00    Sequence
DRB1_0404  110  WRRLEAQAVLSRLLN  RRLEAQAVL      0.3387      1280.2         50.00    Sequence
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DRB1_0404  123  LNAPVSVSATTTDGL  PVSVSATTT      0.3260      1468.9         50.00    Sequence
DRB1_0404  122  LLNAPVSVSATTTDG  LLNAPVSVS      0.3251      1482.9         50.00    Sequence
DRB1_0404  139  LTGRGEGLAAIATAL  GLAAIATAL      0.3243      1496.4         50.00    Sequence
DRB1_0404   4  PRVGLGTDVHPIEPG  RVGLGTDVH      0.3179      1604.5         50.00    Sequence
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DRB1_0404  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.3127      1696.5         50.00    Sequence
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DRB1_0404  58  GDIGEVFGVDDPRWQ  EVFGVDDPR      0.2115      5074.2         50.00    Sequence
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  DRB1_0404   6  VGLGTDVHPIEPGRP  VGLGTDVHP       0.1355      11545.2             50.00     Sequence
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  DRB1_0404  129  VSATTTDGLGLTGRG  VSATTTDGL       0.0995      17046.8             50.00     Sequence
  DRB1_0404  102  IGNRPKIGWRRLEAQ  KIGWRRLEA       0.0993      17074.5             50.00     Sequence
  DRB1_0404   9  GTDVHPIEPGRPCWL  DVHPIEPGR       0.0944      18006.1             50.00     Sequence
  DRB1_0404  136  GLGLTGRGEGLAAIA  LGLTGRGEG       0.0837      20224.5             50.00     Sequence
  DRB1_0404  130  SATTTDGLGLTGRGE  TTDGLGLTG       0.0801      21014.4             50.00     Sequence
  DRB1_0404  32  DGCAGHSDGDVAVHA  DGCAGHSDG       0.0799      21070.6             50.00     Sequence
  DRB1_0404   8  LGTDVHPIEPGRPCW  VHPIEPGRP       0.0778      21538.8             50.00     Sequence
  DRB1_0404  31  ADGCAGHSDGDVAVH  DGCAGHSDG       0.0745      22325.3             50.00     Sequence
  DRB1_0404  131  ATTTDGLGLTGRGEG  TTTDGLGLT       0.0743      22389.7             50.00     Sequence
  DRB1_0404  132  TTTDGLGLTGRGEGL  TTDGLGLTG       0.0691      23676.3             50.00     Sequence
  DRB1_0404  36  GHSDGDVAVHALCDA  VAVHALCDA       0.0684      23853.7             50.00     Sequence
  DRB1_0404  29  PSADGCAGHSDGDVA  DGCAGHSDG       0.0682      23898.9             50.00     Sequence
  DRB1_0404  30  SADGCAGHSDGDVAV  DGCAGHSDG       0.0682      23917.0             50.00     Sequence
  DRB1_0404  135  DGLGLTGRGEGLAAI  LGLTGRGEG       0.0654      24641.7             50.00     Sequence
  DRB1_0404  133  TTDGLGLTGRGEGLA  TTDGLGLTG       0.0638      25067.4             50.00     Sequence
  DRB1_0404  134  TDGLGLTGRGEGLAA  LGLTGRGEG       0.0594      26293.7             50.00     Sequence
  DRB1_0404  34  CAGHSDGDVAVHALC  CAGHSDGDV       0.0553      27479.2             50.00     Sequence
  DRB1_0404  33  GCAGHSDGDVAVHAL  CAGHSDGDV       0.0547      27659.7             50.00     Sequence
  DRB1_0404  35  AGHSDGDVAVHALCD  GHSDGDVAV       0.0520      28484.9             50.00     Sequence
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Allele: DRB1_0404. Number of high binders 13. Number of weak binders 31. Number of peptides 145

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    Allele  pos        peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_0405  76  GADMLRHVVVLITQH  MLRHVVVLI       0.7197        20.8        SB     2.00     Sequence
  DRB1_0405  77  ADMLRHVVVLITQHG  MLRHVVVLI       0.7117        22.6        SB     2.00     Sequence
  DRB1_0405  78  DMLRHVVVLITQHGY  MLRHVVVLI       0.7078        23.6        SB     4.00     Sequence
  DRB1_0405  75  SGADMLRHVVVLITQ  MLRHVVVLI       0.7061        24.0        SB     4.00     Sequence
  DRB1_0405  79  MLRHVVVLITQHGYR  MLRHVVVLI       0.6802        31.8        SB     4.00     Sequence
  DRB1_0405  74  VSGADMLRHVVVLIT  MLRHVVVLI       0.6760        33.3        SB     4.00     Sequence
  DRB1_0405  117  AVLSRLLNAPVSVSA  LSRLLNAPV       0.6620        38.7        SB     8.00     Sequence
  DRB1_0405  106  PKIGWRRLEAQAVLS  GWRRLEAQA       0.6594        39.9        SB     8.00     Sequence
  DRB1_0405  116  QAVLSRLLNAPVSVS  LSRLLNAPV       0.6559        41.4        SB     8.00     Sequence
  DRB1_0405  107  KIGWRRLEAQAVLSR  GWRRLEAQA       0.6524        43.0        SB     8.00     Sequence
  DRB1_0405  118  VLSRLLNAPVSVSAT  LSRLLNAPV       0.6509        43.7        SB     8.00     Sequence
  DRB1_0405  105  RPKIGWRRLEAQAVL  GWRRLEAQA       0.6386        49.9        SB     8.00     Sequence
  DRB1_0405  108  IGWRRLEAQAVLSRL  GWRRLEAQA       0.6324        53.4        WB     8.00     Sequence
  DRB1_0405  115  AQAVLSRLLNAPVSV  LSRLLNAPV       0.6301        54.7        WB     8.00     Sequence
  DRB1_0405  119  LSRLLNAPVSVSATT  LSRLLNAPV       0.6266        56.9        WB    16.00     Sequence
  DRB1_0405  104  NRPKIGWRRLEAQAV  WRRLEAQAV       0.6100        68.0        WB    16.00     Sequence
  DRB1_0405  114  EAQAVLSRLLNAPVS  LSRLLNAPV       0.6006        75.3        WB    16.00     Sequence
  DRB1_0405  109  GWRRLEAQAVLSRLL  GWRRLEAQA       0.5920        82.6        WB    16.00     Sequence
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DRB1_0405  73  GVSGADMLRHVVVLI  MLRHVVVLI      0.5541      124.5      WB   32.00    Sequence
DRB1_0405  113  LEAQAVLSRLLNAPV  LSRLLNAPV      0.5523      127.0      WB   32.00    Sequence
DRB1_0405  80  LRHVVVLITQHGYRV  LRHVVVLIT      0.5512      128.5      WB   32.00    Sequence
DRB1_0405  120  SRLLNAPVSVSATTT  RLLNAPVSV      0.5472      134.2      WB   32.00    Sequence
DRB1_0405  68  DPRWQGVSGADMLRH  WQGVSGADM      0.5311      159.7      WB   32.00    Sequence
DRB1_0405  20  PCWLVGLLFPSADGC  LVGLLFPSA      0.5266      167.6      WB   32.00    Sequence
DRB1_0405  90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.5264      168.1      WB   32.00    Sequence
DRB1_0405  110  WRRLEAQAVLSRLLN  RLEAQAVLS      0.5212      177.8      WB   32.00    Sequence
DRB1_0405  21  CWLVGLLFPSADGCA  LVGLLFPSA      0.5187      182.7      WB   32.00    Sequence
DRB1_0405  69  PRWQGVSGADMLRHV  WQGVSGADM      0.5173      185.5      WB   32.00    Sequence
DRB1_0405  67  DDPRWQGVSGADMLR  WQGVSGADM      0.5152      189.7      WB   32.00    Sequence
DRB1_0405  19  RPCWLVGLLFPSADG  LVGLLFPSA      0.5148      190.6      WB   32.00    Sequence
DRB1_0405  22  WLVGLLFPSADGCAG  LVGLLFPSA      0.4955      234.8      WB   32.00    Sequence
DRB1_0405  95  GNAVVQVIGNRPKIG  VVQVIGNRP      0.4947      236.9      WB   32.00    Sequence
DRB1_0405  88  TQHGYRVGNAVVQVI  GYRVGNAVV      0.4946      237.0      WB   32.00    Sequence
DRB1_0405  89  QHGYRVGNAVVQVIG  GYRVGNAVV      0.4921      243.5      WB   32.00    Sequence
DRB1_0405  96  NAVVQVIGNRPKIGW  VVQVIGNRP      0.4892      251.3      WB   32.00    Sequence
DRB1_0405  91  GYRVGNAVVQVIGNR  GYRVGNAVV      0.4887      252.8      WB   32.00    Sequence
DRB1_0405  81  RHVVVLITQHGYRVG  VVVLITQHG      0.4867      258.1      WB   32.00    Sequence
DRB1_0405  93  RVGNAVVQVIGNRPK  VVQVIGNRP      0.4859      260.4      WB   32.00    Sequence
DRB1_0405  70  RWQGVSGADMLRHVV  WQGVSGADM      0.4832      268.1      WB   32.00    Sequence
DRB1_0405  66  VDDPRWQGVSGADML  WQGVSGADM      0.4827      269.5      WB   32.00    Sequence
DRB1_0405  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.4822      271.1      WB   32.00    Sequence
DRB1_0405  111  RRLEAQAVLSRLLNA  RLEAQAVLS      0.4820      271.6      WB   32.00    Sequence
DRB1_0405  87  ITQHGYRVGNAVVQV  GYRVGNAVV      0.4799      277.8      WB   32.00    Sequence
DRB1_0405  141  GRGEGLAAIATALVV  LAAIATALV      0.4771      286.6      WB   32.00    Sequence
DRB1_0405  94  VGNAVVQVIGNRPKI  VVQVIGNRP      0.4769      287.0      WB   32.00    Sequence
DRB1_0405  92  YRVGNAVVQVIGNRP  VVQVIGNRP      0.4744      294.9      WB   50.00    Sequence
DRB1_0405  140  TGRGEGLAAIATALV  LAAIATALV      0.4705      307.7      WB   50.00    Sequence
DRB1_0405  23  LVGLLFPSADGCAGH  LVGLLFPSA      0.4704      307.9      WB   50.00    Sequence
DRB1_0405  82  HVVVLITQHGYRVGN  HVVVLITQH      0.4639      330.3      WB   50.00    Sequence
DRB1_0405  65  GVDDPRWQGVSGADM  WQGVSGADM      0.4551      363.5      WB   50.00    Sequence
DRB1_0405  112  RLEAQAVLSRLLNAP  RLEAQAVLS      0.4491      388.0      WB   50.00    Sequence
DRB1_0405  18  GRPCWLVGLLFPSAD  WLVGLLFPS      0.4398      428.8      WB   50.00    Sequence
DRB1_0405  103  GNRPKIGWRRLEAQA  IGWRRLEAQ      0.4395      430.2      WB   50.00    Sequence
DRB1_0405  86  LITQHGYRVGNAVVQ  HGYRVGNAV      0.4382      436.2      WB   50.00    Sequence
DRB1_0405  142  RGEGLAAIATALVVS  EGLAAIATA      0.4369      442.3      WB   50.00    Sequence
DRB1_0405  72  QGVSGADMLRHVVVL  DMLRHVVVL      0.4340      456.9      WB   50.00    Sequence
DRB1_0405  71  WQGVSGADMLRHVVV  WQGVSGADM      0.4308      472.7      WB   50.00    Sequence
DRB1_0405  97  AVVQVIGNRPKIGWR  VVQVIGNRP      0.4192      536.0           50.00    Sequence
DRB1_0405   3  LPRVGLGTDVHPIEP  LPRVGLGTD      0.4169      549.3           50.00    Sequence
DRB1_0405   2  QLPRVGLGTDVHPIE  LPRVGLGTD      0.4157      556.8           50.00    Sequence
DRB1_0405  122  LLNAPVSVSATTTDG  LLNAPVSVS      0.4139      567.6           50.00    Sequence
DRB1_0405  85  VLITQHGYRVGNAVV  GYRVGNAVV      0.4119      580.2           50.00    Sequence
DRB1_0405  40  GDVAVHALCDAVLSA  AVHALCDAV      0.4096      594.7           50.00    Sequence
DRB1_0405   1  NQLPRVGLGTDVHPI  LPRVGLGTD      0.4077      607.3           50.00    Sequence
DRB1_0405  41  DVAVHALCDAVLSAA  AVHALCDAV      0.4053      623.1           50.00    Sequence
DRB1_0405  143  GEGLAAIATALVVSL  GLAAIATAL      0.4052      623.6           50.00    Sequence
DRB1_0405  39  DGDVAVHALCDAVLS  AVHALCDAV      0.4030      638.8           50.00    Sequence
DRB1_0405   0  VNQLPRVGLGTDVHP  LPRVGLGTD      0.4023      643.4           50.00    Sequence
DRB1_0405  83  VVVLITQHGYRVGNA  VVVLITQHG      0.3962      687.7           50.00    Sequence
DRB1_0405  42  VAVHALCDAVLSAAG  AVHALCDAV      0.3944      700.7           50.00    Sequence
DRB1_0405  139  LTGRGEGLAAIATAL  GEGLAAIAT      0.3864      764.6           50.00    Sequence
DRB1_0405  24  VGLLFPSADGCAGHS  VGLLFPSAD      0.3850      775.7           50.00    Sequence
DRB1_0405  144  EGLAAIATALVVSLR  GLAAIATAL      0.3826      796.3           50.00    Sequence
DRB1_0405  43  AVHALCDAVLSAAGL  AVHALCDAV      0.3771      845.7           50.00    Sequence
DRB1_0405  17  PGRPCWLVGLLFPSA  WLVGLLFPS      0.3670      943.3           50.00    Sequence
DRB1_0405  124  NAPVSVSATTTDGLG  VSVSATTTD      0.3623      991.8           50.00    Sequence
DRB1_0405  125  APVSVSATTTDGLGL  VSVSATTTD      0.3606      1010.0          50.00    Sequence
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DRB1_0405  126  PVSVSATTTDGLGLT  VSVSATTTD      0.3537      1088.7            50.00     Sequence
DRB1_0405   98  VVQVIGNRPKIGWRR  VVQVIGNRP      0.3521      1108.0            50.00     Sequence
DRB1_0405  138  GLTGRGEGLAAIATA  RGEGLAAIA      0.3494      1141.1            50.00     Sequence
DRB1_0405   84  VVLITQHGYRVGNAV  VVLITQHGY      0.3486      1151.2            50.00     Sequence
DRB1_0405  123  LNAPVSVSATTTDGL  VSVSATTTD      0.3438      1212.0            50.00     Sequence
DRB1_0405   64  FGVDDPRWQGVSGAD  PRWQGVSGA      0.3266      1459.1            50.00     Sequence
DRB1_0405   16  EPGRPCWLVGLLFPS  WLVGLLFPS      0.3265      1460.8            50.00     Sequence
DRB1_0405   38  SDGDVAVHALCDAVL  AVHALCDAV      0.3231      1515.8            50.00     Sequence
DRB1_0405   44  VHALCDAVLSAAGLG  HALCDAVLS      0.3120      1708.8            50.00     Sequence
DRB1_0405   45  HALCDAVLSAAGLGD  HALCDAVLS      0.3006      1934.5            50.00     Sequence
DRB1_0405  127  VSVSATTTDGLGLTG  VSVSATTTD      0.2991      1965.8            50.00     Sequence
DRB1_0405   50  AVLSAAGLGDIGEVF  LSAAGLGDI      0.2982      1984.6            50.00     Sequence
DRB1_0405   49  DAVLSAAGLGDIGEV  SAAGLGDIG      0.2944      2068.3            50.00     Sequence
DRB1_0405  137  LGLTGRGEGLAAIAT  GRGEGLAAI      0.2862      2260.4            50.00     Sequence
DRB1_0405   58  GDIGEVFGVDDPRWQ  GEVFGVDDP      0.2848      2294.2            50.00     Sequence
DRB1_0405   51  VLSAAGLGDIGEVFG  LSAAGLGDI      0.2831      2336.2            50.00     Sequence
DRB1_0405   48  CDAVLSAAGLGDIGE  VLSAAGLGD      0.2816      2376.2            50.00     Sequence
DRB1_0405    4  PRVGLGTDVHPIEPG  GLGTDVHPI      0.2773      2487.5            50.00     Sequence
DRB1_0405   25  GLLFPSADGCAGHSD  GLLFPSADG      0.2749      2554.4            50.00     Sequence
DRB1_0405   59  DIGEVFGVDDPRWQG  IGEVFGVDD      0.2726      2619.4            50.00     Sequence
DRB1_0405   47  LCDAVLSAAGLGDIG  DAVLSAAGL      0.2713      2656.8            50.00     Sequence
DRB1_0405   37  HSDGDVAVHALCDAV  AVHALCDAV      0.2668      2788.1            50.00     Sequence
DRB1_0405   63  VFGVDDPRWQGVSGA  FGVDDPRWQ      0.2647      2851.4            50.00     Sequence
DRB1_0405   56  GLGDIGEVFGVDDPR  GEVFGVDDP      0.2636      2884.8            50.00     Sequence
DRB1_0405   46  ALCDAVLSAAGLGDI  DAVLSAAGL      0.2633      2894.2            50.00     Sequence
DRB1_0405   57  LGDIGEVFGVDDPRW  IGEVFGVDD      0.2627      2915.6            50.00     Sequence
DRB1_0405   60  IGEVFGVDDPRWQGV  IGEVFGVDD      0.2613      2957.7            50.00     Sequence
DRB1_0405  102  IGNRPKIGWRRLEAQ  KIGWRRLEA      0.2596      3015.0            50.00     Sequence
DRB1_0405    5  RVGLGTDVHPIEPGR  GLGTDVHPI      0.2576      3078.8            50.00     Sequence
DRB1_0405  136  GLGLTGRGEGLAAIA  RGEGLAAIA      0.2573      3088.7            50.00     Sequence
DRB1_0405   61  GEVFGVDDPRWQGVS  FGVDDPRWQ      0.2559      3137.4            50.00     Sequence
DRB1_0405   52  LSAAGLGDIGEVFGV  SAAGLGDIG      0.2522      3264.4            50.00     Sequence
DRB1_0405   55  AGLGDIGEVFGVDDP  GLGDIGEVF      0.2503      3332.8            50.00     Sequence
DRB1_0405   99  VQVIGNRPKIGWRRL  QVIGNRPKI      0.2449      3533.7            50.00     Sequence
DRB1_0405   15  IEPGRPCWLVGLLFP  RPCWLVGLL      0.2390      3768.2            50.00     Sequence
DRB1_0405   62  EVFGVDDPRWQGVSG  FGVDDPRWQ      0.2283      4230.3            50.00     Sequence
DRB1_0405    6  VGLGTDVHPIEPGRP  GLGTDVHPI      0.2272      4277.0            50.00     Sequence
DRB1_0405   54  AAGLGDIGEVFGVDD  GLGDIGEVF      0.2225      4503.7            50.00     Sequence
DRB1_0405  132  TTTDGLGLTGRGEGL  GLGLTGRGE      0.2214      4556.9            50.00     Sequence
DRB1_0405  130  SATTTDGLGLTGRGE  GLGLTGRGE      0.2197      4639.9            50.00     Sequence
DRB1_0405  131  ATTTDGLGLTGRGEG  GLGLTGRGE      0.2156      4848.9            50.00     Sequence
DRB1_0405   53  SAAGLGDIGEVFGVD  GLGDIGEVF      0.2136      4956.7            50.00     Sequence
DRB1_0405   36  GHSDGDVAVHALCDA  DVAVHALCD      0.2124      5020.2            50.00     Sequence
DRB1_0405  135  DGLGLTGRGEGLAAI  GRGEGLAAI      0.2114      5077.8            50.00     Sequence
DRB1_0405  133  TTDGLGLTGRGEGLA  GLGLTGRGE      0.2068      5336.6            50.00     Sequence
DRB1_0405   35  AGHSDGDVAVHALCD  DVAVHALCD      0.2034      5537.0            50.00     Sequence
DRB1_0405   14  PIEPGRPCWLVGLLF  PCWLVGLLF      0.2011      5673.2            50.00     Sequence
DRB1_0405   33  GCAGHSDGDVAVHAL  CAGHSDGDV      0.1986      5828.4            50.00     Sequence
DRB1_0405  134  TDGLGLTGRGEGLAA  DGLGLTGRG      0.1913      6310.3            50.00     Sequence
DRB1_0405   34  CAGHSDGDVAVHALC  CAGHSDGDV      0.1903      6377.7            50.00     Sequence
DRB1_0405  100  QVIGNRPKIGWRRLE  QVIGNRPKI      0.1900      6402.0            50.00     Sequence
DRB1_0405   32  DGCAGHSDGDVAVHA  CAGHSDGDV      0.1899      6406.4            50.00     Sequence
DRB1_0405    7  GLGTDVHPIEPGRPC  GLGTDVHPI      0.1857      6701.7            50.00     Sequence
DRB1_0405   31  ADGCAGHSDGDVAVH  CAGHSDGDV      0.1782      7270.2            50.00     Sequence
DRB1_0405  128  SVSATTTDGLGLTGR  VSATTTDGL      0.1665      8251.0            50.00     Sequence
DRB1_0405  101  VIGNRPKIGWRRLEA  KIGWRRLEA      0.1639      8486.6            50.00     Sequence
DRB1_0405   13  HPIEPGRPCWLVGLL  RPCWLVGLL      0.1584      9008.7            50.00     Sequence
DRB1_0405  129  VSATTTDGLGLTGRG  VSATTTDGL      0.1486      10019.2           50.00     Sequence
DRB1_0405   30  SADGCAGHSDGDVAV  CAGHSDGDV      0.1481      10073.8           50.00     Sequence
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  DRB1_0405   8  LGTDVHPIEPGRPCW  GTDVHPIEP     0.1309    12133.4          50.00   Sequence
  DRB1_0405  29  PSADGCAGHSDGDVA  CAGHSDGDV     0.1226    13275.3          50.00   Sequence
  DRB1_0405   9  GTDVHPIEPGRPCWL  DVHPIEPGR     0.1163    14205.5          50.00   Sequence
  DRB1_0405  12  VHPIEPGRPCWLVGL  EPGRPCWLV     0.1125    14803.7          50.00   Sequence
  DRB1_0405  28  FPSADGCAGHSDGDV  CAGHSDGDV     0.1115    14960.8          50.00   Sequence
  DRB1_0405  11  DVHPIEPGRPCWLVG  EPGRPCWLV     0.1027    16458.0          50.00   Sequence
  DRB1_0405  26  LLFPSADGCAGHSDG  LLFPSADGC     0.1012    16725.1          50.00   Sequence
  DRB1_0405  10  TDVHPIEPGRPCWLV  EPGRPCWLV     0.0979    17334.2          50.00   Sequence
  DRB1_0405  27  LFPSADGCAGHSDGD  GCAGHSDGD     0.0855    19827.6          50.00   Sequence
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Allele: DRB1_0405. Number of high binders 12. Number of weak binders 45. Number of peptides 145

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   Allele  pos        peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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  DRB1_0701 109  GWRRLEAQAVLSRLL  AQAVLSRLL     0.8197      7.0     SB    4.00   Sequence
  DRB1_0701 110  WRRLEAQAVLSRLLN  AQAVLSRLL     0.7955      9.1     SB    4.00   Sequence
  DRB1_0701 111  RRLEAQAVLSRLLNA  AQAVLSRLL     0.7573     13.8     SB    8.00   Sequence
  DRB1_0701 113  LEAQAVLSRLLNAPV  AQAVLSRLL     0.7418     16.3     SB    8.00   Sequence
  DRB1_0701 141  GRGEGLAAIATALVV  GLAAIATAL     0.7365     17.3     SB    8.00   Sequence
  DRB1_0701 140  TGRGEGLAAIATALV  GLAAIATAL     0.7348     17.6     SB    8.00   Sequence
  DRB1_0701 112  RLEAQAVLSRLLNAP  AQAVLSRLL     0.7086     23.4     SB    8.00   Sequence
  DRB1_0701 114  EAQAVLSRLLNAPVS  AQAVLSRLL     0.7076     23.7     SB    8.00   Sequence
  DRB1_0701 139  LTGRGEGLAAIATAL  GLAAIATAL     0.7011     25.4     SB   16.00   Sequence
  DRB1_0701 142  RGEGLAAIATALVVS  GLAAIATAL     0.7011     25.4     SB   16.00   Sequence
  DRB1_0701  85  VLITQHGYRVGNAVV  GYRVGNAVV     0.6966     26.7     SB   16.00   Sequence
  DRB1_0701  80  LRHVVVLITQHGYRV  LITQHGYRV     0.6931     27.7     SB   16.00   Sequence
  DRB1_0701 143  GEGLAAIATALVVSL  GLAAIATAL     0.6782     32.5     SB   16.00   Sequence
  DRB1_0701 115  AQAVLSRLLNAPVSV  AQAVLSRLL     0.6747     33.8     SB   16.00   Sequence
  DRB1_0701  86  LITQHGYRVGNAVVQ  GYRVGNAVV     0.6631     38.3     SB   16.00   Sequence
  DRB1_0701 144  EGLAAIATALVVSLR  GLAAIATAL     0.6467     45.7     SB   16.00   Sequence
  DRB1_0701  81  RHVVVLITQHGYRVG  LITQHGYRV     0.6311     54.1     WB   16.00   Sequence
  DRB1_0701  74  VSGADMLRHVVVLIT  LRHVVVLIT     0.6139     65.2     WB   16.00   Sequence
  DRB1_0701  88  TQHGYRVGNAVVQVI  GYRVGNAVV     0.5984     77.1     WB   32.00   Sequence
  DRB1_0701 104  NRPKIGWRRLEAQAV  WRRLEAQAV     0.5976     77.8     WB   32.00   Sequence
  DRB1_0701 105  RPKIGWRRLEAQAVL  WRRLEAQAV     0.5937     81.2     WB   32.00   Sequence
  DRB1_0701  46  ALCDAVLSAAGLGDI  LSAAGLGDI     0.5934     81.4     WB   32.00   Sequence
  DRB1_0701 123  LNAPVSVSATTTDGL  VSATTTDGL     0.5913     83.3     WB   32.00   Sequence
  DRB1_0701  82  HVVVLITQHGYRVGN  LITQHGYRV     0.5869     87.3     WB   32.00   Sequence
  DRB1_0701  75  SGADMLRHVVVLITQ  LRHVVVLIT     0.5817     92.4     WB   32.00   Sequence
  DRB1_0701  65  GVDDPRWQGVSGADM  WQGVSGADM     0.5804     93.7     WB   32.00   Sequence
  DRB1_0701  87  ITQHGYRVGNAVVQV  GYRVGNAVV     0.5798     94.3     WB   32.00   Sequence
  DRB1_0701 120  SRLLNAPVSVSATTT  PVSVSATTT     0.5703    104.5     WB   32.00   Sequence
  DRB1_0701  66  VDDPRWQGVSGADML  WQGVSGADM     0.5621    114.2     WB   32.00   Sequence
  DRB1_0701 106  PKIGWRRLEAQAVLS  WRRLEAQAV     0.5610    115.6     WB   32.00   Sequence
  DRB1_0701  79  MLRHVVVLITQHGYR  VLITQHGYR     0.5607    115.9     WB   32.00   Sequence
  DRB1_0701  67  DDPRWQGVSGADMLR  WQGVSGADM     0.5559    122.2     WB   32.00   Sequence
  DRB1_0701  89  QHGYRVGNAVVQVIG  GYRVGNAVV     0.5506    129.3     WB   32.00   Sequence
  DRB1_0701  76  GADMLRHVVVLITQH  LRHVVVLIT     0.5462    135.6     WB   32.00   Sequence
  DRB1_0701 121  RLLNAPVSVSATTTD  PVSVSATTT     0.5452    137.2     WB   32.00   Sequence
  DRB1_0701 116  QAVLSRLLNAPVSVS  LLNAPVSVS     0.5441    138.7     WB   32.00   Sequence
  DRB1_0701  83  VVVLITQHGYRVGNA  LITQHGYRV     0.5419    142.0     WB   32.00   Sequence
  DRB1_0701 124  NAPVSVSATTTDGLG  VSATTTDGL     0.5395    145.9     WB   32.00   Sequence
  DRB1_0701  47  LCDAVLSAAGLGDIG  LSAAGLGDI     0.5376    148.8     WB   32.00   Sequence
  DRB1_0701  78  DMLRHVVVLITQHGY  LRHVVVLIT     0.5322    157.9     WB   32.00   Sequence
  DRB1_0701  84  VVLITQHGYRVGNAV  LITQHGYRV     0.5277    165.7     WB   32.00   Sequence
  DRB1_0701  38  SDGDVAVHALCDAVL  VHALCDAVL     0.5253    170.1     WB   32.00   Sequence
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DRB1_0701  125  APVSVSATTTDGLGL  VSATTTDGL      0.5227      174.9       WB   32.00    Sequence
DRB1_0701  117  AVLSRLLNAPVSVSA  LLNAPVSVS      0.5189      182.3       WB   32.00    Sequence
DRB1_0701  68  DPRWQGVSGADMLRH  WQGVSGADM      0.5137      192.7       WB   32.00    Sequence
DRB1_0701  77  ADMLRHVVVLITQHG  LRHVVVLIT      0.5130      194.2       WB   32.00    Sequence
DRB1_0701  73  GVSGADMLRHVVVLI  MLRHVVVLI      0.5040      214.1       WB   32.00    Sequence
DRB1_0701  71  WQGVSGADMLRHVVV  WQGVSGADM      0.5019      219.1       WB   32.00    Sequence
DRB1_0701  90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.5001      223.3       WB   32.00    Sequence
DRB1_0701  48  CDAVLSAAGLGDIGE  LSAAGLGDI      0.4880      254.6       WB   32.00    Sequence
DRB1_0701  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.4868      258.0       WB   32.00    Sequence
DRB1_0701  39  DGDVAVHALCDAVLS  VHALCDAVL      0.4804      276.3       WB   32.00    Sequence
DRB1_0701  118  VLSRLLNAPVSVSAT  LLNAPVSVS      0.4798      278.1       WB   32.00    Sequence
DRB1_0701  69  PRWQGVSGADMLRHV  WQGVSGADM      0.4798      278.3       WB   32.00    Sequence
DRB1_0701  126  PVSVSATTTDGLGLT  VSATTTDGL      0.4742      295.6       WB   32.00    Sequence
DRB1_0701  122  LLNAPVSVSATTTDG  PVSVSATTT      0.4735      297.9       WB   32.00    Sequence
DRB1_0701  49  DAVLSAAGLGDIGEV  LSAAGLGDI      0.4491      388.0       WB   50.00    Sequence
DRB1_0701  70  RWQGVSGADMLRHVV  WQGVSGADM      0.4484      390.7       WB   50.00    Sequence
DRB1_0701  108  IGWRRLEAQAVLSRL  WRRLEAQAV      0.4437      411.2       WB   50.00    Sequence
DRB1_0701  91  GYRVGNAVVQVIGNR  GYRVGNAVV      0.4379      438.0       WB   50.00    Sequence
DRB1_0701  44  VHALCDAVLSAAGLG  AVLSAAGLG      0.4373      440.8       WB   50.00    Sequence
DRB1_0701  119  LSRLLNAPVSVSATT  LLNAPVSVS      0.4352      450.9       WB   50.00    Sequence
DRB1_0701  40  GDVAVHALCDAVLSA  VHALCDAVL      0.4297      478.2       WB   50.00    Sequence
DRB1_0701  50  AVLSAAGLGDIGEVF  LSAAGLGDI      0.4236      511.2            50.00    Sequence
DRB1_0701  45  HALCDAVLSAAGLGD  AVLSAAGLG      0.4138      568.2            50.00    Sequence
DRB1_0701  127  VSVSATTTDGLGLTG  VSATTTDGL      0.4051      624.1            50.00    Sequence
DRB1_0701  72  QGVSGADMLRHVVVL  ADMLRHVVV      0.3975      677.9            50.00    Sequence
DRB1_0701  41  DVAVHALCDAVLSAA  VHALCDAVL      0.3891      742.1            50.00    Sequence
DRB1_0701  51  VLSAAGLGDIGEVFG  LSAAGLGDI      0.3878      753.2            50.00    Sequence
DRB1_0701  37  HSDGDVAVHALCDAV  AVHALCDAV      0.3695      917.8            50.00    Sequence
DRB1_0701  42  VAVHALCDAVLSAAG  VHALCDAVL      0.3660      953.3            50.00    Sequence
DRB1_0701  95  GNAVVQVIGNRPKIG  VIGNRPKIG      0.3616      999.7            50.00    Sequence
DRB1_0701  128  SVSATTTDGLGLTGR  VSATTTDGL      0.3586      1032.8           50.00    Sequence
DRB1_0701  92  YRVGNAVVQVIGNRP  VVQVIGNRP      0.3530      1097.1           50.00    Sequence
DRB1_0701  43  AVHALCDAVLSAAGL  VHALCDAVL      0.3442      1206.0           50.00    Sequence
DRB1_0701  93  RVGNAVVQVIGNRPK  VGNAVVQVI      0.3433      1218.3           50.00    Sequence
DRB1_0701  129  VSATTTDGLGLTGRG  VSATTTDGL      0.3286      1428.5           50.00    Sequence
DRB1_0701  52  LSAAGLGDIGEVFGV  LSAAGLGDI      0.3277      1442.7           50.00    Sequence
DRB1_0701  96  NAVVQVIGNRPKIGW  VIGNRPKIG      0.3270      1453.7           50.00    Sequence
DRB1_0701  10  TDVHPIEPGRPCWLV  IEPGRPCWL      0.3264      1463.1           50.00    Sequence
DRB1_0701   9  GTDVHPIEPGRPCWL  IEPGRPCWL      0.3135      1681.6           50.00    Sequence
DRB1_0701  94  VGNAVVQVIGNRPKI  VVQVIGNRP      0.3109      1729.2           50.00    Sequence
DRB1_0701  97  AVVQVIGNRPKIGWR  VIGNRPKIG      0.2891      2191.2           50.00    Sequence
DRB1_0701  11  DVHPIEPGRPCWLVG  IEPGRPCWL      0.2859      2268.2           50.00    Sequence
DRB1_0701  12  VHPIEPGRPCWLVGL  IEPGRPCWL      0.2840      2315.5           50.00    Sequence
DRB1_0701  15  IEPGRPCWLVGLLFP  IEPGRPCWL      0.2835      2326.2           50.00    Sequence
DRB1_0701  14  PIEPGRPCWLVGLLF  IEPGRPCWL      0.2817      2371.6           50.00    Sequence
DRB1_0701   1  NQLPRVGLGTDVHPI  GLGTDVHPI      0.2814      2381.3           50.00    Sequence
DRB1_0701  13  HPIEPGRPCWLVGLL  IEPGRPCWL      0.2703      2684.8           50.00    Sequence
DRB1_0701  98  VVQVIGNRPKIGWRR  VIGNRPKIG      0.2462      3484.2           50.00    Sequence
DRB1_0701   2  QLPRVGLGTDVHPIE  GLGTDVHPI      0.2446      3546.5           50.00    Sequence
DRB1_0701  20  PCWLVGLLFPSADGC  LLFPSADGC      0.2159      4836.8           50.00    Sequence
DRB1_0701  133  TTDGLGLTGRGEGLA  LTGRGEGLA      0.2153      4868.0           50.00    Sequence
DRB1_0701  99  VQVIGNRPKIGWRRL  VIGNRPKIG      0.2137      4951.0           50.00    Sequence
DRB1_0701   3  LPRVGLGTDVHPIEP  GLGTDVHPI      0.2061      5378.5           50.00    Sequence
DRB1_0701  22  WLVGLLFPSADGCAG  LLFPSADGC      0.2056      5406.1           50.00    Sequence
DRB1_0701  21  CWLVGLLFPSADGCA  LLFPSADGC      0.1967      5950.3           50.00    Sequence
DRB1_0701  134  TDGLGLTGRGEGLAA  LTGRGEGLA      0.1947      6085.7           50.00    Sequence
DRB1_0701  135  DGLGLTGRGEGLAAI  LTGRGEGLA      0.1938      6144.1           50.00    Sequence
DRB1_0701  100  QVIGNRPKIGWRRLE  VIGNRPKIG      0.1853      6735.8           50.00    Sequence
DRB1_0701  132  TTTDGLGLTGRGEGL  GLTGRGEGL      0.1814      7021.6           50.00    Sequence
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  DRB1_0701  23  LVGLLFPSADGCAGH  LLFPSADGC      0.1763     7424.7           50.00    Sequence
  DRB1_0701  136  GLGLTGRGEGLAAIA  GLTGRGEGL      0.1734     7662.2           50.00    Sequence
  DRB1_0701  28  FPSADGCAGHSDGDV  CAGHSDGDV      0.1714     7827.0           50.00    Sequence
  DRB1_0701  30  SADGCAGHSDGDVAV  CAGHSDGDV      0.1695     7992.2           50.00    Sequence
  DRB1_0701   4  PRVGLGTDVHPIEPG  GLGTDVHPI     0.1676     8156.6          50.00    Sequence
  DRB1_0701  137  LGLTGRGEGLAAIAT  LTGRGEGLA     0.1645     8431.1          50.00    Sequence
  DRB1_0701  16  EPGRPCWLVGLLFPS  CWLVGLLFP     0.1633     8540.5          50.00    Sequence
  DRB1_0701  101  VIGNRPKIGWRRLEA  VIGNRPKIG     0.1609     8768.2          50.00    Sequence
  DRB1_0701  24  VGLLFPSADGCAGHS  LLFPSADGC      0.1599     8862.2          50.00    Sequence
  DRB1_0701  34  CAGHSDGDVAVHALC  GDVAVHALC      0.1550     9345.7          50.00    Sequence
  DRB1_0701   6  VGLGTDVHPIEPGRP  GLGTDVHPI     0.1493     9946.0          50.00    Sequence
  DRB1_0701  29  PSADGCAGHSDGDVA  CAGHSDGDV      0.1492     9950.3           50.00    Sequence
  DRB1_0701  31  ADGCAGHSDGDVAVH  CAGHSDGDV      0.1472     10167.1          50.00    Sequence
  DRB1_0701   5  RVGLGTDVHPIEPGR  GLGTDVHPI     0.1472     10168.2          50.00    Sequence
  DRB1_0701  138  GLTGRGEGLAAIATA  LTGRGEGLA     0.1449     10424.9          50.00    Sequence
  DRB1_0701  57  LGDIGEVFGVDDPRW  VFGVDDPRW      0.1439     10542.3          50.00    Sequence
  DRB1_0701  25  GLLFPSADGCAGHSD  LLFPSADGC      0.1422     10736.0          50.00    Sequence
  DRB1_0701  58  GDIGEVFGVDDPRWQ  VFGVDDPRW      0.1362     11459.3          50.00    Sequence
  DRB1_0701   7  GLGTDVHPIEPGRPC  GLGTDVHPI     0.1359     11486.5          50.00    Sequence
  DRB1_0701  32  DGCAGHSDGDVAVHA  CAGHSDGDV      0.1346     11650.2          50.00    Sequence
  DRB1_0701  26  LLFPSADGCAGHSDG  LLFPSADGC      0.1318     12017.0          50.00    Sequence
  DRB1_0701  35  AGHSDGDVAVHALCD  GDVAVHALC      0.1313     12079.8          50.00    Sequence
  DRB1_0701  59  DIGEVFGVDDPRWQG  VFGVDDPRW      0.1313     12084.3          50.00    Sequence
  DRB1_0701   0  VNQLPRVGLGTDVHP  VNQLPRVGL      0.1311     12110.3          50.00    Sequence
  DRB1_0701  36  GHSDGDVAVHALCDA  GDVAVHALC      0.1289     12398.3          50.00    Sequence
  DRB1_0701  33  GCAGHSDGDVAVHAL  CAGHSDGDV      0.1277     12554.6          50.00    Sequence
  DRB1_0701  60  IGEVFGVDDPRWQGV  VFGVDDPRW      0.1266     12711.0          50.00    Sequence
  DRB1_0701  17  PGRPCWLVGLLFPSA  CWLVGLLFP      0.1237     13112.4          50.00    Sequence
  DRB1_0701  61  GEVFGVDDPRWQGVS  VFGVDDPRW      0.1137     14616.3          50.00    Sequence
  DRB1_0701  130  SATTTDGLGLTGRGE  ATTTDGLGL      0.1118     14922.7          50.00    Sequence
  DRB1_0701  131  ATTTDGLGLTGRGEG  ATTTDGLGL      0.1094     15304.6          50.00    Sequence
  DRB1_0701  19  RPCWLVGLLFPSADG  GLLFPSADG      0.1088     15409.3          50.00    Sequence
  DRB1_0701  18  GRPCWLVGLLFPSAD  CWLVGLLFP      0.1081     15526.8          50.00    Sequence
  DRB1_0701  62  EVFGVDDPRWQGVSG  VFGVDDPRW      0.1031     16386.2          50.00    Sequence
  DRB1_0701  27  LFPSADGCAGHSDGD  LFPSADGCA      0.1018     16614.4          50.00    Sequence
  DRB1_0701  63  VFGVDDPRWQGVSGA  VFGVDDPRW      0.0960     17703.6          50.00    Sequence
  DRB1_0701  54  AAGLGDIGEVFGVDD  GLGDIGEVF      0.0839     20175.8          50.00    Sequence
  DRB1_0701  55  AGLGDIGEVFGVDDP  GLGDIGEVF      0.0781     21466.9          50.00    Sequence
  DRB1_0701   8  LGTDVHPIEPGRPCW  VHPIEPGRP      0.0752     22167.4          50.00    Sequence
  DRB1_0701  102  IGNRPKIGWRRLEAQ  GNRPKIGWR      0.0751     22180.6          50.00    Sequence
  DRB1_0701  53  SAAGLGDIGEVFGVD  GLGDIGEVF      0.0724     22849.8          50.00    Sequence
  DRB1_0701  56  GLGDIGEVFGVDDPR  GLGDIGEVF      0.0710     23183.5          50.00    Sequence
  DRB1_0701  103  GNRPKIGWRRLEAQA  GNRPKIGWR      0.0670     24229.3          50.00    Sequence
  DRB1_0701  64  FGVDDPRWQGVSGAD  GVDDPRWQG      0.0450     30723.4          50.00    Sequence
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Allele: DRB1_0701. Number of high binders 16. Number of weak binders 47. Number of peptides 145

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     Allele  pos       peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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  DRB1_0802  105  RPKIGWRRLEAQAVL  RPKIGWRRL      0.6229       59.2      WB    2.00    Sequence
  DRB1_0802  104  NRPKIGWRRLEAQAV  RPKIGWRRL      0.6061       71.0      WB    2.00    Sequence
  DRB1_0802  90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.5645      111.3      WB    4.00    Sequence
  DRB1_0802  103  GNRPKIGWRRLEAQA  RPKIGWRRL      0.5585      118.8      WB    4.00    Sequence
  DRB1_0802  91  GYRVGNAVVQVIGNR  GYRVGNAVV      0.5584      118.8      WB    4.00    Sequence
  DRB1_0802  89  QHGYRVGNAVVQVIG  GYRVGNAVV      0.5446      138.0      WB    8.00    Sequence
  DRB1_0802  86  LITQHGYRVGNAVVQ  ITQHGYRVG      0.5426      141.0      WB    8.00    Sequence
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DRB1_0802	87	ITQHGYRVGNAVVQV	ITQHGYRVG	0.5342	154.4	WB	8.00	Sequence
DRB1_0802	98	VVQVIGNRPKIGWRR	VVQVIGNRP	0.5151	189.9	WB	8.00	Sequence
DRB1_0802	85	VLITQHGYRVGNAVV	GYRVGNAVV	0.5127	194.8	WB	8.00	Sequence
DRB1_0802	106	PKIGWRRLEAQAVLS	PKIGWRRLE	0.5106	199.5	WB	8.00	Sequence
DRB1_0802	99	VQVIGNRPKIGWRRL	VQVIGNRPK	0.5092	202.5	WB	8.00	Sequence
DRB1_0802	100	QVIGNRPKIGWRRLE	RPKIGWRRL	0.5079	205.4	WB	8.00	Sequence
DRB1_0802	102	IGNRPKIGWRRLEAQ	RPKIGWRRL	0.5014	220.3	WB	8.00	Sequence
DRB1_0802	88	TQHGYRVGNAVVQVI	GYRVGNAVV	0.4982	228.0	WB	8.00	Sequence
DRB1_0802	92	YRVGNAVVQVIGNRP	YRVGNAVVQ	0.4906	247.6	WB	8.00	Sequence
DRB1_0802	101	VIGNRPKIGWRRLEA	RPKIGWRRL	0.4848	263.7	WB	16.00	Sequence
DRB1_0802	97	AVVQVIGNRPKIGWR	VVQVIGNRP	0.4805	276.3	WB	16.00	Sequence
DRB1_0802	107	KIGWRRLEAQAVLSR	GWRRLEAQA	0.4745	294.7	WB	16.00	Sequence
DRB1_0802	95	GNAVVQVIGNRPKIG	GNAVVQVIG	0.4640	330.1	WB	16.00	Sequence
DRB1_0802	96	NAVVQVIGNRPKIGW	VVQVIGNRP	0.4607	342.1	WB	16.00	Sequence
DRB1_0802	93	RVGNAVVQVIGNRPK	GNAVVQVIG	0.4540	367.9	WB	16.00	Sequence
DRB1_0802	115	AQAVLSRLLNAPVSV	VLSRLLNAP	0.4500	384.1	WB	16.00	Sequence
DRB1_0802	94	VGNAVVQVIGNRPKI	GNAVVQVIG	0.4471	396.5	WB	16.00	Sequence
DRB1_0802	108	IGWRRLEAQAVLSRL	GWRRLEAQA	0.4390	432.5	WB	16.00	Sequence
DRB1_0802	114	EAQAVLSRLLNAPVS	QAVLSRLLN	0.4389	432.9	WB	16.00	Sequence
DRB1_0802	116	QAVLSRLLNAPVSVS	VLSRLLNAP	0.4355	449.3	WB	16.00	Sequence
DRB1_0802	82	HVVVLITQHGYRVGN	VVVLITQHG	0.4305	474.2	WB	16.00	Sequence
DRB1_0802	81	RHVVVLITQHGYRVG	ITQHGYRVG	0.4276	489.2	WB	16.00	Sequence
DRB1_0802	75	SGADMLRHVVVLITQ	GADMLRHVV	0.4204	528.9		16.00	Sequence
DRB1_0802	76	GADMLRHVVVLITQH	GADMLRHVV	0.4204	529.2		16.00	Sequence
DRB1_0802	109	GWRRLEAQAVLSRLL	GWRRLEAQA	0.4202	530.4		16.00	Sequence
DRB1_0802	83	VVVLITQHGYRVGNA	VVVLITQHG	0.4102	591.0		16.00	Sequence
DRB1_0802	118	VLSRLLNAPVSVSAT	VLSRLLNAP	0.4050	624.7		32.00	Sequence
DRB1_0802	74	VSGADMLRHVVVLIT	GADMLRHVV	0.4039	632.7		32.00	Sequence
DRB1_0802	113	LEAQAVLSRLLNAPV	AQAVLSRLL	0.4004	657.2		32.00	Sequence
DRB1_0802	84	VVLITQHGYRVGNAV	LITQHGYRV	0.4000	659.7		32.00	Sequence
DRB1_0802	117	AVLSRLLNAPVSVSA	VLSRLLNAP	0.3958	690.5		32.00	Sequence
DRB1_0802	73	GVSGADMLRHVVVLI	MLRHVVVLI	0.3781	835.8		32.00	Sequence
DRB1_0802	80	LRHVVVLITQHGYRV	VVVLITQHG	0.3779	838.3		32.00	Sequence
DRB1_0802	79	MLRHVVVLITQHGYR	MLRHVVVLI	0.3754	861.0		32.00	Sequence
DRB1_0802	112	RLEAQAVLSRLLNAP	AQAVLSRLL	0.3735	878.7		32.00	Sequence
DRB1_0802	110	WRRLEAQAVLSRLLN	WRRLEAQAV	0.3682	930.4		32.00	Sequence
DRB1_0802	71	WQGVSGADMLRHVVV	WQGVSGADM	0.3559	1063.1		32.00	Sequence
DRB1_0802	77	ADMLRHVVVLITQHG	MLRHVVVLI	0.3546	1078.4		32.00	Sequence
DRB1_0802	78	DMLRHVVVLITQHGY	MLRHVVVLI	0.3449	1196.9		32.00	Sequence
DRB1_0802	69	PRWQGVSGADMLRHV	PRWQGVSGA	0.3405	1255.9		32.00	Sequence
DRB1_0802	111	RRLEAQAVLSRLLNA	AQAVLSRLL	0.3390	1275.8		32.00	Sequence
DRB1_0802	68	DPRWQGVSGADMLRH	PRWQGVSGA	0.3371	1303.3		32.00	Sequence
DRB1_0802	67	DDPRWQGVSGADMLR	PRWQGVSGA	0.3339	1348.8		32.00	Sequence
DRB1_0802	70	RWQGVSGADMLRHVV	WQGVSGADM	0.3329	1363.8		32.00	Sequence
DRB1_0802	72	QGVSGADMLRHVVVL	GVSGADMLR	0.3299	1408.9		32.00	Sequence
DRB1_0802	119	LSRLLNAPVSVSATT	LSRLLNAPV	0.3139	1674.6		50.00	Sequence
DRB1_0802	21	CWLVGLLFPSADGCA	WLVGLLFPS	0.3054	1836.0		50.00	Sequence
DRB1_0802	66	VDDPRWQGVSGADML	PRWQGVSGA	0.3019	1907.2		50.00	Sequence
DRB1_0802	136	GLGLTGRGEGLAAIA	GLGLTGRGE	0.3016	1913.2		50.00	Sequence
DRB1_0802	19	RPCWLVGLLFPSADG	WLVGLLFPS	0.3010	1926.7		50.00	Sequence
DRB1_0802	63	VFGVDDPRWQGVSGA	VFGVDDPRW	0.2920	2122.8		50.00	Sequence
DRB1_0802	20	PCWLVGLLFPSADGC	WLVGLLFPS	0.2915	2133.1		50.00	Sequence
DRB1_0802	22	WLVGLLFPSADGCAG	WLVGLLFPS	0.2830	2338.9		50.00	Sequence
DRB1_0802	139	LTGRGEGLAAIATAL	LTGRGEGLA	0.2827	2346.9		50.00	Sequence
DRB1_0802	137	LGLTGRGEGLAAIAT	RGEGLAAIA	0.2818	2369.0		50.00	Sequence
DRB1_0802	17	PGRPCWLVGLLFPSA	WLVGLLFPS	0.2798	2421.8		50.00	Sequence
DRB1_0802	18	GRPCWLVGLLFPSAD	WLVGLLFPS	0.2768	2502.8		50.00	Sequence
DRB1_0802	141	GRGEGLAAIATALVV	GLAAIATAL	0.2748	2556.0		50.00	Sequence
DRB1_0802	64	FGVDDPRWQGVSGAD	FGVDDPRWQ	0.2708	2670.2		50.00	Sequence

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DRB1_0802  140  TGRGEGLAAIATALV  GLAAIATAL      0.2680      2750.8            50.00     Sequence
DRB1_0802  138  GLTGRGEGLAAIATA  LTGRGEGLA      0.2651      2839.3            50.00     Sequence
DRB1_0802  142  RGEGLAAIATALVVS  GLAAIATAL      0.2621      2933.3            50.00     Sequence
DRB1_0802  65  GVDDPRWQGVSGADM  RWQGVSGAD      0.2618      2943.6            50.00     Sequence
DRB1_0802  120  SRLLNAPVSVSATTT  LNAPVSVSA      0.2548      3173.4            50.00     Sequence
DRB1_0802  135  DGLGLTGRGEGLAAI  GLGLTGRGE      0.2530      3238.3            50.00     Sequence
DRB1_0802  16  EPGRPCWLVGLLFPS  WLVGLLFPS      0.2480      3416.1            50.00     Sequence
DRB1_0802  62  EVFGVDDPRWQGVSG  VFGVDDPRW      0.2437      3579.2            50.00     Sequence
DRB1_0802  121  RLLNAPVSVSATTTD  LNAPVSVSA      0.2359      3894.8            50.00     Sequence
DRB1_0802  143  GEGLAAIATALVVSL  GLAAIATAL      0.2343      3962.2            50.00     Sequence
DRB1_0802  134  TDGLGLTGRGEGLAA  GLGLTGRGE      0.2318      4073.4            50.00     Sequence
DRB1_0802  133  TTDGLGLTGRGEGLA  GLGLTGRGE      0.2290      4197.0            50.00     Sequence
DRB1_0802  144  EGLAAIATALVVSLR  GLAAIATAL      0.2266      4309.1            50.00     Sequence
DRB1_0802   5  RVGLGTDVHPIEPGR  GLGTDVHPI      0.2159      4833.1            50.00     Sequence
DRB1_0802  122  LLNAPVSVSATTTDG  LNAPVSVSA      0.2150      4880.5            50.00     Sequence
DRB1_0802  23  LVGLLFPSADGCAGH  LVGLLFPSA      0.2111      5092.5            50.00     Sequence
DRB1_0802   6  VGLGTDVHPIEPGRP  GLGTDVHPI      0.2060      5381.7            50.00     Sequence
DRB1_0802  61  GEVFGVDDPRWQGVS  FGVDDPRWQ      0.2045      5471.3            50.00     Sequence
DRB1_0802   7  GLGTDVHPIEPGRPC  GLGTDVHPI      0.1990      5808.7            50.00     Sequence
DRB1_0802  47  LCDAVLSAAGLGDIG  CDAVLSAAG      0.1970      5933.8            50.00     Sequence
DRB1_0802   0  VNQLPRVGLGTDVHP  VNQLPRVGL      0.1945      6096.0            50.00     Sequence
DRB1_0802  48  CDAVLSAAGLGDIGE  CDAVLSAAG      0.1936      6156.2            50.00     Sequence
DRB1_0802  45  HALCDAVLSAAGLGD  CDAVLSAAG      0.1924      6235.8            50.00     Sequence
DRB1_0802  46  ALCDAVLSAAGLGDI  CDAVLSAAG      0.1912      6314.6            50.00     Sequence
DRB1_0802   2  QLPRVGLGTDVHPIE  QLPRVGLGT      0.1885      6507.5            50.00     Sequence
DRB1_0802  132  TTTDGLGLTGRGEGL  GLGLTGRGE      0.1874      6579.2            50.00     Sequence
DRB1_0802  123  LNAPVSVSATTTDGL  LNAPVSVSA      0.1871      6604.2            50.00     Sequence
DRB1_0802   4  PRVGLGTDVHPIEPG  GLGTDVHPI      0.1859      6693.3            50.00     Sequence
DRB1_0802  60  IGEVFGVDDPRWQGV  FGVDDPRWQ      0.1795      7171.9            50.00     Sequence
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DRB1_0802  44  VHALCDAVLSAAGLG  CDAVLSAAG      0.1763      7420.3            50.00     Sequence
DRB1_0802   1  NQLPRVGLGTDVHPI  QLPRVGLGT      0.1753      7504.6            50.00     Sequence
DRB1_0802  15  IEPGRPCWLVGLLFP  CWLVGLLFP      0.1719      7780.3            50.00     Sequence
DRB1_0802  59  DIGEVFGVDDPRWQG  FGVDDPRWQ      0.1688      8053.3            50.00     Sequence
DRB1_0802  131  ATTTDGLGLTGRGEG  GLGLTGRGE      0.1664      8264.6            50.00     Sequence
DRB1_0802  14  PIEPGRPCWLVGLLF  PIEPGRPCW      0.1642      8456.3            50.00     Sequence
DRB1_0802   3  LPRVGLGTDVHPIEP  GLGTDVHPI      0.1638      8493.5            50.00     Sequence
DRB1_0802  42  VAVHALCDAVLSAAG  HALCDAVLS      0.1623      8633.8            50.00     Sequence
DRB1_0802  13  HPIEPGRPCWLVGLL  PIEPGRPCW      0.1572      9128.1            50.00     Sequence
DRB1_0802  24  VGLLFPSADGCAGHS  GLLFPSADG      0.1487      10002.3           50.00     Sequence
DRB1_0802  58  GDIGEVFGVDDPRWQ  VFGVDDPRW      0.1449      10424.0           50.00     Sequence
DRB1_0802  124  NAPVSVSATTTDGLG  PVSVSATTT      0.1443      10489.7           50.00     Sequence
DRB1_0802  49  DAVLSAAGLGDIGEV  AVLSAAGLG      0.1442      10509.9           50.00     Sequence
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DRB1_0802  25  GLLFPSADGCAGHSD  GLLFPSADG      0.1375      11290.9           50.00     Sequence
DRB1_0802  126  PVSVSATTTDGLGLT  PVSVSATTT      0.1374      11302.4           50.00     Sequence
DRB1_0802  12  VHPIEPGRPCWLVGL  PIEPGRPCW      0.1370      11360.4           50.00     Sequence
DRB1_0802  125  APVSVSATTTDGLGL  PVSVSATTT      0.1351      11591.9           50.00     Sequence
DRB1_0802  11  DVHPIEPGRPCWLVG  PIEPGRPCW      0.1304      12200.3           50.00     Sequence
DRB1_0802  39  DGDVAVHALCDAVLS  GDVAVHALC      0.1247      12978.1           50.00     Sequence
DRB1_0802  10  TDVHPIEPGRPCWLV  PIEPGRPCW      0.1209      13519.6           50.00     Sequence
DRB1_0802   9  GTDVHPIEPGRPCWL  PIEPGRPCW      0.1196      13704.7           50.00     Sequence
DRB1_0802   8  LGTDVHPIEPGRPCW  LGTDVHPIE      0.1194      13738.0           50.00     Sequence
DRB1_0802  40  GDVAVHALCDAVLSA  AVHALCDAV      0.1187      13836.1           50.00     Sequence
DRB1_0802  41  DVAVHALCDAVLSAA  HALCDAVLS      0.1187      13841.5           50.00     Sequence
DRB1_0802  50  AVLSAAGLGDIGEVF  AVLSAAGLG      0.1139      14586.9           50.00     Sequence
DRB1_0802  38  SDGDVAVHALCDAVL  GDVAVHALC      0.1076      15604.4           50.00     Sequence
DRB1_0802  37  HSDGDVAVHALCDAV  GDVAVHALC      0.1068      15738.2           50.00     Sequence
DRB1_0802  57  LGDIGEVFGVDDPRW  VFGVDDPRW      0.1053      16002.8           50.00     Sequence
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  DRB1_0802  56  GLGDIGEVFGVDDPR  GLGDIGEVF       0.1022      16555.3            50.00     Sequence
  DRB1_0802  127  VSVSATTTDGLGLTG  VSVSATTTD       0.1012      16720.7            50.00     Sequence
  DRB1_0802  51  VLSAAGLGDIGEVFG  LGDIGEVFG       0.0989     17154.7            50.00     Sequence
  DRB1_0802  128  SVSATTTDGLGLTGR  SVSATTTDG       0.0969      17530.1            50.00     Sequence
  DRB1_0802  52  LSAAGLGDIGEVFGV  GLGDIGEVF       0.0936     18156.2            50.00     Sequence
  DRB1_0802  55  AGLGDIGEVFGVDDP  GLGDIGEVF       0.0933     18215.2            50.00     Sequence
  DRB1_0802  129  VSATTTDGLGLTGRG  SATTTDGLG       0.0909      18707.8            50.00     Sequence
  DRB1_0802  27  LFPSADGCAGHSDGD  FPSADGCAG        0.0895      18982.4            50.00     Sequence
  DRB1_0802  53  SAAGLGDIGEVFGVD  GLGDIGEVF       0.0861     19690.3            50.00     Sequence
  DRB1_0802  54  AAGLGDIGEVFGVDD  GLGDIGEVF       0.0835     20263.9            50.00     Sequence
  DRB1_0802  26  LLFPSADGCAGHSDG  FPSADGCAG        0.0811      20796.1            50.00     Sequence
  DRB1_0802  35  AGHSDGDVAVHALCD  GDVAVHALC       0.0789      21284.2            50.00     Sequence
  DRB1_0802  36  GHSDGDVAVHALCDA  GDVAVHALC       0.0774      21628.9            50.00     Sequence
  DRB1_0802  34  CAGHSDGDVAVHALC  GDVAVHALC       0.0761      21943.1            50.00     Sequence
  DRB1_0802  28  FPSADGCAGHSDGDV  FPSADGCAG        0.0668      24257.4            50.00     Sequence
  DRB1_0802  33  GCAGHSDGDVAVHAL  AGHSDGDVA       0.0413      31996.3            50.00     Sequence
  DRB1_0802  32  DGCAGHSDGDVAVHA  GHSDGDVAV       0.0353      34111.7            50.00     Sequence
  DRB1_0802  31  ADGCAGHSDGDVAVH  AGHSDGDVA       0.0343      34506.7            50.00     Sequence
  DRB1_0802  30  SADGCAGHSDGDVAV  AGHSDGDVA       0.0318      35459.7            50.00     Sequence
  DRB1_0802  29  PSADGCAGHSDGDVA  AGHSDGDVA       0.0288      36632.4            50.00     Sequence
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Allele: DRB1_0802. Number of high binders 0. Number of weak binders 29. Number of peptides 145

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    Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_0901  110  WRRLEAQAVLSRLLN  WRRLEAQAV       0.6715        35.0        SB     1.00     Sequence
  DRB1_0901  109  GWRRLEAQAVLSRLL  WRRLEAQAV       0.6673        36.6        SB     1.00     Sequence
  DRB1_0901  108  IGWRRLEAQAVLSRL  WRRLEAQAV      0.6567        41.0        SB     2.00     Sequence
  DRB1_0901  68  DPRWQGVSGADMLRH  QGVSGADML       0.6490        44.6        SB     2.00     Sequence
  DRB1_0901  67  DDPRWQGVSGADMLR  QGVSGADML       0.6472        45.5        SB     2.00     Sequence
  DRB1_0901  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.6362        51.2        WB     2.00     Sequence
  DRB1_0901  66  VDDPRWQGVSGADML  WQGVSGADM       0.6291        55.3        WB     4.00     Sequence
  DRB1_0901  69  PRWQGVSGADMLRHV  QGVSGADML       0.6233        58.9        WB     4.00     Sequence
  DRB1_0901  117  AVLSRLLNAPVSVSA  LSRLLNAPV      0.6114        67.0        WB     4.00     Sequence
  DRB1_0901  89  QHGYRVGNAVVQVIG  HGYRVGNAV       0.6088        68.9        WB     4.00     Sequence
  DRB1_0901  90  HGYRVGNAVVQVIGN  HGYRVGNAV       0.6067        70.5        WB     4.00     Sequence
  DRB1_0901  118  VLSRLLNAPVSVSAT  LSRLLNAPV      0.6065        70.6        WB     4.00     Sequence
  DRB1_0901  106  PKIGWRRLEAQAVLS  WRRLEAQAV       0.6042        72.4        WB     4.00     Sequence
  DRB1_0901  111  RRLEAQAVLSRLLNA  RRLEAQAVL       0.5962        79.0        WB     4.00     Sequence
  DRB1_0901  88  TQHGYRVGNAVVQVI  YRVGNAVVQ       0.5958        79.3        WB     4.00     Sequence
  DRB1_0901  86  LITQHGYRVGNAVVQ  GYRVGNAVV       0.5940        80.9        WB     4.00     Sequence
  DRB1_0901  87  ITQHGYRVGNAVVQV  YRVGNAVVQ       0.5937        81.2        WB     4.00     Sequence
  DRB1_0901  70  RWQGVSGADMLRHVV  QGVSGADML       0.5889        85.5        WB     8.00     Sequence
  DRB1_0901  119  LSRLLNAPVSVSATT  LSRLLNAPV       0.5867        87.5        WB     8.00     Sequence
  DRB1_0901  142  RGEGLAAIATALVVS  LAAIATALV       0.5865        87.7        WB     8.00     Sequence
  DRB1_0901  141  GRGEGLAAIATALVV  LAAIATALV       0.5842        89.9        WB     8.00     Sequence
  DRB1_0901  144  EGLAAIATALVVSLR  EGLAAIATA       0.5822        91.9        WB     8.00     Sequence
  DRB1_0901  143  GEGLAAIATALVVSL  LAAIATALV       0.5677       107.5        WB     8.00     Sequence
  DRB1_0901  140  TGRGEGLAAIATALV  LAAIATALV       0.5653       110.3        WB     8.00     Sequence
  DRB1_0901  116  QAVLSRLLNAPVSVS  LSRLLNAPV       0.5619       114.5        WB     8.00     Sequence
  DRB1_0901  139  LTGRGEGLAAIATAL  RGEGLAAIA       0.5466       135.1        WB    16.00     Sequence
  DRB1_0901  91  GYRVGNAVVQVIGNR  YRVGNAVVQ       0.5387       147.1        WB    16.00     Sequence
  DRB1_0901  120  SRLLNAPVSVSATTT  LLNAPVSVS       0.5308       160.3        WB    16.00     Sequence
  DRB1_0901  121  RLLNAPVSVSATTTD  LLNAPVSVS       0.5302       161.3        WB    16.00     Sequence
  DRB1_0901  105  RPKIGWRRLEAQAVL  WRRLEAQAV       0.5297       162.2        WB    16.00     Sequence
  DRB1_0901  71  WQGVSGADMLRHVVV  QGVSGADML       0.5247       171.2        WB    16.00     Sequence
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DRB1_0901   41  DVAVHALCDAVLSAA  VHALCDAVL     0.5163    187.5     WB   16.00   Sequence
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DRB1_0901   39  DGDVAVHALCDAVLS  VHALCDAVL     0.5123    195.7     WB   16.00   Sequence
DRB1_0901  113  LEAQAVLSRLLNAPV  LSRLLNAPV     0.5094    202.0     WB   16.00   Sequence
DRB1_0901  115  AQAVLSRLLNAPVSV  LSRLLNAPV     0.5092    202.5     WB   16.00   Sequence
DRB1_0901   42  VAVHALCDAVLSAAG  VHALCDAVL     0.5053    211.1     WB   16.00   Sequence
DRB1_0901  138  GLTGRGEGLAAIATA  RGEGLAAIA     0.5029    216.7     WB   16.00   Sequence
DRB1_0901   92  YRVGNAVVQVIGNRP  YRVGNAVVQ     0.5028    216.8     WB   16.00   Sequence
DRB1_0901  122  LLNAPVSVSATTTDG  LLNAPVSVS     0.5006    222.3     WB   16.00   Sequence
DRB1_0901  114  EAQAVLSRLLNAPVS  LSRLLNAPV     0.4985    227.3     WB   16.00   Sequence
DRB1_0901  112  RLEAQAVLSRLLNAP  RLEAQAVLS     0.4978    228.9     WB   16.00   Sequence
DRB1_0901   77  ADMLRHVVVLITQHG  MLRHVVVLI     0.4947    236.8     WB   16.00   Sequence
DRB1_0901   65  GVDDPRWQGVSGADM  WQGVSGADM     0.4910    246.5     WB   32.00   Sequence
DRB1_0901   78  DMLRHVVVLITQHGY  MLRHVVVLI     0.4873    256.7     WB   32.00   Sequence
DRB1_0901   44  VHALCDAVLSAAGLG  VHALCDAVL     0.4764    288.5     WB   32.00   Sequence
DRB1_0901   43  AVHALCDAVLSAAGL  VHALCDAVL     0.4751    292.8     WB   32.00   Sequence
DRB1_0901   76  GADMLRHVVVLITQH  MLRHVVVLI     0.4736    297.6     WB   32.00   Sequence
DRB1_0901  137  LGLTGRGEGLAAIAT  RGEGLAAIA     0.4663    322.1     WB   32.00   Sequence
DRB1_0901   85  VLITQHGYRVGNAVV  GYRVGNAVV     0.4613    340.1     WB   32.00   Sequence
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DRB1_0901   38  SDGDVAVHALCDAVL  VHALCDAVL     0.4474    395.0     WB   32.00   Sequence
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DRB1_0901   75  SGADMLRHVVVLITQ  MLRHVVVLI     0.4450    405.4     WB   32.00   Sequence
DRB1_0901  123  LNAPVSVSATTTDGL  LNAPVSVSA     0.4401    427.6     WB   32.00   Sequence
DRB1_0901  104  NRPKIGWRRLEAQAV  WRRLEAQAV     0.4329    462.1     WB   32.00   Sequence
DRB1_0901  136  GLGLTGRGEGLAAIA  RGEGLAAIA     0.4306    473.8     WB   32.00   Sequence
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DRB1_0901   49  DAVLSAAGLGDIGEV  AVLSAAGLG     0.4106    588.4          50.00   Sequence
DRB1_0901   47  LCDAVLSAAGLGDIG  DAVLSAAGL     0.4024    642.8          50.00   Sequence
DRB1_0901   46  ALCDAVLSAAGLGDI  DAVLSAAGL     0.4003    657.8          50.00   Sequence
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DRB1_0901   73  GVSGADMLRHVVVLI  MLRHVVVLI     0.3952    694.9          50.00   Sequence
DRB1_0901  124  NAPVSVSATTTDGLG  VSVSATTTD     0.3939    705.1          50.00   Sequence
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DRB1_0901  125  APVSVSATTTDGLGL  VSVSATTTD     0.3858    769.6          50.00   Sequence
DRB1_0901  126  PVSVSATTTDGLGLT  VSVSATTTD     0.3840    784.1          50.00   Sequence
DRB1_0901   48  CDAVLSAAGLGDIGE  DAVLSAAGL     0.3826    796.7          50.00   Sequence
DRB1_0901   95  GNAVVQVIGNRPKIG  VQVIGNRPK     0.3750    864.8          50.00   Sequence
DRB1_0901    0  VNQLPRVGLGTDVHP  VNQLPRVGL     0.3744    870.3          50.00   Sequence
DRB1_0901   45  HALCDAVLSAAGLGD  DAVLSAAGL     0.3740    874.4          50.00   Sequence
DRB1_0901   50  AVLSAAGLGDIGEVF  AVLSAAGLG     0.3618    997.3          50.00   Sequence
DRB1_0901   97  AVVQVIGNRPKIGWR  VQVIGNRPK     0.3605   1011.5          50.00   Sequence
DRB1_0901   84  VVLITQHGYRVGNAV  HGYRVGNAV     0.3506   1125.6          50.00   Sequence
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DRB1_0901  127  VSVSATTTDGLGLTG  VSVSATTTD     0.3457   1187.6          50.00   Sequence
DRB1_0901   24  VGLLFPSADGCAGHS  VGLLFPSAD     0.3447   1200.0          50.00   Sequence
DRB1_0901   21  CWLVGLLFPSADGCA  WLVGLLFPS     0.3426   1227.9          50.00   Sequence
DRB1_0901   23  LVGLLFPSADGCAGH  VGLLFPSAD     0.3297   1412.1          50.00   Sequence
DRB1_0901   98  VVQVIGNRPKIGWRR  VQVIGNRPK     0.3259   1471.1          50.00   Sequence
DRB1_0901   20  PCWLVGLLFPSADGC  VGLLFPSAD     0.3230   1518.4          50.00   Sequence
DRB1_0901   19  RPCWLVGLLFPSADG  VGLLFPSAD     0.3230   1518.4          50.00   Sequence
DRB1_0901  135  DGLGLTGRGEGLAAI  LTGRGEGLA     0.3215   1542.2          50.00   Sequence
DRB1_0901   25  GLLFPSADGCAGHSD  GLLFPSADG     0.3183   1596.4          50.00   Sequence
DRB1_0901   37  HSDGDVAVHALCDAV  VAVHALCDA     0.3150   1655.0          50.00   Sequence
DRB1_0901   64  FGVDDPRWQGVSGAD  RWQGVSGAD     0.3129   1693.2          50.00   Sequence
DRB1_0901   18  GRPCWLVGLLFPSAD  VGLLFPSAD     0.3075   1794.7          50.00   Sequence
DRB1_0901   17  PGRPCWLVGLLFPSA  LVGLLFPSA     0.3056   1832.2          50.00   Sequence
DRB1_0901   51  VLSAAGLGDIGEVFG  LSAAGLGDI     0.2990   1968.3          50.00   Sequence
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  DRB1_0901  16  EPGRPCWLVGLLFPS  WLVGLLFPS      0.2989      1970.9             50.00     Sequence
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  DRB1_0901  15  IEPGRPCWLVGLLFP  PGRPCWLVG      0.2885      2205.6             50.00     Sequence
  DRB1_0901  26  LLFPSADGCAGHSDG  LLFPSADGC      0.2831      2336.1             50.00     Sequence
  DRB1_0901  83  VVVLITQHGYRVGNA  ITQHGYRVG      0.2807      2399.4             50.00     Sequence
  DRB1_0901   3  LPRVGLGTDVHPIEP  LPRVGLGTD      0.2774      2486.5             50.00     Sequence
  DRB1_0901  57  LGDIGEVFGVDDPRW  DIGEVFGVD      0.2703      2684.7             50.00     Sequence
  DRB1_0901  80  LRHVVVLITQHGYRV  LRHVVVLIT      0.2691      2719.3             50.00     Sequence
  DRB1_0901  36  GHSDGDVAVHALCDA  VAVHALCDA      0.2687      2731.4             50.00     Sequence
  DRB1_0901   4  PRVGLGTDVHPIEPG  PRVGLGTDV      0.2644      2860.1             50.00     Sequence
  DRB1_0901   8  LGTDVHPIEPGRPCW  TDVHPIEPG      0.2640      2874.2             50.00     Sequence
  DRB1_0901  52  LSAAGLGDIGEVFGV  LSAAGLGDI      0.2614      2955.4             50.00     Sequence
  DRB1_0901  30  SADGCAGHSDGDVAV  AGHSDGDVA      0.2596      3012.6             50.00     Sequence
  DRB1_0901 100  QVIGNRPKIGWRRLE  QVIGNRPKI      0.2591      3030.3             50.00     Sequence
  DRB1_0901  14  PIEPGRPCWLVGLLF  IEPGRPCWL      0.2586      3047.2             50.00     Sequence
  DRB1_0901   6  VGLGTDVHPIEPGRP  LGTDVHPIE      0.2571      3095.4             50.00     Sequence
  DRB1_0901   2  QLPRVGLGTDVHPIE  LPRVGLGTD      0.2546      3181.7             50.00     Sequence
  DRB1_0901  31  ADGCAGHSDGDVAVH  DGCAGHSDG      0.2544      3187.4             50.00     Sequence
  DRB1_0901   5  RVGLGTDVHPIEPGR  LGTDVHPIE      0.2543      3192.4             50.00     Sequence
  DRB1_0901   1  NQLPRVGLGTDVHPI  LPRVGLGTD      0.2534      3223.2             50.00     Sequence
  DRB1_0901 134  TDGLGLTGRGEGLAA  LTGRGEGLA      0.2515      3289.1             50.00     Sequence
  DRB1_0901   7  GLGTDVHPIEPGRPC  LGTDVHPIE      0.2502      3336.4             50.00     Sequence
  DRB1_0901  81  RHVVVLITQHGYRVG  ITQHGYRVG      0.2501      3341.5             50.00     Sequence
  DRB1_0901  29  PSADGCAGHSDGDVA  AGHSDGDVA      0.2496      3357.5             50.00     Sequence
  DRB1_0901   9  GTDVHPIEPGRPCWL  TDVHPIEPG      0.2487      3391.1             50.00     Sequence
  DRB1_0901  55  AGLGDIGEVFGVDDP  LGDIGEVFG      0.2472      3444.7             50.00     Sequence
  DRB1_0901 102  IGNRPKIGWRRLEAQ  IGNRPKIGW      0.2468      3459.9             50.00     Sequence
  DRB1_0901  32  DGCAGHSDGDVAVHA  AGHSDGDVA      0.2460      3492.0             50.00     Sequence
  DRB1_0901  82  HVVVLITQHGYRVGN  ITQHGYRVG      0.2457      3503.1             50.00     Sequence
  DRB1_0901  56  GLGDIGEVFGVDDPR  LGDIGEVFG      0.2443      3556.4             50.00     Sequence
  DRB1_0901  10  TDVHPIEPGRPCWLV  TDVHPIEPG      0.2441      3564.3             50.00     Sequence
  DRB1_0901  58  GDIGEVFGVDDPRWQ  DIGEVFGVD      0.2437      3580.0             50.00     Sequence
  DRB1_0901  34  CAGHSDGDVAVHALC  AGHSDGDVA      0.2428      3614.0             50.00     Sequence
  DRB1_0901 103  GNRPKIGWRRLEAQA  GWRRLEAQA      0.2425      3626.2             50.00     Sequence
  DRB1_0901  54  AAGLGDIGEVFGVDD  DIGEVFGVD      0.2375      3827.6             50.00     Sequence
  DRB1_0901  13  HPIEPGRPCWLVGLL  IEPGRPCWL      0.2371      3843.5             50.00     Sequence
  DRB1_0901  28  FPSADGCAGHSDGDV  CAGHSDGDV      0.2353      3922.2             50.00     Sequence
  DRB1_0901  27  LFPSADGCAGHSDGD  LFPSADGCA      0.2345      3956.1             50.00     Sequence
  DRB1_0901  35  AGHSDGDVAVHALCD  AGHSDGDVA      0.2334      3999.8             50.00     Sequence
  DRB1_0901  59  DIGEVFGVDDPRWQG  DIGEVFGVD      0.2285      4220.4             50.00     Sequence
  DRB1_0901 133  TTDGLGLTGRGEGLA  LGLTGRGEG      0.2270      4289.9             50.00     Sequence
  DRB1_0901 101  VIGNRPKIGWRRLEA  IGNRPKIGW      0.2270      4290.1             50.00     Sequence
  DRB1_0901  33  GCAGHSDGDVAVHAL  CAGHSDGDV      0.2209      4578.6             50.00     Sequence
  DRB1_0901 128  SVSATTTDGLGLTGR  VSATTTDGL      0.2140      4934.4             50.00     Sequence
  DRB1_0901  63  VFGVDDPRWQGVSGA  VFGVDDPRW      0.2138      4945.5             50.00     Sequence
  DRB1_0901  53  SAAGLGDIGEVFGVD  LGDIGEVFG      0.2126      5012.7             50.00     Sequence
  DRB1_0901 132  TTTDGLGLTGRGEGL  TTTDGLGLT      0.2059      5385.9             50.00     Sequence
  DRB1_0901 129  VSATTTDGLGLTGRG  TTTDGLGLT      0.2057      5400.4             50.00     Sequence
  DRB1_0901  11  DVHPIEPGRPCWLVG  HPIEPGRPC      0.2009      5686.2             50.00     Sequence
  DRB1_0901  60  IGEVFGVDDPRWQGV  IGEVFGVDD      0.1926      6220.0             50.00     Sequence
  DRB1_0901 131  ATTTDGLGLTGRGEG  TTTDGLGLT      0.1912      6318.2             50.00     Sequence
  DRB1_0901  62  EVFGVDDPRWQGVSG  EVFGVDDPR      0.1912      6318.8             50.00     Sequence
  DRB1_0901  12  VHPIEPGRPCWLVGL  PGRPCWLVG      0.1877      6564.0             50.00     Sequence
  DRB1_0901  61  GEVFGVDDPRWQGVS  EVFGVDDPR      0.1732      7673.3             50.00     Sequence
  DRB1_0901 130  SATTTDGLGLTGRGE  TTTDGLGLT      0.1722      7757.6             50.00     Sequence
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Allele: DRB1_0901. Number of high binders 5. Number of weak binders 52. Number of peptides 145
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     Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  115  AQAVLSRLLNAPVSV  QAVLSRLLN       0.6444        46.9        SB     4.00     Sequence
   DRB1_1101  116  QAVLSRLLNAPVSVS  LSRLLNAPV       0.6387        49.9        SB     8.00     Sequence
   DRB1_1101  114  EAQAVLSRLLNAPVS  QAVLSRLLN       0.6346        52.1        WB     8.00     Sequence
   DRB1_1101  117  AVLSRLLNAPVSVSA  LSRLLNAPV       0.6206        60.7        WB     8.00     Sequence
   DRB1_1101  113  LEAQAVLSRLLNAPV  QAVLSRLLN       0.6125        66.2        WB     8.00     Sequence
   DRB1_1101  118  VLSRLLNAPVSVSAT  LSRLLNAPV       0.5767        97.5        WB     8.00     Sequence
   DRB1_1101   79  MLRHVVVLITQHGYR  LRHVVVLIT       0.5665       108.9        WB    16.00     Sequence
   DRB1_1101   82  HVVVLITQHGYRVGN  VVVLITQHG       0.5528       126.3        WB    16.00     Sequence
   DRB1_1101  112  RLEAQAVLSRLLNAP  QAVLSRLLN       0.5507       129.1        WB    16.00     Sequence
   DRB1_1101   78  DMLRHVVVLITQHGY  LRHVVVLIT       0.5487       132.0        WB    16.00     Sequence
   DRB1_1101   77  ADMLRHVVVLITQHG  LRHVVVLIT       0.5324       157.5        WB    16.00     Sequence
   DRB1_1101   80  LRHVVVLITQHGYRV  HVVVLITQH       0.5320       158.2        WB    16.00     Sequence
   DRB1_1101   81  RHVVVLITQHGYRVG  VVVLITQHG       0.5254       169.9        WB    16.00     Sequence
   DRB1_1101   98  VVQVIGNRPKIGWRR  VVQVIGNRP       0.5181       183.7        WB    16.00     Sequence
   DRB1_1101  107  KIGWRRLEAQAVLSR  WRRLEAQAV       0.5150       190.1        WB    16.00     Sequence
   DRB1_1101  119  LSRLLNAPVSVSATT  LSRLLNAPV       0.5150       190.2        WB    16.00     Sequence
   DRB1_1101   76  GADMLRHVVVLITQH  LRHVVVLIT       0.5078       205.5        WB    16.00     Sequence
   DRB1_1101   83  VVVLITQHGYRVGNA  VVVLITQHG       0.5025       217.7        WB    16.00     Sequence
   DRB1_1101   97  AVVQVIGNRPKIGWR  VVQVIGNRP       0.5006       222.1        WB    16.00     Sequence
   DRB1_1101  111  RRLEAQAVLSRLLNA  QAVLSRLLN       0.4970       230.9        WB    16.00     Sequence
   DRB1_1101   96  NAVVQVIGNRPKIGW  VVQVIGNRP       0.4879       255.0        WB    16.00     Sequence
   DRB1_1101  108  IGWRRLEAQAVLSRL  WRRLEAQAV       0.4846       264.2        WB    16.00     Sequence
   DRB1_1101  106  PKIGWRRLEAQAVLS  WRRLEAQAV       0.4743       295.2        WB    16.00     Sequence
   DRB1_1101   75  SGADMLRHVVVLITQ  LRHVVVLIT       0.4718       303.3        WB    32.00     Sequence
   DRB1_1101  110  WRRLEAQAVLSRLLN  QAVLSRLLN       0.4717       303.9        WB    32.00     Sequence
   DRB1_1101   74  VSGADMLRHVVVLIT  MLRHVVVLI       0.4650       326.5        WB    32.00     Sequence
   DRB1_1101  109  GWRRLEAQAVLSRLL  WRRLEAQAV       0.4636       331.7        WB    32.00     Sequence
   DRB1_1101   99  VQVIGNRPKIGWRRL  IGNRPKIGW       0.4357       448.5        WB    32.00     Sequence
   DRB1_1101  105  RPKIGWRRLEAQAVL  KIGWRRLEA       0.4347       453.5        WB    32.00     Sequence
   DRB1_1101   95  GNAVVQVIGNRPKIG  VVQVIGNRP       0.4324       464.9        WB    32.00     Sequence
   DRB1_1101   84  VVLITQHGYRVGNAV  VVLITQHGY       0.4277       488.9        WB    32.00     Sequence
   DRB1_1101   85  VLITQHGYRVGNAVV  VLITQHGYR       0.4082       604.0              32.00     Sequence
   DRB1_1101   73  GVSGADMLRHVVVLI  VSGADMLRH       0.3991       666.0              32.00     Sequence
   DRB1_1101   88  TQHGYRVGNAVVQVI  GYRVGNAVV       0.3965       685.4              32.00     Sequence
   DRB1_1101   86  LITQHGYRVGNAVVQ  GYRVGNAVV       0.3957       691.1              32.00     Sequence
   DRB1_1101  104  NRPKIGWRRLEAQAV  KIGWRRLEA       0.3899       735.7              32.00     Sequence
   DRB1_1101  135  DGLGLTGRGEGLAAI  LGLTGRGEG       0.3880       751.1              32.00     Sequence
   DRB1_1101   87  ITQHGYRVGNAVVQV  GYRVGNAVV       0.3872       758.0              32.00     Sequence
   DRB1_1101   94  VGNAVVQVIGNRPKI  VVQVIGNRP       0.3807       812.6              32.00     Sequence
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   DRB1_1101   89  QHGYRVGNAVVQVIG  YRVGNAVVQ       0.3763       853.0              32.00     Sequence
   DRB1_1101  134  TDGLGLTGRGEGLAA  LGLTGRGEG       0.3717       896.5              32.00     Sequence
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   DRB1_1101  120  SRLLNAPVSVSATTT  RLLNAPVSV       0.3605      1011.5              32.00     Sequence
   DRB1_1101  137  LGLTGRGEGLAAIAT  GLTGRGEGL       0.3529      1097.7              50.00     Sequence
   DRB1_1101   90  HGYRVGNAVVQVIGN  YRVGNAVVQ       0.3478      1160.7              50.00     Sequence
   DRB1_1101   71  WQGVSGADMLRHVVV  VSGADMLRH       0.3435      1215.8              50.00     Sequence
   DRB1_1101   72  QGVSGADMLRHVVVL  VSGADMLRH       0.3435      1216.0              50.00     Sequence
   DRB1_1101  101  VIGNRPKIGWRRLEA  VIGNRPKIG       0.3349      1334.1              50.00     Sequence
   DRB1_1101   93  RVGNAVVQVIGNRPK  VVQVIGNRP       0.3326      1367.9              50.00     Sequence
   DRB1_1101   70  RWQGVSGADMLRHVV  VSGADMLRH       0.3235      1509.4              50.00     Sequence
   DRB1_1101  133  TTDGLGLTGRGEGLA  LGLTGRGEG       0.3153      1649.1              50.00     Sequence
   DRB1_1101  103  GNRPKIGWRRLEAQA  KIGWRRLEA       0.2971      2007.8              50.00     Sequence
   DRB1_1101   69  PRWQGVSGADMLRHV  VSGADMLRH       0.2863      2258.7              50.00     Sequence
   DRB1_1101   92  YRVGNAVVQVIGNRP  YRVGNAVVQ       0.2821      2363.4              50.00     Sequence
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DRB1_1101  20  PCWLVGLLFPSADGC  LVGLLFPSA      0.2786      2454.1            50.00    Sequence
DRB1_1101  68  DPRWQGVSGADMLRH  VSGADMLRH      0.2749      2554.6            50.00    Sequence
DRB1_1101  138  GLTGRGEGLAAIATA  LTGRGEGLA      0.2721      2633.3            50.00    Sequence
DRB1_1101  91  GYRVGNAVVQVIGNR  YRVGNAVVQ      0.2710      2665.3            50.00    Sequence
DRB1_1101  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.2687      2732.0            50.00    Sequence
DRB1_1101  19  RPCWLVGLLFPSADG  LVGLLFPSA      0.2678      2757.7            50.00    Sequence
DRB1_1101  102  IGNRPKIGWRRLEAQ  KIGWRRLEA      0.2654      2831.8            50.00    Sequence
DRB1_1101  22  WLVGLLFPSADGCAG  LVGLLFPSA      0.2619      2938.9            50.00    Sequence
DRB1_1101  21  CWLVGLLFPSADGCA  LVGLLFPSA      0.2612      2962.0            50.00    Sequence
DRB1_1101  42  VAVHALCDAVLSAAG  HALCDAVLS      0.2608      2975.2            50.00    Sequence
DRB1_1101  132  TTTDGLGLTGRGEGL  LGLTGRGEG      0.2495      3362.3            50.00    Sequence
DRB1_1101  18  GRPCWLVGLLFPSAD  WLVGLLFPS      0.2446      3543.6            50.00    Sequence
DRB1_1101  41  DVAVHALCDAVLSAA  HALCDAVLS      0.2439      3571.9            50.00    Sequence
DRB1_1101  45  HALCDAVLSAAGLGD  HALCDAVLS      0.2331      4015.5            50.00    Sequence
DRB1_1101  47  LCDAVLSAAGLGDIG  AVLSAAGLG      0.2328      4026.9            50.00    Sequence
DRB1_1101  44  VHALCDAVLSAAGLG  HALCDAVLS      0.2307      4120.7            50.00    Sequence
DRB1_1101  49  DAVLSAAGLGDIGEV  AVLSAAGLG      0.2305      4129.8            50.00    Sequence
DRB1_1101  144  EGLAAIATALVVSLR  LAAIATALV      0.2298      4159.3            50.00    Sequence
DRB1_1101  48  CDAVLSAAGLGDIGE  AVLSAAGLG      0.2287      4208.3            50.00    Sequence
DRB1_1101  50  AVLSAAGLGDIGEVF  AVLSAAGLG      0.2268      4296.5            50.00    Sequence
DRB1_1101  40  GDVAVHALCDAVLSA  HALCDAVLS      0.2241      4424.2            50.00    Sequence
DRB1_1101  17  PGRPCWLVGLLFPSA  LVGLLFPSA      0.2200      4625.9            50.00    Sequence
DRB1_1101  139  LTGRGEGLAAIATAL  LTGRGEGLA      0.2151      4876.4            50.00    Sequence
DRB1_1101  43  AVHALCDAVLSAAGL  HALCDAVLS      0.2141      4932.0            50.00    Sequence
DRB1_1101  143  GEGLAAIATALVVSL  LAAIATALV      0.2121      5037.9            50.00    Sequence
DRB1_1101   0  VNQLPRVGLGTDVHP  VNQLPRVGL      0.2073      5309.7            50.00    Sequence
DRB1_1101  46  ALCDAVLSAAGLGDI  AVLSAAGLG      0.2068      5335.9            50.00    Sequence
DRB1_1101  67  DDPRWQGVSGADMLR  WQGVSGADM      0.1996      5765.7            50.00    Sequence
DRB1_1101  23  LVGLLFPSADGCAGH  LVGLLFPSA      0.1979      5874.5            50.00    Sequence
DRB1_1101  39  DGDVAVHALCDAVLS  HALCDAVLS      0.1895      6437.2            50.00    Sequence
DRB1_1101  131  ATTTDGLGLTGRGEG  LGLTGRGEG      0.1861      6672.2            50.00    Sequence
DRB1_1101  142  RGEGLAAIATALVVS  LAAIATALV      0.1847      6776.3            50.00    Sequence
DRB1_1101  122  LLNAPVSVSATTTDG  LLNAPVSVS      0.1732      7671.7            50.00    Sequence
DRB1_1101  141  GRGEGLAAIATALVV  GEGLAAIAT      0.1727      7717.8            50.00    Sequence
DRB1_1101  140  TGRGEGLAAIATALV  GLAAIATAL      0.1695      7989.7            50.00    Sequence
DRB1_1101  16  EPGRPCWLVGLLFPS  CWLVGLLFP      0.1640      8481.8            50.00    Sequence
DRB1_1101  53  SAAGLGDIGEVFGVD  LGDIGEVFG      0.1526      9596.3            50.00    Sequence
DRB1_1101  66  VDDPRWQGVSGADML  WQGVSGADM      0.1467      10224.4            50.00    Sequence
DRB1_1101  51  VLSAAGLGDIGEVFG  VLSAAGLGD      0.1466      10240.2            50.00    Sequence
DRB1_1101  54  AAGLGDIGEVFGVDD  LGDIGEVFG      0.1457      10333.5            50.00    Sequence
DRB1_1101  52  LSAAGLGDIGEVFGV  LGDIGEVFG      0.1431      10632.9            50.00    Sequence
DRB1_1101   2  QLPRVGLGTDVHPIE  RVGLGTDVH      0.1396      11043.9            50.00    Sequence
DRB1_1101   3  LPRVGLGTDVHPIEP  RVGLGTDVH      0.1358      11506.4            50.00    Sequence
DRB1_1101  55  AGLGDIGEVFGVDDP  LGDIGEVFG      0.1346      11652.6            50.00    Sequence
DRB1_1101  123  LNAPVSVSATTTDGL  PVSVSATTT      0.1297      12293.2            50.00    Sequence
DRB1_1101   1  NQLPRVGLGTDVHPI  RVGLGTDVH      0.1290      12376.3            50.00    Sequence
DRB1_1101  38  SDGDVAVHALCDAVL  VAVHALCDA      0.1283      12471.9            50.00    Sequence
DRB1_1101   4  PRVGLGTDVHPIEPG  RVGLGTDVH      0.1262      12769.2            50.00    Sequence
DRB1_1101  60  IGEVFGVDDPRWQGV  VFGVDDPRW      0.1246      12979.9            50.00    Sequence
DRB1_1101  24  VGLLFPSADGCAGHS  GLLFPSADG      0.1226      13275.0            50.00    Sequence
DRB1_1101  65  GVDDPRWQGVSGADM  WQGVSGADM      0.1222      13321.4            50.00    Sequence
DRB1_1101  61  GEVFGVDDPRWQGVS  VFGVDDPRW      0.1190      13795.3            50.00    Sequence
DRB1_1101  15  IEPGRPCWLVGLLFP  PCWLVGLLF      0.1187      13844.7            50.00    Sequence
DRB1_1101  62  EVFGVDDPRWQGVSG  VFGVDDPRW      0.1169      14121.7            50.00    Sequence
DRB1_1101  25  GLLFPSADGCAGHSD  GLLFPSADG      0.1162      14221.8            50.00    Sequence
DRB1_1101  56  GLGDIGEVFGVDDPR  LGDIGEVFG      0.1148      14444.6            50.00    Sequence
DRB1_1101  57  LGDIGEVFGVDDPRW  VFGVDDPRW      0.1125      14805.7            50.00    Sequence
DRB1_1101   5  RVGLGTDVHPIEPGR  RVGLGTDVH      0.1103      15152.5            50.00    Sequence
DRB1_1101  59  DIGEVFGVDDPRWQG  VFGVDDPRW      0.1099      15228.0            50.00    Sequence
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  DRB1_1101  124  NAPVSVSATTTDGLG  PVSVSATTT       0.1081      15524.8             50.00     Sequence
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  DRB1_1101   63  VFGVDDPRWQGVSGA  VFGVDDPRW       0.0997      17001.9             50.00     Sequence
  DRB1_1101   37  HSDGDVAVHALCDAV  VAVHALCDA       0.0974      17428.2             50.00     Sequence
  DRB1_1101  125  APVSVSATTTDGLGL  PVSVSATTT       0.0964      17619.7             50.00     Sequence
  DRB1_1101   58  GDIGEVFGVDDPRWQ  VFGVDDPRW       0.0900      18876.5             50.00     Sequence
  DRB1_1101  129  VSATTTDGLGLTGRG  TTDGLGLTG       0.0833      20298.2             50.00     Sequence
  DRB1_1101   14  PIEPGRPCWLVGLLF  PCWLVGLLF       0.0818      20624.9             50.00     Sequence
  DRB1_1101  126  PVSVSATTTDGLGLT  VSVSATTTD       0.0756      22059.5             50.00     Sequence
  DRB1_1101   26  LLFPSADGCAGHSDG  FPSADGCAG       0.0678      24016.8             50.00     Sequence
  DRB1_1101   27  LFPSADGCAGHSDGD  FPSADGCAG       0.0665      24343.6             50.00     Sequence
  DRB1_1101  128  SVSATTTDGLGLTGR  TTDGLGLTG       0.0646      24847.4             50.00     Sequence
  DRB1_1101    6  VGLGTDVHPIEPGRP  VGLGTDVHP       0.0619      25602.2             50.00     Sequence
  DRB1_1101   28  FPSADGCAGHSDGDV  FPSADGCAG       0.0603      26043.4             50.00     Sequence
  DRB1_1101   64  FGVDDPRWQGVSGAD  RWQGVSGAD       0.0595      26269.2             50.00     Sequence
  DRB1_1101  127  VSVSATTTDGLGLTG  VSVSATTTD       0.0574      26866.2             50.00     Sequence
  DRB1_1101   36  GHSDGDVAVHALCDA  VAVHALCDA       0.0547      27669.5             50.00     Sequence
  DRB1_1101    7  GLGTDVHPIEPGRPC  GLGTDVHPI       0.0412      32009.5             50.00     Sequence
  DRB1_1101   13  HPIEPGRPCWLVGLL  HPIEPGRPC       0.0400      32442.2             50.00     Sequence
  DRB1_1101   12  VHPIEPGRPCWLVGL  HPIEPGRPC       0.0376      33279.8             50.00     Sequence
  DRB1_1101   35  AGHSDGDVAVHALCD  HSDGDVAVH       0.0374      33364.5             50.00     Sequence
  DRB1_1101   34  CAGHSDGDVAVHALC  HSDGDVAVH       0.0368      33564.7             50.00     Sequence
  DRB1_1101   11  DVHPIEPGRPCWLVG  HPIEPGRPC       0.0341      34577.3             50.00     Sequence
  DRB1_1101   10  TDVHPIEPGRPCWLV  HPIEPGRPC       0.0320      35379.2             50.00     Sequence
  DRB1_1101   29  PSADGCAGHSDGDVA  DGCAGHSDG       0.0320      35384.2             50.00     Sequence
  DRB1_1101   30  SADGCAGHSDGDVAV  DGCAGHSDG       0.0299      36173.5             50.00     Sequence
  DRB1_1101    9  GTDVHPIEPGRPCWL  VHPIEPGRP       0.0298      36236.6             50.00     Sequence
  DRB1_1101    8  LGTDVHPIEPGRPCW  HPIEPGRPC       0.0291      36485.2             50.00     Sequence
  DRB1_1101   32  DGCAGHSDGDVAVHA  DGCAGHSDG       0.0264      37567.2             50.00     Sequence
  DRB1_1101   31  ADGCAGHSDGDVAVH  DGCAGHSDG       0.0263      37619.7             50.00     Sequence
  DRB1_1101   33  GCAGHSDGDVAVHAL  HSDGDVAVH       0.0251      38122.9             50.00     Sequence
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Allele: DRB1_1101. Number of high binders 2. Number of weak binders 29. Number of peptides 145

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    Allele  pos        peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_1302  141  GRGEGLAAIATALVV  LAAIATALV       0.7209        20.5        SB     0.80     Sequence
  DRB1_1302   81  RHVVVLITQHGYRVG  LITQHGYRV       0.7170        21.4        SB     1.00     Sequence
  DRB1_1302  143  GEGLAAIATALVVSL  LAAIATALV       0.7168        21.4        SB     1.00     Sequence
  DRB1_1302   82  HVVVLITQHGYRVGN  LITQHGYRV       0.7065        23.9        SB     2.00     Sequence
  DRB1_1302  142  RGEGLAAIATALVVS  LAAIATALV       0.7052        24.3        SB     2.00     Sequence
  DRB1_1302  140  TGRGEGLAAIATALV  LAAIATALV       0.7008        25.5        SB     2.00     Sequence
  DRB1_1302   80  LRHVVVLITQHGYRV  LITQHGYRV       0.6952        27.0        SB     2.00     Sequence
  DRB1_1302  144  EGLAAIATALVVSLR  LAAIATALV       0.6952        27.1        SB     2.00     Sequence
  DRB1_1302   83  VVVLITQHGYRVGNA  LITQHGYRV       0.6870        29.6        SB     2.00     Sequence
  DRB1_1302   84  VVLITQHGYRVGNAV  LITQHGYRV       0.6794        32.1        SB     2.00     Sequence
  DRB1_1302   86  LITQHGYRVGNAVVQ  LITQHGYRV       0.6755        33.5        SB     2.00     Sequence
  DRB1_1302   94  VGNAVVQVIGNRPKI  VVQVIGNRP       0.6712        35.1        SB     2.00     Sequence
  DRB1_1302   85  VLITQHGYRVGNAVV  LITQHGYRV       0.6674        36.5        SB     2.00     Sequence
  DRB1_1302   95  GNAVVQVIGNRPKIG  VVQVIGNRP       0.6505        43.9        SB     4.00     Sequence
  DRB1_1302  115  AQAVLSRLLNAPVSV  LSRLLNAPV       0.6485        44.8        SB     4.00     Sequence
  DRB1_1302   96  NAVVQVIGNRPKIGW  VVQVIGNRP       0.6407        48.8        SB     4.00     Sequence
  DRB1_1302  113  LEAQAVLSRLLNAPV  LSRLLNAPV       0.6357        51.5        WB     4.00     Sequence
  DRB1_1302  116  QAVLSRLLNAPVSVS  LSRLLNAPV       0.6326        53.3        WB     4.00     Sequence
  DRB1_1302   97  AVVQVIGNRPKIGWR  VVQVIGNRP       0.6247        58.0        WB     4.00     Sequence
  DRB1_1302  117  AVLSRLLNAPVSVSA  LSRLLNAPV       0.6153        64.2        WB     4.00     Sequence
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DRB1_1302  114  EAQAVLSRLLNAPVS  LSRLLNAPV      0.6150    64.5     WB   4.00   Sequence
DRB1_1302   92  YRVGNAVVQVIGNRP  VVQVIGNRP      0.6146    64.7     WB   4.00   Sequence
DRB1_1302  119  LSRLLNAPVSVSATT  LSRLLNAPV      0.6011    74.9     WB   8.00   Sequence
DRB1_1302  118  VLSRLLNAPVSVSAT  LSRLLNAPV      0.5958    79.3     WB   8.00   Sequence
DRB1_1302   98  VVQVIGNRPKIGWRR  VVQVIGNRP      0.5930    81.8     WB   8.00   Sequence
DRB1_1302   93  RVGNAVVQVIGNRPK  VVQVIGNRP      0.5848    89.3     WB   8.00   Sequence
DRB1_1302   88  TQHGYRVGNAVVQVI  GYRVGNAVV      0.5158   188.5     WB  16.00   Sequence
DRB1_1302   89  QHGYRVGNAVVQVIG  GYRVGNAVV      0.5099   200.9     WB  16.00   Sequence
DRB1_1302   90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.5002   223.2     WB  16.00   Sequence
DRB1_1302   87  ITQHGYRVGNAVVQV  GYRVGNAVV      0.4968   231.4     WB  16.00   Sequence
DRB1_1302   91  GYRVGNAVVQVIGNR  VGNAVVQVI      0.4956   234.4     WB  16.00   Sequence
DRB1_1302  108  IGWRRLEAQAVLSRL  WRRLEAQAV      0.4938   239.2     WB  16.00   Sequence
DRB1_1302  109  GWRRLEAQAVLSRLL  WRRLEAQAV      0.4935   239.9     WB  16.00   Sequence
DRB1_1302   78  DMLRHVVVLITQHGY  VVLITQHGY      0.4881   254.3     WB  16.00   Sequence
DRB1_1302  107  KIGWRRLEAQAVLSR  WRRLEAQAV      0.4861   259.8     WB  16.00   Sequence
DRB1_1302  110  WRRLEAQAVLSRLLN  WRRLEAQAV      0.4645   328.3     WB  16.00   Sequence
DRB1_1302   79  MLRHVVVLITQHGYR  VVLITQHGY      0.4642   329.6     WB  16.00   Sequence
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DRB1_1302  106  PKIGWRRLEAQAVLS  WRRLEAQAV      0.4566   357.5     WB  16.00   Sequence
DRB1_1302   77  ADMLRHVVVLITQHG  LRHVVVLIT      0.4262   496.9     WB  32.00   Sequence
DRB1_1302   76  GADMLRHVVVLITQH  LRHVVVLIT      0.4245   506.1         32.00   Sequence
DRB1_1302   75  SGADMLRHVVVLITQ  LRHVVVLIT      0.4194   534.9         32.00   Sequence
DRB1_1302   74  VSGADMLRHVVVLIT  LRHVVVLIT      0.4185   539.9         32.00   Sequence
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DRB1_1302  139  LTGRGEGLAAIATAL  GLAAIATAL      0.4015   649.4         32.00   Sequence
DRB1_1302  105  RPKIGWRRLEAQAVL  WRRLEAQAV      0.4010   653.0         32.00   Sequence
DRB1_1302  120  SRLLNAPVSVSATTT  RLLNAPVSV      0.4003   657.8         32.00   Sequence
DRB1_1302  111  RRLEAQAVLSRLLNA  RLEAQAVLS      0.3982   673.0         32.00   Sequence
DRB1_1302  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.3868   761.0         32.00   Sequence
DRB1_1302  112  RLEAQAVLSRLLNAP  RLEAQAVLS      0.3473  1167.3         32.00   Sequence
DRB1_1302   38  SDGDVAVHALCDAVL  AVHALCDAV      0.3435  1215.8         32.00   Sequence
DRB1_1302   73  GVSGADMLRHVVVLI  MLRHVVVLI      0.3358  1321.8         32.00   Sequence
DRB1_1302   39  DGDVAVHALCDAVLS  AVHALCDAV      0.3265  1461.5         50.00   Sequence
DRB1_1302  104  NRPKIGWRRLEAQAV  WRRLEAQAV      0.3264  1462.9         50.00   Sequence
DRB1_1302   68  DPRWQGVSGADMLRH  WQGVSGADM      0.3196  1573.9         50.00   Sequence
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DRB1_1302   69  PRWQGVSGADMLRHV  WQGVSGADM      0.3150  1655.3         50.00   Sequence
DRB1_1302   70  RWQGVSGADMLRHVV  WQGVSGADM      0.3137  1678.2         50.00   Sequence
DRB1_1302   37  HSDGDVAVHALCDAV  AVHALCDAV      0.3113  1722.0         50.00   Sequence
DRB1_1302   67  DDPRWQGVSGADMLR  WQGVSGADM      0.3051  1842.6         50.00   Sequence
DRB1_1302   46  ALCDAVLSAAGLGDI  DAVLSAAGL      0.3031  1882.5         50.00   Sequence
DRB1_1302   66  VDDPRWQGVSGADML  WQGVSGADM      0.3027  1891.4         50.00   Sequence
DRB1_1302   71  WQGVSGADMLRHVVV  WQGVSGADM      0.3011  1922.7         50.00   Sequence
DRB1_1302   40  GDVAVHALCDAVLSA  AVHALCDAV      0.3008  1929.2         50.00   Sequence
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DRB1_1302   47  LCDAVLSAAGLGDIG  DAVLSAAGL      0.2861  2263.4         50.00   Sequence
DRB1_1302  137  LGLTGRGEGLAAIAT  GRGEGLAAI      0.2791  2439.4         50.00   Sequence
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DRB1_1302   48  CDAVLSAAGLGDIGE  DAVLSAAGL      0.2674  2769.9         50.00   Sequence
DRB1_1302   45  HALCDAVLSAAGLGD  DAVLSAAGL      0.2542  3195.3         50.00   Sequence
DRB1_1302   72  QGVSGADMLRHVVVL  DMLRHVVVL      0.2432  3598.2         50.00   Sequence
DRB1_1302  122  LLNAPVSVSATTTDG  VSVSATTTD      0.2429  3611.3         50.00   Sequence
DRB1_1302  135  DGLGLTGRGEGLAAI  GLTGRGEGL      0.2421  3640.2         50.00   Sequence
DRB1_1302   65  GVDDPRWQGVSGADM  WQGVSGADM      0.2384  3791.3         50.00   Sequence
DRB1_1302  123  LNAPVSVSATTTDGL  VSATTTDGL      0.2376  3825.5         50.00   Sequence
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DRB1_1302  101  VIGNRPKIGWRRLEA  IGNRPKIGW   0.2227   4494.1   50.00   Sequence
DRB1_1302  124  NAPVSVSATTTDGLG  VSATTTDGL   0.2216   4546.3   50.00   Sequence
DRB1_1302  125  APVSVSATTTDGLGL  ATTTDGLGL   0.2163   4812.6   50.00   Sequence
DRB1_1302  126  PVSVSATTTDGLGLT  VSATTTDGL   0.2053   5421.4   50.00   Sequence
DRB1_1302  102  IGNRPKIGWRRLEAQ  RPKIGWRRL   0.1918   6278.5   50.00   Sequence
DRB1_1302  127  VSVSATTTDGLGLTG  VSATTTDGL   0.1715   7817.9   50.00   Sequence
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DRB1_1302  134  TDGLGLTGRGEGLAA  GLTGRGEGL   0.1673   8183.3   50.00   Sequence
DRB1_1302    1  NQLPRVGLGTDVHPI  GLGTDVHPI   0.1665   8250.4   50.00   Sequence
DRB1_1302    2  QLPRVGLGTDVHPIE  GLGTDVHPI   0.1639   8489.1   50.00   Sequence
DRB1_1302   54  AAGLGDIGEVFGVDD  IGEVFGVDD   0.1639   8489.4   50.00   Sequence
DRB1_1302   50  AVLSAAGLGDIGEVF  LSAAGLGDI   0.1638   8499.6   50.00   Sequence
DRB1_1302   52  LSAAGLGDIGEVFGV  LSAAGLGDI   0.1606   8795.5   50.00   Sequence
DRB1_1302    3  LPRVGLGTDVHPIEP  GLGTDVHPI   0.1605   8808.7   50.00   Sequence
DRB1_1302    6  VGLGTDVHPIEPGRP  GLGTDVHPI   0.1568   9168.7   50.00   Sequence
DRB1_1302  133  TTDGLGLTGRGEGLA  GLTGRGEGL   0.1560   9241.3   50.00   Sequence
DRB1_1302  132  TTTDGLGLTGRGEGL  GLTGRGEGL   0.1541   9439.2   50.00   Sequence
DRB1_1302    7  GLGTDVHPIEPGRPC  VHPIEPGRP   0.1525   9606.3   50.00   Sequence
DRB1_1302    4  PRVGLGTDVHPIEPG  GLGTDVHPI   0.1505   9815.5   50.00   Sequence
DRB1_1302    0  VNQLPRVGLGTDVHP  VNQLPRVGL   0.1503   9837.2   50.00   Sequence
DRB1_1302   58  GDIGEVFGVDDPRWQ  VFGVDDPRW   0.1502   9844.7   50.00   Sequence
DRB1_1302   36  GHSDGDVAVHALCDA  DGDVAVHAL   0.1481  10072.8   50.00   Sequence
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DRB1_1302   55  AGLGDIGEVFGVDDP  IGEVFGVDD   0.1449  10428.7   50.00   Sequence
DRB1_1302   60  IGEVFGVDDPRWQGV  VFGVDDPRW   0.1424  10711.6   50.00   Sequence
DRB1_1302  129  VSATTTDGLGLTGRG  VSATTTDGL   0.1399  11005.8   50.00   Sequence
DRB1_1302   10  TDVHPIEPGRPCWLV  IEPGRPCWL   0.1398  11019.6   50.00   Sequence
DRB1_1302    5  RVGLGTDVHPIEPGR  GLGTDVHPI   0.1335  11797.7   50.00   Sequence
DRB1_1302   33  GCAGHSDGDVAVHAL  DGDVAVHAL   0.1310  12123.8   50.00   Sequence
DRB1_1302   57  LGDIGEVFGVDDPRW  VFGVDDPRW   0.1291  12371.6   50.00   Sequence
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DRB1_1302  103  GNRPKIGWRRLEAQA  RPKIGWRRL   0.1274  12599.2   50.00   Sequence
DRB1_1302   11  DVHPIEPGRPCWLVG  IEPGRPCWL   0.1269  12661.6   50.00   Sequence
DRB1_1302   34  CAGHSDGDVAVHALC  DGDVAVHAL   0.1266  12708.0   50.00   Sequence
DRB1_1302   53  SAAGLGDIGEVFGVD  AGLGDIGEV   0.1239  13080.0   50.00   Sequence
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DRB1_1302   64  FGVDDPRWQGVSGAD  RWQGVSGAD   0.1219  13371.5   50.00   Sequence
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DRB1_1302   56  GLGDIGEVFGVDDPR  GDIGEVFGV   0.1198  13684.4   50.00   Sequence
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DRB1_1302    8  LGTDVHPIEPGRPCW  VHPIEPGRP   0.1117  14936.1   50.00   Sequence
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DRB1_1302  131  ATTTDGLGLTGRGEG  ATTTDGLGL   0.1089  15389.3   50.00   Sequence
DRB1_1302   61  GEVFGVDDPRWQGVS  VFGVDDPRW   0.1057  15937.5   50.00   Sequence
DRB1_1302   18  GRPCWLVGLLFPSAD  RPCWLVGLL   0.0986  17206.9   50.00   Sequence
DRB1_1302   19  RPCWLVGLLFPSADG  VGLLFPSAD   0.0982  17277.3   50.00   Sequence
DRB1_1302   63  VFGVDDPRWQGVSGA  VFGVDDPRW   0.0958  17735.8   50.00   Sequence
DRB1_1302   62  EVFGVDDPRWQGVSG  VFGVDDPRW   0.0951  17861.0   50.00   Sequence
DRB1_1302   30  SADGCAGHSDGDVAV  GHSDGDVAV   0.0903  18819.0   50.00   Sequence
DRB1_1302   16  EPGRPCWLVGLLFPS  GRPCWLVGL   0.0893  19024.8   50.00   Sequence
DRB1_1302   17  PGRPCWLVGLLFPSA  GRPCWLVGL   0.0886  19162.8   50.00   Sequence
DRB1_1302   31  ADGCAGHSDGDVAVH  GHSDGDVAV   0.0860  19726.6   50.00   Sequence
DRB1_1302   32  DGCAGHSDGDVAVHA  GHSDGDVAV   0.0852  19893.1   50.00   Sequence
DRB1_1302   20  PCWLVGLLFPSADGC  VGLLFPSAD   0.0830  20379.4   50.00   Sequence
DRB1_1302   21  CWLVGLLFPSADGCA  VGLLFPSAD   0.0810  20810.3   50.00   Sequence
DRB1_1302   22  WLVGLLFPSADGCAG  VGLLFPSAD   0.0786  21372.6   50.00   Sequence
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  DRB1_1302  23  LVGLLFPSADGCAGH  VGLLFPSAD      0.0703     23355.9            50.00    Sequence
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  DRB1_1302  25  GLLFPSADGCAGHSD  LLFPSADGC      0.0518     28556.8            50.00    Sequence
  DRB1_1302  29  PSADGCAGHSDGDVA  AGHSDGDVA      0.0392     32708.3            50.00    Sequence
  DRB1_1302  26  LLFPSADGCAGHSDG  LLFPSADGC      0.0340     34628.3            50.00    Sequence
  DRB1_1302  27  LFPSADGCAGHSDGD  LFPSADGCA      0.0258     37827.9            50.00    Sequence
  DRB1_1302  28  FPSADGCAGHSDGDV  CAGHSDGDV      0.0242     38461.8            50.00    Sequence
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Allele: DRB1_1302. Number of high binders 16. Number of weak binders 24. Number of peptides 145

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    Allele  pos        peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB1_1501  96  NAVVQVIGNRPKIGW  VVQVIGNRP      0.7244       19.7       SB     1.00     Sequence
  DRB1_1501  95  GNAVVQVIGNRPKIG  VVQVIGNRP      0.7227       20.1       SB     1.00     Sequence
  DRB1_1501  81  RHVVVLITQHGYRVG  HVVVLITQH      0.7226       20.1       SB     1.00     Sequence
  DRB1_1501  97  AVVQVIGNRPKIGWR  VVQVIGNRP      0.7196       20.8       SB     1.00     Sequence
  DRB1_1501  82  HVVVLITQHGYRVGN  HVVVLITQH      0.7157       21.7       SB     2.00     Sequence
  DRB1_1501  80  LRHVVVLITQHGYRV  HVVVLITQH      0.6962       26.8       SB     2.00     Sequence
  DRB1_1501 116  QAVLSRLLNAPVSVS  LSRLLNAPV      0.6853       30.1       SB     2.00     Sequence
  DRB1_1501 115  AQAVLSRLLNAPVSV  VLSRLLNAP      0.6815       31.4       SB     2.00     Sequence
  DRB1_1501  94  VGNAVVQVIGNRPKI  VVQVIGNRP      0.6724       34.6       SB     4.00     Sequence
  DRB1_1501  79  MLRHVVVLITQHGYR  HVVVLITQH      0.6695       35.7       SB     4.00     Sequence
  DRB1_1501 114  EAQAVLSRLLNAPVS  VLSRLLNAP      0.6559       41.4       SB     4.00     Sequence
  DRB1_1501 117  AVLSRLLNAPVSVSA  LSRLLNAPV      0.6515       43.4       SB     4.00     Sequence
  DRB1_1501  78  DMLRHVVVLITQHGY  HVVVLITQH      0.6508       43.8       SB     4.00     Sequence
  DRB1_1501  93  RVGNAVVQVIGNRPK  VVQVIGNRP      0.6285       55.7       WB     4.00     Sequence
  DRB1_1501 113  LEAQAVLSRLLNAPV  VLSRLLNAP      0.6256       57.4       WB     8.00     Sequence
  DRB1_1501  83  VVVLITQHGYRVGNA  VLITQHGYR      0.6245       58.1       WB     8.00     Sequence
  DRB1_1501  85  VLITQHGYRVGNAVV  VLITQHGYR      0.6231       59.0       WB     8.00     Sequence
  DRB1_1501  84  VVLITQHGYRVGNAV  VLITQHGYR      0.6225       59.4       WB     8.00     Sequence
  DRB1_1501  77  ADMLRHVVVLITQHG  HVVVLITQH      0.6208       60.5       WB     8.00     Sequence
  DRB1_1501  76  GADMLRHVVVLITQH  HVVVLITQH      0.6000       75.8       WB     8.00     Sequence
  DRB1_1501 118  VLSRLLNAPVSVSAT  VLSRLLNAP      0.5861       88.1       WB     8.00     Sequence
  DRB1_1501 112  RLEAQAVLSRLLNAP  VLSRLLNAP      0.5800       94.1       WB     8.00     Sequence
  DRB1_1501  98  VVQVIGNRPKIGWRR  VVQVIGNRP      0.5790       95.1       WB     8.00     Sequence
  DRB1_1501  92  YRVGNAVVQVIGNRP  VVQVIGNRP      0.5727      101.9       WB     8.00     Sequence
  DRB1_1501 108  IGWRRLEAQAVLSRL  GWRRLEAQA      0.5701      104.7       WB     8.00     Sequence
  DRB1_1501 107  KIGWRRLEAQAVLSR  GWRRLEAQA      0.5624      113.8       WB    16.00     Sequence
  DRB1_1501 105  RPKIGWRRLEAQAVL  GWRRLEAQA      0.5564      121.5       WB    16.00     Sequence
  DRB1_1501 106  PKIGWRRLEAQAVLS  GWRRLEAQA      0.5490      131.6       WB    16.00     Sequence
  DRB1_1501 109  GWRRLEAQAVLSRLL  GWRRLEAQA      0.5382      147.9       WB    16.00     Sequence
  DRB1_1501 104  NRPKIGWRRLEAQAV  KIGWRRLEA      0.5267      167.6       WB    16.00     Sequence
  DRB1_1501 111  RRLEAQAVLSRLLNA  EAQAVLSRL      0.5240      172.6       WB    16.00     Sequence
  DRB1_1501  86  LITQHGYRVGNAVVQ  ITQHGYRVG      0.5174      185.2       WB    16.00     Sequence
  DRB1_1501  87  ITQHGYRVGNAVVQV  ITQHGYRVG      0.4959      233.7       WB    16.00     Sequence
  DRB1_1501 103  GNRPKIGWRRLEAQA  KIGWRRLEA      0.4837      266.9       WB    32.00     Sequence
  DRB1_1501  91  GYRVGNAVVQVIGNR  AVVQVIGNR      0.4758      290.4       WB    32.00     Sequence
  DRB1_1501 110  WRRLEAQAVLSRLLN  EAQAVLSRL      0.4693      311.8       WB    32.00     Sequence
  DRB1_1501  73  GVSGADMLRHVVVLI  DMLRHVVVL      0.4638      330.8       WB    32.00     Sequence
  DRB1_1501  74  VSGADMLRHVVVLIT  DMLRHVVVL      0.4567      357.3       WB    32.00     Sequence
  DRB1_1501  72  QGVSGADMLRHVVVL  DMLRHVVVL      0.4544      366.1       WB    32.00     Sequence
  DRB1_1501  75  SGADMLRHVVVLITQ  DMLRHVVVL      0.4476      394.4       WB    32.00     Sequence
  DRB1_1501  88  TQHGYRVGNAVVQVI  HGYRVGNAV      0.4428      415.4       WB    32.00     Sequence
  DRB1_1501 119  LSRLLNAPVSVSATT  LSRLLNAPV      0.4385      435.2       WB    32.00     Sequence
  DRB1_1501  43  AVHALCDAVLSAAGL  AVHALCDAV      0.4181      542.7             32.00     Sequence
  DRB1_1501 142  RGEGLAAIATALVVS  GLAAIATAL      0.4154      558.4             32.00     Sequence
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DRB1_1501  102  IGNRPKIGWRRLEAQ  KIGWRRLEA      0.4151       560.3            32.00     Sequence
DRB1_1501   19  RPCWLVGLLFPSADG  LVGLLFPSA      0.4140       566.7            32.00     Sequence
DRB1_1501   18  GRPCWLVGLLFPSAD  LVGLLFPSA      0.4091       597.8            32.00     Sequence
DRB1_1501  141  GRGEGLAAIATALVV  GLAAIATAL      0.4083       603.0            32.00     Sequence
DRB1_1501   89  QHGYRVGNAVVQVIG  HGYRVGNAV      0.4071       610.7            32.00     Sequence
DRB1_1501   17  PGRPCWLVGLLFPSA  LVGLLFPSA      0.3988       668.4            32.00     Sequence
DRB1_1501   99  VQVIGNRPKIGWRRL  QVIGNRPKI      0.3978       675.9            32.00     Sequence
DRB1_1501   42  VAVHALCDAVLSAAG  AVHALCDAV      0.3966       684.4            32.00     Sequence
DRB1_1501  143  GEGLAAIATALVVSL  GLAAIATAL      0.3955       692.3            32.00     Sequence
DRB1_1501   40  GDVAVHALCDAVLSA  AVHALCDAV      0.3938       705.3            32.00     Sequence
DRB1_1501   44  VHALCDAVLSAAGLG  AVLSAAGLG      0.3926       714.6            32.00     Sequence
DRB1_1501  139  LTGRGEGLAAIATAL  EGLAAIATA      0.3901       734.6            32.00     Sequence
DRB1_1501   90  HGYRVGNAVVQVIGN  GYRVGNAVV      0.3899       736.3            32.00     Sequence
DRB1_1501   41  DVAVHALCDAVLSAA  AVHALCDAV      0.3875       755.5            32.00     Sequence
DRB1_1501  140  TGRGEGLAAIATALV  GLAAIATAL      0.3872       757.7            32.00     Sequence
DRB1_1501   20  PCWLVGLLFPSADGC  LVGLLFPSA      0.3844       780.9            50.00     Sequence
DRB1_1501  144  EGLAAIATALVVSLR  EGLAAIATA      0.3810       810.6            50.00     Sequence
DRB1_1501  100  QVIGNRPKIGWRRLE  VIGNRPKIG      0.3702       911.0            50.00     Sequence
DRB1_1501   45  HALCDAVLSAAGLGD  AVLSAAGLG      0.3671       942.1            50.00     Sequence
DRB1_1501   21  CWLVGLLFPSADGCA  LVGLLFPSA      0.3632       982.1            50.00     Sequence
DRB1_1501   46  ALCDAVLSAAGLGDI  CDAVLSAAG      0.3611      1005.5            50.00     Sequence
DRB1_1501   22  WLVGLLFPSADGCAG  LVGLLFPSA      0.3534      1092.6            50.00     Sequence
DRB1_1501  101  VIGNRPKIGWRRLEA  KIGWRRLEA      0.3508      1123.7            50.00     Sequence
DRB1_1501    1  NQLPRVGLGTDVHPI  RVGLGTDVH      0.3460      1183.9            50.00     Sequence
DRB1_1501  138  GLTGRGEGLAAIATA  LTGRGEGLA      0.3450      1196.5            50.00     Sequence
DRB1_1501    0  VNQLPRVGLGTDVHP  RVGLGTDVH      0.3340      1346.8            50.00     Sequence
DRB1_1501   16  EPGRPCWLVGLLFPS  WLVGLLFPS      0.3299      1409.2            50.00     Sequence
DRB1_1501    2  QLPRVGLGTDVHPIE  RVGLGTDVH      0.3237      1506.7            50.00     Sequence
DRB1_1501   39  DGDVAVHALCDAVLS  AVHALCDAV      0.3234      1511.0            50.00     Sequence
DRB1_1501   47  LCDAVLSAAGLGDIG  AVLSAAGLG      0.2996      1955.3            50.00     Sequence
DRB1_1501   23  LVGLLFPSADGCAGH  LVGLLFPSA      0.2959      2035.7            50.00     Sequence
DRB1_1501   38  SDGDVAVHALCDAVL  AVHALCDAV      0.2922      2118.0            50.00     Sequence
DRB1_1501    3  LPRVGLGTDVHPIEP  RVGLGTDVH      0.2791      2439.7            50.00     Sequence
DRB1_1501   48  CDAVLSAAGLGDIGE  AVLSAAGLG      0.2721      2631.4            50.00     Sequence
DRB1_1501   71  WQGVSGADMLRHVVV  GVSGADMLR      0.2703      2683.6            50.00     Sequence
DRB1_1501    4  PRVGLGTDVHPIEPG  RVGLGTDVH      0.2629      2907.1            50.00     Sequence
DRB1_1501  137  LGLTGRGEGLAAIAT  LTGRGEGLA      0.2622      2930.4            50.00     Sequence
DRB1_1501   15  IEPGRPCWLVGLLFP  RPCWLVGLL      0.2621      2933.2            50.00     Sequence
DRB1_1501  136  GLGLTGRGEGLAAIA  LTGRGEGLA      0.2564      3121.3            50.00     Sequence
DRB1_1501  135  DGLGLTGRGEGLAAI  LTGRGEGLA      0.2536      3217.6            50.00     Sequence
DRB1_1501   50  AVLSAAGLGDIGEVF  AVLSAAGLG      0.2455      3510.0            50.00     Sequence
DRB1_1501   70  RWQGVSGADMLRHVV  GVSGADMLR      0.2449      3531.8            50.00     Sequence
DRB1_1501   49  DAVLSAAGLGDIGEV  AVLSAAGLG      0.2420      3646.3            50.00     Sequence
DRB1_1501  120  SRLLNAPVSVSATTT  LLNAPVSVS      0.2387      3779.1            50.00     Sequence
DRB1_1501    5  RVGLGTDVHPIEPGR  RVGLGTDVH      0.2368      3856.7            50.00     Sequence
DRB1_1501   14  PIEPGRPCWLVGLLF  RPCWLVGLL      0.2319      4067.3            50.00     Sequence
DRB1_1501   69  PRWQGVSGADMLRHV  GVSGADMLR      0.2313      4092.5            50.00     Sequence
DRB1_1501   11  DVHPIEPGRPCWLVG  DVHPIEPGR      0.2269      4292.5            50.00     Sequence
DRB1_1501   13  HPIEPGRPCWLVGLL  RPCWLVGLL      0.2251      4378.0            50.00     Sequence
DRB1_1501   12  VHPIEPGRPCWLVGL  PGRPCWLVG      0.2190      4676.4            50.00     Sequence
DRB1_1501  133  TTDGLGLTGRGEGLA  LTGRGEGLA      0.2139      4941.4            50.00     Sequence
DRB1_1501  121  RLLNAPVSVSATTTD  LLNAPVSVS      0.2126      5011.0            50.00     Sequence
DRB1_1501   68  DPRWQGVSGADMLRH  GVSGADMLR      0.2125      5016.8            50.00     Sequence
DRB1_1501  134  TDGLGLTGRGEGLAA  LTGRGEGLA      0.2107      5113.6            50.00     Sequence
DRB1_1501   10  TDVHPIEPGRPCWLV  DVHPIEPGR      0.2021      5612.5            50.00     Sequence
DRB1_1501   51  VLSAAGLGDIGEVFG  GLGDIGEVF      0.2009      5689.2            50.00     Sequence
DRB1_1501   37  HSDGDVAVHALCDAV  AVHALCDAV      0.2005      5713.6            50.00     Sequence
DRB1_1501   52  LSAAGLGDIGEVFGV  GLGDIGEVF      0.1896      6427.8            50.00     Sequence
DRB1_1501  132  TTTDGLGLTGRGEGL  DGLGLTGRG      0.1866      6639.2            50.00     Sequence
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  DRB1_1501  58  GDIGEVFGVDDPRWQ  EVFGVDDPR      0.1819      6985.1            50.00     Sequence
  DRB1_1501   9  GTDVHPIEPGRPCWL  DVHPIEPGR      0.1818      6996.8            50.00     Sequence
  DRB1_1501  53  SAAGLGDIGEVFGVD  AGLGDIGEV      0.1746      7560.1            50.00     Sequence
  DRB1_1501  57  LGDIGEVFGVDDPRW  EVFGVDDPR      0.1720      7776.8            50.00     Sequence
  DRB1_1501  56  GLGDIGEVFGVDDPR  EVFGVDDPR      0.1602      8830.1            50.00     Sequence
  DRB1_1501 131  ATTTDGLGLTGRGEG  TDGLGLTGR      0.1591      8939.4            50.00     Sequence
  DRB1_1501   8  LGTDVHPIEPGRPCW  DVHPIEPGR      0.1581      9042.2            50.00     Sequence
  DRB1_1501  59  DIGEVFGVDDPRWQG  EVFGVDDPR      0.1576      9090.2            50.00     Sequence
  DRB1_1501 122  LLNAPVSVSATTTDG  LLNAPVSVS      0.1571      9135.1            50.00     Sequence
  DRB1_1501 130  SATTTDGLGLTGRGE  TDGLGLTGR      0.1559      9258.9            50.00     Sequence
  DRB1_1501   6  VGLGTDVHPIEPGRP  DVHPIEPGR      0.1543      9414.9            50.00     Sequence
  DRB1_1501  67  DDPRWQGVSGADMLR  RWQGVSGAD      0.1534      9513.7            50.00     Sequence
  DRB1_1501  61  GEVFGVDDPRWQGVS  EVFGVDDPR      0.1518      9677.7            50.00     Sequence
  DRB1_1501  55  AGLGDIGEVFGVDDP  GLGDIGEVF      0.1515      9710.3            50.00     Sequence
  DRB1_1501  60  IGEVFGVDDPRWQGV  EVFGVDDPR      0.1503      9837.1            50.00     Sequence
  DRB1_1501   7  GLGTDVHPIEPGRPC  DVHPIEPGR      0.1485     10023.2            50.00     Sequence
  DRB1_1501  54  AAGLGDIGEVFGVDD  GLGDIGEVF      0.1473     10162.6            50.00     Sequence
  DRB1_1501  32  DGCAGHSDGDVAVHA  DGCAGHSDG      0.1449     10422.4            50.00     Sequence
  DRB1_1501  31  ADGCAGHSDGDVAVH  GCAGHSDGD      0.1411     10866.8            50.00     Sequence
  DRB1_1501  24  VGLLFPSADGCAGHS  GLLFPSADG      0.1400     10996.0            50.00     Sequence
  DRB1_1501 123  LNAPVSVSATTTDGL  APVSVSATT      0.1339     11740.3            50.00     Sequence
  DRB1_1501  62  EVFGVDDPRWQGVSG  EVFGVDDPR      0.1316     12039.6            50.00     Sequence
  DRB1_1501 124  NAPVSVSATTTDGLG  APVSVSATT      0.1299     12266.5            50.00     Sequence
  DRB1_1501 128  SVSATTTDGLGLTGR  TDGLGLTGR      0.1278     12550.7            50.00     Sequence
  DRB1_1501 125  APVSVSATTTDGLGL  APVSVSATT      0.1255     12860.4            50.00     Sequence
  DRB1_1501  25  GLLFPSADGCAGHSD  GLLFPSADG      0.1246     12992.6            50.00     Sequence
  DRB1_1501 129  VSATTTDGLGLTGRG  TDGLGLTGR      0.1243     13024.1            50.00     Sequence
  DRB1_1501  66  VDDPRWQGVSGADML  RWQGVSGAD      0.1209     13521.3            50.00     Sequence
  DRB1_1501  26  LLFPSADGCAGHSDG  LLFPSADGC      0.1193     13759.1            50.00     Sequence
  DRB1_1501  30  SADGCAGHSDGDVAV  DGCAGHSDG      0.1188     13822.2            50.00     Sequence
  DRB1_1501  29  PSADGCAGHSDGDVA  DGCAGHSDG      0.1180     13941.3            50.00     Sequence
  DRB1_1501  33  GCAGHSDGDVAVHAL  HSDGDVAVH      0.1153     14353.4            50.00     Sequence
  DRB1_1501  34  CAGHSDGDVAVHALC  HSDGDVAVH      0.1131     14700.7            50.00     Sequence
  DRB1_1501 127  VSVSATTTDGLGLTG  SVSATTTDG      0.1113     14995.6            50.00     Sequence
  DRB1_1501  65  GVDDPRWQGVSGADM  RWQGVSGAD      0.1076     15614.7            50.00     Sequence
  DRB1_1501  35  AGHSDGDVAVHALCD  HSDGDVAVH      0.1041     16208.6            50.00     Sequence
  DRB1_1501  28  FPSADGCAGHSDGDV  DGCAGHSDG      0.1040     16222.8            50.00     Sequence
  DRB1_1501  36  GHSDGDVAVHALCDA  HSDGDVAVH      0.1029     16424.5            50.00     Sequence
  DRB1_1501  63  VFGVDDPRWQGVSGA  VFGVDDPRW      0.1006     16834.9            50.00     Sequence
  DRB1_1501 126  PVSVSATTTDGLGLT  PVSVSATTT      0.0980     17317.5            50.00     Sequence
  DRB1_1501  64  FGVDDPRWQGVSGAD  DPRWQGVSG      0.0872     19472.5            50.00     Sequence
  DRB1_1501  27  LFPSADGCAGHSDGD  PSADGCAGH      0.0843     20074.9            50.00     Sequence
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Allele: DRB1_1501. Number of high binders 13. Number of weak binders 29. Number of peptides 145

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    Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB3_0101  58  GDIGEVFGVDDPRWQ  FGVDDPRWQ      0.6141        65.0       WB    0.80     Sequence
  DRB3_0101  59  DIGEVFGVDDPRWQG  FGVDDPRWQ      0.5920        82.6       WB    2.00     Sequence
  DRB3_0101  60  IGEVFGVDDPRWQGV  FGVDDPRWQ      0.5765        97.7       WB    2.00     Sequence
  DRB3_0101  61  GEVFGVDDPRWQGVS  FGVDDPRWQ      0.5436       139.4       WB    2.00     Sequence
  DRB3_0101  62  EVFGVDDPRWQGVSG  FGVDDPRWQ      0.5160       188.1       WB    4.00     Sequence
  DRB3_0101  63  VFGVDDPRWQGVSGA  FGVDDPRWQ      0.5010       221.2       WB    4.00     Sequence
  DRB3_0101  64  FGVDDPRWQGVSGAD  FGVDDPRWQ      0.4443       408.5       WB    8.00     Sequence
  DRB3_0101  73  GVSGADMLRHVVVLI  MLRHVVVLI      0.3645       968.7             16.00     Sequence
  DRB3_0101  74  VSGADMLRHVVVLIT  MLRHVVVLI      0.3517      1112.3             16.00     Sequence
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DRB3_0101	75	SGADMLRHVVVLITQ	MLRHVVVLI	0.3284	1431.3	16.00	Sequence
DRB3_0101	88	TQHGYRVGNAVVQVI	VGNAVVQVI	0.3213	1546.7	16.00	Sequence
DRB3_0101	76	GADMLRHVVVLITQH	MLRHVVVLI	0.3055	1834.3	16.00	Sequence
DRB3_0101	89	QHGYRVGNAVVQVIG	VGNAVVQVI	0.3044	1856.2	16.00	Sequence
DRB3_0101	78	DMLRHVVVLITQHGY	MLRHVVVLI	0.3018	1909.7	16.00	Sequence
DRB3_0101	90	HGYRVGNAVVQVIGN	VGNAVVQVI	0.2912	2140.9	32.00	Sequence
DRB3_0101	77	ADMLRHVVVLITQHG	MLRHVVVLI	0.2905	2158.3	32.00	Sequence
DRB3_0101	52	LSAAGLGDIGEVFGV	GLGDIGEVF	0.2863	2256.7	32.00	Sequence
DRB3_0101	79	MLRHVVVLITQHGYR	MLRHVVVLI	0.2785	2457.7	32.00	Sequence
DRB3_0101	53	SAAGLGDIGEVFGVD	GLGDIGEVF	0.2773	2487.3	32.00	Sequence
DRB3_0101	91	GYRVGNAVVQVIGNR	VGNAVVQVI	0.2710	2664.7	32.00	Sequence
DRB3_0101	50	AVLSAAGLGDIGEVF	GLGDIGEVF	0.2669	2785.3	32.00	Sequence
DRB3_0101	54	AAGLGDIGEVFGVDD	GLGDIGEVF	0.2594	3021.5	32.00	Sequence
DRB3_0101	51	VLSAAGLGDIGEVFG	GLGDIGEVF	0.2588	3040.4	32.00	Sequence
DRB3_0101	55	AGLGDIGEVFGVDDP	GLGDIGEVF	0.2582	3061.0	32.00	Sequence
DRB3_0101	92	YRVGNAVVQVIGNRP	VGNAVVQVI	0.2491	3378.1	32.00	Sequence
DRB3_0101	56	GLGDIGEVFGVDDPR	GLGDIGEVF	0.2467	3464.2	32.00	Sequence
DRB3_0101	116	QAVLSRLLNAPVSVS	LLNAPVSVS	0.2445	3550.1	32.00	Sequence
DRB3_0101	93	RVGNAVVQVIGNRPK	VGNAVVQVI	0.2402	3718.9	32.00	Sequence
DRB3_0101	105	RPKIGWRRLEAQAVL	WRRLEAQAV	0.2378	3814.1	32.00	Sequence
DRB3_0101	104	NRPKIGWRRLEAQAV	WRRLEAQAV	0.2326	4037.1	32.00	Sequence
DRB3_0101	40	GDVAVHALCDAVLSA	AVHALCDAV	0.2313	4093.5	32.00	Sequence
DRB3_0101	80	LRHVVVLITQHGYRV	VVLITQHGY	0.2270	4287.1	32.00	Sequence
DRB3_0101	41	DVAVHALCDAVLSAA	AVHALCDAV	0.2248	4390.4	32.00	Sequence
DRB3_0101	106	PKIGWRRLEAQAVLS	WRRLEAQAV	0.2237	4444.3	32.00	Sequence
DRB3_0101	117	AVLSRLLNAPVSVSA	LLNAPVSVS	0.2234	4459.7	32.00	Sequence
DRB3_0101	94	VGNAVVQVIGNRPKI	VGNAVVQVI	0.2087	5225.5	32.00	Sequence
DRB3_0101	81	RHVVVLITQHGYRVG	LITQHGYRV	0.2080	5265.3	32.00	Sequence
DRB3_0101	42	VAVHALCDAVLSAAG	AVHALCDAV	0.2078	5276.2	32.00	Sequence
DRB3_0101	118	VLSRLLNAPVSVSAT	LLNAPVSVS	0.2047	5460.8	50.00	Sequence
DRB3_0101	82	HVVVLITQHGYRVGN	LITQHGYRV	0.2045	5469.5	50.00	Sequence
DRB3_0101	10	TDVHPIEPGRPCWLV	IEPGRPCWL	0.1996	5765.7	50.00	Sequence
DRB3_0101	12	VHPIEPGRPCWLVGL	IEPGRPCWL	0.1976	5893.8	50.00	Sequence
DRB3_0101	107	KIGWRRLEAQAVLSR	WRRLEAQAV	0.1967	5950.4	50.00	Sequence
DRB3_0101	84	VVLITQHGYRVGNAV	LITQHGYRV	0.1953	6040.5	50.00	Sequence
DRB3_0101	43	AVHALCDAVLSAAGL	AVHALCDAV	0.1951	6054.2	50.00	Sequence
DRB3_0101	39	DGDVAVHALCDAVLS	AVHALCDAV	0.1951	6056.4	50.00	Sequence
DRB3_0101	87	ITQHGYRVGNAVVQV	RVGNAVVQV	0.1914	6303.4	50.00	Sequence
DRB3_0101	83	VVVLITQHGYRVGNA	LITQHGYRV	0.1912	6315.4	50.00	Sequence
DRB3_0101	115	AQAVLSRLLNAPVSV	RLLNAPVSV	0.1899	6408.0	50.00	Sequence
DRB3_0101	11	DVHPIEPGRPCWLVG	IEPGRPCWL	0.1894	6441.3	50.00	Sequence
DRB3_0101	13	HPIEPGRPCWLVGLL	IEPGRPCWL	0.1868	6622.6	50.00	Sequence
DRB3_0101	119	LSRLLNAPVSVSATT	LLNAPVSVS	0.1839	6839.8	50.00	Sequence
DRB3_0101	14	PIEPGRPCWLVGLLF	IEPGRPCWL	0.1837	6854.7	50.00	Sequence
DRB3_0101	38	SDGDVAVHALCDAVL	AVHALCDAV	0.1826	6935.9	50.00	Sequence
DRB3_0101	108	IGWRRLEAQAVLSRL	WRRLEAQAV	0.1825	6937.5	50.00	Sequence
DRB3_0101	15	IEPGRPCWLVGLLFP	IEPGRPCWL	0.1817	6998.8	50.00	Sequence
DRB3_0101	37	HSDGDVAVHALCDAV	AVHALCDAV	0.1810	7053.9	50.00	Sequence
DRB3_0101	33	GCAGHSDGDVAVHAL	GHSDGDVAV	0.1807	7078.3	50.00	Sequence
DRB3_0101	32	DGCAGHSDGDVAVHA	GHSDGDVAV	0.1793	7183.6	50.00	Sequence
DRB3_0101	34	CAGHSDGDVAVHALC	GHSDGDVAV	0.1780	7284.5	50.00	Sequence
DRB3_0101	109	GWRRLEAQAVLSRLL	WRRLEAQAV	0.1767	7387.9	50.00	Sequence
DRB3_0101	110	WRRLEAQAVLSRLLN	WRRLEAQAV	0.1738	7622.6	50.00	Sequence
DRB3_0101	120	SRLLNAPVSVSATTT	LLNAPVSVS	0.1734	7661.5	50.00	Sequence
DRB3_0101	35	AGHSDGDVAVHALCD	GHSDGDVAV	0.1697	7975.7	50.00	Sequence
DRB3_0101	85	VLITQHGYRVGNAVV	LITQHGYRV	0.1686	8070.4	50.00	Sequence
DRB3_0101	72	QGVSGADMLRHVVVL	SGADMLRHV	0.1673	8183.8	50.00	Sequence
DRB3_0101	36	GHSDGDVAVHALCDA	GHSDGDVAV	0.1670	8205.0	50.00	Sequence
DRB3_0101	9	GTDVHPIEPGRPCWL	IEPGRPCWL	0.1664	8258.2	50.00	Sequence

DRB3_0101	121	RLLNAPVSVSATTTD	LLNAPVSVS	0.1654	8351.6	50.00	Sequence
DRB3_0101	16	EPGRPCWLVGLLFPS	WLVGLLFPS	0.1604	8814.0	50.00	Sequence
DRB3_0101	2	QLPRVGLGTDVHPIE	GLGTDVHPI	0.1598	8869.6	50.00	Sequence
DRB3_0101	86	LITQHGYRVGNAVVQ	LITQHGYRV	0.1582	9026.7	50.00	Sequence
DRB3_0101	69	PRWQGVSGADMLRHV	SGADMLRHV	0.1575	9096.6	50.00	Sequence
DRB3_0101	31	ADGCAGHSDGDVAVH	GHSDGDVAV	0.1559	9259.1	50.00	Sequence
DRB3_0101	70	RWQGVSGADMLRHVV	SGADMLRHV	0.1546	9384.0	50.00	Sequence
DRB3_0101	44	VHALCDAVLSAAGLG	ALCDAVLSA	0.1525	9598.0	50.00	Sequence
DRB3_0101	3	LPRVGLGTDVHPIEP	GLGTDVHPI	0.1517	9684.5	50.00	Sequence
DRB3_0101	71	WQGVSGADMLRHVVV	SGADMLRHV	0.1517	9685.6	50.00	Sequence
DRB3_0101	57	LGDIGEVFGVDDPRW	GDIGEVFGV	0.1515	9711.2	50.00	Sequence
DRB3_0101	46	ALCDAVLSAAGLGDI	LSAAGLGDI	0.1514	9717.7	50.00	Sequence
DRB3_0101	30	SADGCAGHSDGDVAV	GHSDGDVAV	0.1509	9768.8	50.00	Sequence
DRB3_0101	122	LLNAPVSVSATTTDG	LLNAPVSVS	0.1499	9881.5	50.00	Sequence
DRB3_0101	143	GEGLAAIATALVVSL	IATALVVSL	0.1480	10076.7	50.00	Sequence
DRB3_0101	18	GRPCWLVGLLFPSAD	WLVGLLFPS	0.1439	10540.1	50.00	Sequence
DRB3_0101	141	GRGEGLAAIATALVV	LAAIATALV	0.1411	10861.8	50.00	Sequence
DRB3_0101	126	PVSVSATTTDGLGLT	TTTDGLGLT	0.1407	10906.8	50.00	Sequence
DRB3_0101	4	PRVGLGTDVHPIEPG	GLGTDVHPI	0.1405	10935.8	50.00	Sequence
DRB3_0101	17	PGRPCWLVGLLFPSA	WLVGLLFPS	0.1378	11257.5	50.00	Sequence
DRB3_0101	144	EGLAAIATALVVSLR	IATALVVSL	0.1358	11505.9	50.00	Sequence
DRB3_0101	140	TGRGEGLAAIATALV	LAAIATALV	0.1326	11904.3	50.00	Sequence
DRB3_0101	22	WLVGLLFPSADGCAG	WLVGLLFPS	0.1324	11939.1	50.00	Sequence
DRB3_0101	19	RPCWLVGLLFPSADG	WLVGLLFPS	0.1309	12135.4	50.00	Sequence
DRB3_0101	127	VSVSATTTDGLGLTG	TTTDGLGLT	0.1306	12167.3	50.00	Sequence
DRB3_0101	45	HALCDAVLSAAGLGD	ALCDAVLSA	0.1294	12332.5	50.00	Sequence
DRB3_0101	20	PCWLVGLLFPSADGC	VGLLFPSAD	0.1289	12400.3	50.00	Sequence
DRB3_0101	5	RVGLGTDVHPIEPGR	GLGTDVHPI	0.1282	12487.8	50.00	Sequence
DRB3_0101	1	NQLPRVGLGTDVHPI	GLGTDVHPI	0.1280	12519.1	50.00	Sequence
DRB3_0101	21	CWLVGLLFPSADGCA	WLVGLLFPS	0.1265	12728.3	50.00	Sequence
DRB3_0101	142	RGEGLAAIATALVVS	LAAIATALV	0.1226	13276.9	50.00	Sequence
DRB3_0101	128	SVSATTTDGLGLTGR	TTTDGLGLT	0.1196	13711.5	50.00	Sequence
DRB3_0101	66	VDDPRWQGVSGADML	QGVSGADML	0.1166	14164.1	50.00	Sequence
DRB3_0101	49	DAVLSAAGLGDIGEV	AGLGDIGEV	0.1163	14211.9	50.00	Sequence
DRB3_0101	7	GLGTDVHPIEPGRPC	GLGTDVHPI	0.1082	15510.2	50.00	Sequence
DRB3_0101	6	VGLGTDVHPIEPGRP	GLGTDVHPI	0.1080	15544.9	50.00	Sequence
DRB3_0101	68	DPRWQGVSGADMLRH	QGVSGADML	0.1061	15865.3	50.00	Sequence
DRB3_0101	67	DDPRWQGVSGADMLR	QGVSGADML	0.1058	15913.6	50.00	Sequence
DRB3_0101	23	LVGLLFPSADGCAGH	VGLLFPSAD	0.1039	16252.0	50.00	Sequence
DRB3_0101	129	VSATTTDGLGLTGRG	TTTDGLGLT	0.1012	16730.3	50.00	Sequence
DRB3_0101	95	GNAVVQVIGNRPKIG	VIGNRPKIG	0.0984	17233.6	50.00	Sequence
DRB3_0101	24	VGLLFPSADGCAGHS	VGLLFPSAD	0.0980	17314.9	50.00	Sequence
DRB3_0101	96	NAVVQVIGNRPKIGW	VIGNRPKIG	0.0975	17413.9	50.00	Sequence
DRB3_0101	65	GVDDPRWQGVSGADM	WQGVSGADM	0.0968	17543.8	50.00	Sequence
DRB3_0101	47	LCDAVLSAAGLGDIG	LSAAGLGDI	0.0964	17616.1	50.00	Sequence
DRB3_0101	48	CDAVLSAAGLGDIGE	LSAAGLGDI	0.0903	18828.2	50.00	Sequence
DRB3_0101	113	LEAQAVLSRLLNAPV	LSRLLNAPV	0.0889	19116.6	50.00	Sequence
DRB3_0101	111	RRLEAQAVLSRLLNA	AQAVLSRLL	0.0888	19121.5	50.00	Sequence
DRB3_0101	114	EAQAVLSRLLNAPVS	AQAVLSRLL	0.0886	19161.1	50.00	Sequence
DRB3_0101	97	AVVQVIGNRPKIGWR	VIGNRPKIG	0.0881	19277.5	50.00	Sequence
DRB3_0101	29	PSADGCAGHSDGDVA	CAGHSDGDV	0.0861	19695.6	50.00	Sequence
DRB3_0101	123	LNAPVSVSATTTDGL	VSATTTDGL	0.0854	19854.6	50.00	Sequence
DRB3_0101	28	FPSADGCAGHSDGDV	CAGHSDGDV	0.0845	20037.4	50.00	Sequence
DRB3_0101	98	VVQVIGNRPKIGWRR	VIGNRPKIG	0.0825	20486.8	50.00	Sequence
DRB3_0101	25	GLLFPSADGCAGHSD	LLFPSADGC	0.0811	20795.4	50.00	Sequence
DRB3_0101	124	NAPVSVSATTTDGLG	VSATTTDGL	0.0789	21281.2	50.00	Sequence
DRB3_0101	112	RLEAQAVLSRLLNAP	AQAVLSRLL	0.0783	21426.3	50.00	Sequence
DRB3_0101	130	SATTTDGLGLTGRGE	TTTDGLGLT	0.0761	21955.7	50.00	Sequence
DRB3_0101	100	QVIGNRPKIGWRRLE	VIGNRPKIG	0.0751	22185.7	50.00	Sequence

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  DRB3_0101  125  APVSVSATTTDGLGL  VSATTTDGL       0.0750      22210.2             50.00     Sequence
  DRB3_0101  139  LTGRGEGLAAIATAL  GLAAIATAL       0.0726      22790.0             50.00     Sequence
  DRB3_0101  101  VIGNRPKIGWRRLEA  VIGNRPKIG       0.0717      23006.1             50.00     Sequence
  DRB3_0101  135  DGLGLTGRGEGLAAI  GRGEGLAAI       0.0716      23049.4             50.00     Sequence
  DRB3_0101  131  ATTTDGLGLTGRGEG  TTTDGLGLT       0.0710      23204.8             50.00     Sequence
  DRB3_0101  136  GLGLTGRGEGLAAIA  GRGEGLAAI       0.0693      23627.9             50.00     Sequence
  DRB3_0101  138  GLTGRGEGLAAIATA  GRGEGLAAI       0.0671      24203.4             50.00     Sequence
  DRB3_0101  137  LGLTGRGEGLAAIAT  GRGEGLAAI       0.0668      24278.6             50.00     Sequence
  DRB3_0101  132  TTTDGLGLTGRGEGL  TTTDGLGLT       0.0659      24506.4             50.00     Sequence
  DRB3_0101   99  VQVIGNRPKIGWRRL  VIGNRPKIG       0.0650      24746.2             50.00     Sequence
  DRB3_0101  102  IGNRPKIGWRRLEAQ  IGNRPKIGW       0.0598      26170.5             50.00     Sequence
  DRB3_0101    0  VNQLPRVGLGTDVHP  PRVGLGTDV       0.0589      26439.4             50.00     Sequence
  DRB3_0101    8  LGTDVHPIEPGRPCW  LGTDVHPIE       0.0584      26586.3             50.00     Sequence
  DRB3_0101   26  LLFPSADGCAGHSDG  LLFPSADGC       0.0491      29387.7             50.00     Sequence
  DRB3_0101  103  GNRPKIGWRRLEAQA  IGWRRLEAQ       0.0462      30320.8             50.00     Sequence
  DRB3_0101   27  LFPSADGCAGHSDGD  FPSADGCAG       0.0385      32975.5             50.00     Sequence
  DRB3_0101  134  TDGLGLTGRGEGLAA  LTGRGEGLA       0.0369      33546.2             50.00     Sequence
  DRB3_0101  133  TTDGLGLTGRGEGLA  LTGRGEGLA       0.0352      34155.3             50.00     Sequence
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Allele: DRB3_0101. Number of high binders 0. Number of weak binders 7. Number of peptides 145

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     Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random      Identity
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  DRB4_0101   80  LRHVVVLITQHGYRV  LRHVVVLIT       0.7230        20.0       SB     1.00     Sequence
  DRB4_0101   79  MLRHVVVLITQHGYR  LRHVVVLIT       0.7219        20.3       SB     1.00     Sequence
  DRB4_0101   78  DMLRHVVVLITQHGY  LRHVVVLIT       0.7169        21.4       SB     2.00     Sequence
  DRB4_0101   77  ADMLRHVVVLITQHG  LRHVVVLIT       0.6963        26.7       SB     2.00     Sequence
  DRB4_0101   76  GADMLRHVVVLITQH  LRHVVVLIT       0.6656        37.3       SB     4.00     Sequence
  DRB4_0101   81  RHVVVLITQHGYRVG  VVLITQHGY       0.6650        37.5       SB     4.00     Sequence
  DRB4_0101   82  HVVVLITQHGYRVGN  VVVLITQHG       0.6635        38.1       SB     4.00     Sequence
  DRB4_0101   75  SGADMLRHVVVLITQ  LRHVVVLIT       0.6372        50.7       WB     4.00     Sequence
  DRB4_0101   74  VSGADMLRHVVVLIT  LRHVVVLIT       0.6205        60.7       WB     8.00     Sequence
  DRB4_0101   83  VVVLITQHGYRVGNA  VVLITQHGY       0.6143        64.9       WB     8.00     Sequence
  DRB4_0101  105  RPKIGWRRLEAQAVL  IGWRRLEAQ       0.5713       103.4       WB     8.00     Sequence
  DRB4_0101  106  PKIGWRRLEAQAVLS  KIGWRRLEA       0.5626       113.6       WB    16.00     Sequence
  DRB4_0101  104  NRPKIGWRRLEAQAV  WRRLEAQAV       0.5516       127.9       WB    16.00     Sequence
  DRB4_0101  115  AQAVLSRLLNAPVSV  AQAVLSRLL       0.5443       138.5       WB    16.00     Sequence
  DRB4_0101   84  VVLITQHGYRVGNAV  VVLITQHGY       0.5436       139.5       WB    16.00     Sequence
  DRB4_0101  114  EAQAVLSRLLNAPVS  QAVLSRLLN       0.5285       164.2       WB    16.00     Sequence
  DRB4_0101  113  LEAQAVLSRLLNAPV  AQAVLSRLL       0.5201       180.0       WB    16.00     Sequence
  DRB4_0101  107  KIGWRRLEAQAVLSR  RRLEAQAVL       0.5175       185.1       WB    16.00     Sequence
  DRB4_0101  103  GNRPKIGWRRLEAQA  IGWRRLEAQ       0.5157       188.7       WB    16.00     Sequence
  DRB4_0101  116  QAVLSRLLNAPVSVS  QAVLSRLLN       0.4939       239.0       WB    32.00     Sequence
  DRB4_0101   73  GVSGADMLRHVVVLI  ADMLRHVVV       0.4901       248.9       WB    32.00     Sequence
  DRB4_0101  111  RRLEAQAVLSRLLNA  RRLEAQAVL       0.4820       271.7       WB    32.00     Sequence
  DRB4_0101  108  IGWRRLEAQAVLSRL  RRLEAQAVL       0.4783       282.9       WB    32.00     Sequence
  DRB4_0101  109  GWRRLEAQAVLSRLL  RRLEAQAVL       0.4782       283.0       WB    32.00     Sequence
  DRB4_0101  110  WRRLEAQAVLSRLLN  WRRLEAQAV       0.4766       288.0       WB    32.00     Sequence
  DRB4_0101  102  IGNRPKIGWRRLEAQ  IGWRRLEAQ       0.4755       291.6       WB    32.00     Sequence
  DRB4_0101  117  AVLSRLLNAPVSVSA  AVLSRLLNA       0.4491       387.9       WB    32.00     Sequence
  DRB4_0101   94  VGNAVVQVIGNRPKI  VQVIGNRPK       0.4454       403.8       WB    32.00     Sequence
  DRB4_0101   72  QGVSGADMLRHVVVL  ADMLRHVVV       0.4447       406.5       WB    32.00     Sequence
  DRB4_0101  112  RLEAQAVLSRLLNAP  AQAVLSRLL       0.4411       423.1       WB    32.00     Sequence
  DRB4_0101   93  RVGNAVVQVIGNRPK  VQVIGNRPK       0.4403       426.6       WB    32.00     Sequence
  DRB4_0101   71  WQGVSGADMLRHVVV  ADMLRHVVV       0.4316       468.7       WB    32.00     Sequence
  DRB4_0101   95  GNAVVQVIGNRPKIG  VQVIGNRPK       0.4157       556.5             32.00     Sequence
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DRB4_0101   92  YRVGNAVVQVIGNRP  VGNAVVQVI       0.4148       562.1              32.00     Sequence
DRB4_0101   97  AVVQVIGNRPKIGWR  VQVIGNRPK       0.4129       573.7              32.00     Sequence
DRB4_0101   96  NAVVQVIGNRPKIGW  VQVIGNRPK       0.4112       584.6              32.00     Sequence
DRB4_0101   91  GYRVGNAVVQVIGNR  VGNAVVQVI       0.3984       671.6              50.00     Sequence
DRB4_0101   98  VVQVIGNRPKIGWRR  VQVIGNRPK       0.3886       746.6              50.00     Sequence
DRB4_0101  101  VIGNRPKIGWRRLEA  KIGWRRLEA       0.3863       765.4              50.00     Sequence
DRB4_0101   99  VQVIGNRPKIGWRRL  VQVIGNRPK       0.3832       791.2              50.00     Sequence
DRB4_0101   70  RWQGVSGADMLRHVV  WQGVSGADM       0.3812       809.0              50.00     Sequence
DRB4_0101  118  VLSRLLNAPVSVSAT  LSRLLNAPV       0.3790       827.9              50.00     Sequence
DRB4_0101   69  PRWQGVSGADMLRHV  WQGVSGADM       0.3753       861.9              50.00     Sequence
DRB4_0101   90  HGYRVGNAVVQVIGN  GYRVGNAVV       0.3718       894.9              50.00     Sequence
DRB4_0101   19  RPCWLVGLLFPSADG  LVGLLFPSA       0.3685       927.2              50.00     Sequence
DRB4_0101   20  PCWLVGLLFPSADGC  LVGLLFPSA       0.3672       941.3              50.00     Sequence
DRB4_0101  141  GRGEGLAAIATALVV  LAAIATALV       0.3634       980.7              50.00     Sequence
DRB4_0101   68  DPRWQGVSGADMLRH  WQGVSGADM       0.3603      1013.4              50.00     Sequence
DRB4_0101   40  GDVAVHALCDAVLSA  VHALCDAVL       0.3603      1014.2              50.00     Sequence
DRB4_0101   21  CWLVGLLFPSADGCA  LVGLLFPSA       0.3596      1021.4              50.00     Sequence
DRB4_0101  140  TGRGEGLAAIATALV  LAAIATALV       0.3585      1034.2              50.00     Sequence
DRB4_0101   89  QHGYRVGNAVVQVIG  VGNAVVQVI       0.3554      1068.7              50.00     Sequence
DRB4_0101  100  QVIGNRPKIGWRRLE  QVIGNRPKI       0.3552      1071.0              50.00     Sequence
DRB4_0101  142  RGEGLAAIATALVVS  LAAIATALV       0.3539      1086.4              50.00     Sequence
DRB4_0101   39  DGDVAVHALCDAVLS  VHALCDAVL       0.3536      1090.1              50.00     Sequence
DRB4_0101   67  DDPRWQGVSGADMLR  WQGVSGADM       0.3526      1102.3              50.00     Sequence
DRB4_0101   16  EPGRPCWLVGLLFPS  EPGRPCWLV       0.3522      1106.3              50.00     Sequence
DRB4_0101  143  GEGLAAIATALVVSL  LAAIATALV       0.3485      1151.3              50.00     Sequence
DRB4_0101   18  GRPCWLVGLLFPSAD  LVGLLFPSA       0.3470      1170.8              50.00     Sequence
DRB4_0101   88  TQHGYRVGNAVVQVI  VGNAVVQVI       0.3467      1174.6              50.00     Sequence
DRB4_0101   38  SDGDVAVHALCDAVL  VHALCDAVL       0.3466      1175.7              50.00     Sequence
DRB4_0101  119  LSRLLNAPVSVSATT  LSRLLNAPV       0.3394      1271.1              50.00     Sequence
DRB4_0101   22  WLVGLLFPSADGCAG  VGLLFPSAD       0.3393      1272.5              50.00     Sequence
DRB4_0101   42  VAVHALCDAVLSAAG  VHALCDAVL       0.3366      1310.7              50.00     Sequence
DRB4_0101    0  VNQLPRVGLGTDVHP  VNQLPRVGL       0.3348      1335.8              50.00     Sequence
DRB4_0101  144  EGLAAIATALVVSLR  LAAIATALV       0.3339      1349.0              50.00     Sequence
DRB4_0101   17  PGRPCWLVGLLFPSA  LVGLLFPSA       0.3315      1383.7              50.00     Sequence
DRB4_0101   66  VDDPRWQGVSGADML  WQGVSGADM       0.3291      1421.5              50.00     Sequence
DRB4_0101   65  GVDDPRWQGVSGADM  WQGVSGADM       0.3288      1425.5              50.00     Sequence
DRB4_0101   85  VLITQHGYRVGNAVV  VLITQHGYR       0.3268      1456.4              50.00     Sequence
DRB4_0101   41  DVAVHALCDAVLSAA  VHALCDAVL       0.3216      1541.4              50.00     Sequence
DRB4_0101   86  LITQHGYRVGNAVVQ  LITQHGYRV       0.3209      1552.5              50.00     Sequence
DRB4_0101   43  AVHALCDAVLSAAGL  VHALCDAVL       0.3171      1617.4              50.00     Sequence
DRB4_0101    4  PRVGLGTDVHPIEPG  RVGLGTDVH       0.3087      1772.2              50.00     Sequence
DRB4_0101   87  ITQHGYRVGNAVVQV  YRVGNAVVQ       0.3070      1804.1              50.00     Sequence
DRB4_0101   15  IEPGRPCWLVGLLFP  EPGRPCWLV       0.3051      1841.6              50.00     Sequence
DRB4_0101   11  DVHPIEPGRPCWLVG  VHPIEPGRP       0.3034      1876.5              50.00     Sequence
DRB4_0101   10  TDVHPIEPGRPCWLV  VHPIEPGRP       0.3003      1939.7              50.00     Sequence
DRB4_0101   12  VHPIEPGRPCWLVGL  VHPIEPGRP       0.2985      1978.1              50.00     Sequence
DRB4_0101   23  LVGLLFPSADGCAGH  GLLFPSADG       0.2921      2119.9              50.00     Sequence
DRB4_0101   44  VHALCDAVLSAAGLG  VHALCDAVL       0.2915      2133.9              50.00     Sequence
DRB4_0101   14  PIEPGRPCWLVGLLF  EPGRPCWLV       0.2880      2217.5              50.00     Sequence
DRB4_0101   56  GLGDIGEVFGVDDPR  LGDIGEVFG       0.2871      2238.3              50.00     Sequence
DRB4_0101    1  NQLPRVGLGTDVHPI  RVGLGTDVH       0.2862      2260.2              50.00     Sequence
DRB4_0101    6  VGLGTDVHPIEPGRP  VHPIEPGRP       0.2843      2305.9              50.00     Sequence
DRB4_0101    3  LPRVGLGTDVHPIEP  PRVGLGTDV       0.2838      2319.3              50.00     Sequence
DRB4_0101   57  LGDIGEVFGVDDPRW  LGDIGEVFG       0.2835      2328.0              50.00     Sequence
DRB4_0101   61  GEVFGVDDPRWQGVS  EVFGVDDPR       0.2805      2405.0              50.00     Sequence
DRB4_0101   13  HPIEPGRPCWLVGLL  EPGRPCWLV       0.2796      2427.9              50.00     Sequence
DRB4_0101    2  QLPRVGLGTDVHPIE  RVGLGTDVH       0.2794      2431.8              50.00     Sequence
DRB4_0101    5  RVGLGTDVHPIEPGR  RVGLGTDVH       0.2775      2483.9              50.00     Sequence
DRB4_0101  139  LTGRGEGLAAIATAL  GLAAIATAL       0.2728      2613.0              50.00     Sequence
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 DRB4_0101  60  IGEVFGVDDPRWQGV  EVFGVDDPR     0.2704    2680.3        50.00    Sequence
 DRB4_0101   9  GTDVHPIEPGRPCWL  VHPIEPGRP     0.2683    2742.0        50.00    Sequence
 DRB4_0101  37  HSDGDVAVHALCDAV  GDVAVHALC     0.2671    2778.0        50.00    Sequence
 DRB4_0101  55  AGLGDIGEVFGVDDP  LGDIGEVFG     0.2644    2862.3        50.00    Sequence
 DRB4_0101   8  LGTDVHPIEPGRPCW  VHPIEPGRP     0.2637    2883.4        50.00    Sequence
 DRB4_0101   7  GLGTDVHPIEPGRPC  VHPIEPGRP     0.2612    2960.7        50.00    Sequence
 DRB4_0101  58  GDIGEVFGVDDPRWQ  GEVFGVDDP     0.2564    3120.6        50.00    Sequence
 DRB4_0101  59  DIGEVFGVDDPRWQG  EVFGVDDPR     0.2559    3136.6        50.00    Sequence
 DRB4_0101  120  SRLLNAPVSVSATTT  SRLLNAPVS    0.2558    3139.5        50.00    Sequence
 DRB4_0101  24  VGLLFPSADGCAGHS  GLLFPSADG     0.2525    3255.9        50.00    Sequence
 DRB4_0101  48  CDAVLSAAGLGDIGE  DAVLSAAGL     0.2270    4288.8        50.00    Sequence
 DRB4_0101  64  FGVDDPRWQGVSGAD  PRWQGVSGA     0.2259    4340.6        50.00    Sequence
 DRB4_0101  121  RLLNAPVSVSATTTD  RLLNAPVSV    0.2206    4597.4        50.00    Sequence
 DRB4_0101  36  GHSDGDVAVHALCDA  VAVHALCDA     0.2189    4681.4        50.00    Sequence
 DRB4_0101  123  LNAPVSVSATTTDGL  APVSVSATT    0.2184    4706.3        50.00    Sequence
 DRB4_0101  125  APVSVSATTTDGLGL  APVSVSATT    0.2179    4733.9        50.00    Sequence
 DRB4_0101  124  NAPVSVSATTTDGLG  APVSVSATT    0.2163    4814.5        50.00    Sequence
 DRB4_0101  63  VFGVDDPRWQGVSGA  PRWQGVSGA     0.2158    4839.9        50.00    Sequence
 DRB4_0101  47  LCDAVLSAAGLGDIG  DAVLSAAGL     0.2145    4908.1        50.00    Sequence
 DRB4_0101  25  GLLFPSADGCAGHSD  GLLFPSADG     0.2114    5076.5        50.00    Sequence
 DRB4_0101  62  EVFGVDDPRWQGVSG  EVFGVDDPR     0.2043    5484.9        50.00    Sequence
 DRB4_0101  46  ALCDAVLSAAGLGDI  DAVLSAAGL     0.2016    5647.7        50.00    Sequence
 DRB4_0101  122  LLNAPVSVSATTTDG  APVSVSATT    0.1987    5823.9        50.00    Sequence
 DRB4_0101  54  AAGLGDIGEVFGVDD  LGDIGEVFG     0.1982    5857.6        50.00    Sequence
 DRB4_0101  45  HALCDAVLSAAGLGD  DAVLSAAGL     0.1977    5887.5        50.00    Sequence
 DRB4_0101  53  SAAGLGDIGEVFGVD  LGDIGEVFG     0.1936    6154.8        50.00    Sequence
 DRB4_0101  138  GLTGRGEGLAAIATA  EGLAAIATA    0.1871    6605.1        50.00    Sequence
 DRB4_0101  52  LSAAGLGDIGEVFGV  LGDIGEVFG     0.1825    6938.9        50.00    Sequence
 DRB4_0101  49  DAVLSAAGLGDIGEV  DAVLSAAGL     0.1711    7848.1        50.00    Sequence
 DRB4_0101  137  LGLTGRGEGLAAIAT  LGLTGRGEG    0.1628    8593.3        50.00    Sequence
 DRB4_0101  136  GLGLTGRGEGLAAIA  LGLTGRGEG    0.1584    9004.6        50.00    Sequence
 DRB4_0101  135  DGLGLTGRGEGLAAI  LGLTGRGEG    0.1565    9197.8        50.00    Sequence
 DRB4_0101  35  AGHSDGDVAVHALCD  GDVAVHALC     0.1522    9629.9        50.00    Sequence
 DRB4_0101  126  PVSVSATTTDGLGLT  VSATTTDGL    0.1522    9632.0        50.00    Sequence
 DRB4_0101  34  CAGHSDGDVAVHALC  GDVAVHALC     0.1502    9847.6        50.00    Sequence
 DRB4_0101  51  VLSAAGLGDIGEVFG  LGDIGEVFG     0.1477    10109.3       50.00    Sequence
 DRB4_0101  133  TTDGLGLTGRGEGLA  LGLTGRGEG    0.1356    11526.5       50.00    Sequence
 DRB4_0101  134  TDGLGLTGRGEGLAA  LGLTGRGEG    0.1297    12287.3       50.00    Sequence
 DRB4_0101  128  SVSATTTDGLGLTGR  VSATTTDGL    0.1289    12397.8       50.00    Sequence
 DRB4_0101  127  VSVSATTTDGLGLTG  VSATTTDGL    0.1236    13126.9       50.00    Sequence
 DRB4_0101  50  AVLSAAGLGDIGEVF  LSAAGLGDI     0.1193    13752.4       50.00    Sequence
 DRB4_0101  132  TTTDGLGLTGRGEGL  LGLTGRGEG    0.1188    13832.2       50.00    Sequence
 DRB4_0101  26  LLFPSADGCAGHSDG  LLFPSADGC     0.1155    14322.3       50.00    Sequence
 DRB4_0101  131  ATTTDGLGLTGRGEG  LGLTGRGEG    0.1117    14934.6       50.00    Sequence
 DRB4_0101  129  VSATTTDGLGLTGRG  VSATTTDGL    0.1110    15038.9       50.00    Sequence
 DRB4_0101  33  GCAGHSDGDVAVHAL  CAGHSDGDV     0.1065    15787.7       50.00    Sequence
 DRB4_0101  30  SADGCAGHSDGDVAV  SADGCAGHS     0.1004    16870.3       50.00    Sequence
 DRB4_0101  32  DGCAGHSDGDVAVHA  HSDGDVAVH     0.0974    17429.9       50.00    Sequence
 DRB4_0101  31  ADGCAGHSDGDVAVH  CAGHSDGDV     0.0956    17768.5       50.00    Sequence
 DRB4_0101  29  PSADGCAGHSDGDVA  CAGHSDGDV     0.0945    17979.1       50.00    Sequence
 DRB4_0101  130  SATTTDGLGLTGRGE  DGLGLTGRG    0.0875    19402.7       50.00    Sequence
 DRB4_0101  28  FPSADGCAGHSDGDV  CAGHSDGDV     0.0868    19537.7       50.00    Sequence
 DRB4_0101  27  LFPSADGCAGHSDGD  SADGCAGHS     0.0599    26144.7       50.00    Sequence
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Allele: DRB4_0101. Number of high binders 7. Number of weak binders 25. Number of peptides 145

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   Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB5_0101   81  RHVVVLITQHGYRVG  VLITQHGYR       0.6658        37.2        SB     8.00     Sequence
  DRB5_0101   82  HVVVLITQHGYRVGN  VLITQHGYR       0.6587        40.1        SB     8.00     Sequence
  DRB5_0101   80  LRHVVVLITQHGYRV  VLITQHGYR       0.6550        41.8        SB     8.00     Sequence
  DRB5_0101  109  GWRRLEAQAVLSRLL  WRRLEAQAV       0.6512        43.5        SB     8.00     Sequence
  DRB5_0101  108  IGWRRLEAQAVLSRL  WRRLEAQAV       0.6474        45.4        SB     8.00     Sequence
  DRB5_0101  110  WRRLEAQAVLSRLLN  WRRLEAQAV       0.6441        47.1        SB     8.00     Sequence
  DRB5_0101   83  VVVLITQHGYRVGNA  VLITQHGYR       0.6438        47.2        SB     8.00     Sequence
  DRB5_0101  107  KIGWRRLEAQAVLSR  WRRLEAQAV       0.6369        50.8        WB     8.00     Sequence
  DRB5_0101   84  VVLITQHGYRVGNAV  VLITQHGYR       0.6253        57.6        WB     8.00     Sequence
  DRB5_0101   97  AVVQVIGNRPKIGWR  VVQVIGNRP       0.6132        65.7        WB     8.00     Sequence
  DRB5_0101   96  NAVVQVIGNRPKIGW  VVQVIGNRP       0.6070        70.2        WB     8.00     Sequence
  DRB5_0101   95  GNAVVQVIGNRPKIG  VVQVIGNRP       0.6018        74.4        WB    16.00     Sequence
  DRB5_0101   79  MLRHVVVLITQHGYR  VLITQHGYR       0.5929        81.8        WB    16.00     Sequence
  DRB5_0101   85  VLITQHGYRVGNAVV  VLITQHGYR       0.5883        86.0        WB    16.00     Sequence
  DRB5_0101   94  VGNAVVQVIGNRPKI  VVQVIGNRP       0.5763        98.0        WB    16.00     Sequence
  DRB5_0101  106  PKIGWRRLEAQAVLS  WRRLEAQAV       0.5760        98.3        WB    16.00     Sequence
  DRB5_0101   98  VVQVIGNRPKIGWRR  VVQVIGNRP       0.5673       108.0        WB    16.00     Sequence
  DRB5_0101  111  RRLEAQAVLSRLLNA  LEAQAVLSR       0.5652       110.4        WB    16.00     Sequence
  DRB5_0101   93  RVGNAVVQVIGNRPK  VVQVIGNRP       0.5566       121.3        WB    16.00     Sequence
  DRB5_0101  118  VLSRLLNAPVSVSAT  RLLNAPVSV       0.5411       143.4        WB    16.00     Sequence
  DRB5_0101  117  AVLSRLLNAPVSVSA  LSRLLNAPV       0.5379       148.4        WB    16.00     Sequence
  DRB5_0101  116  QAVLSRLLNAPVSVS  LSRLLNAPV       0.5337       155.2        WB    16.00     Sequence
  DRB5_0101  115  AQAVLSRLLNAPVSV  LSRLLNAPV       0.5318       158.6        WB    16.00     Sequence
  DRB5_0101   92  YRVGNAVVQVIGNRP  VVQVIGNRP       0.5254       169.9        WB    16.00     Sequence
  DRB5_0101  112  RLEAQAVLSRLLNAP  LEAQAVLSR       0.5006       222.2        WB    32.00     Sequence
  DRB5_0101   99  VQVIGNRPKIGWRRL  VQVIGNRPK       0.4982       227.9        WB    32.00     Sequence
  DRB5_0101  105  RPKIGWRRLEAQAVL  WRRLEAQAV       0.4840       266.0        WB    32.00     Sequence
  DRB5_0101  119  LSRLLNAPVSVSATT  RLLNAPVSV       0.4831       268.3        WB    32.00     Sequence
  DRB5_0101   86  LITQHGYRVGNAVVQ  LITQHGYRV       0.4758       290.4        WB    32.00     Sequence
  DRB5_0101   73  GVSGADMLRHVVVLI  VSGADMLRH       0.4733       298.7        WB    32.00     Sequence
  DRB5_0101   70  RWQGVSGADMLRHVV  GVSGADMLR       0.4711       305.8        WB    32.00     Sequence
  DRB5_0101   71  WQGVSGADMLRHVVV  GVSGADMLR       0.4704       308.0        WB    32.00     Sequence
  DRB5_0101   91  GYRVGNAVVQVIGNR  YRVGNAVVQ       0.4693       311.8        WB    32.00     Sequence
  DRB5_0101   72  QGVSGADMLRHVVVL  GVSGADMLR       0.4680       316.0        WB    32.00     Sequence
  DRB5_0101  113  LEAQAVLSRLLNAPV  LSRLLNAPV       0.4615       339.3        WB    32.00     Sequence
  DRB5_0101  114  EAQAVLSRLLNAPVS  LSRLLNAPV       0.4605       342.9        WB    32.00     Sequence
  DRB5_0101   69  PRWQGVSGADMLRHV  GVSGADMLR       0.4544       366.4        WB    32.00     Sequence
  DRB5_0101   68  DPRWQGVSGADMLRH  GVSGADMLR       0.4415       421.2        WB    32.00     Sequence
  DRB5_0101   78  DMLRHVVVLITQHGY  RHVVVLITQ       0.4386       434.7        WB    32.00     Sequence
  DRB5_0101  104  NRPKIGWRRLEAQAV  WRRLEAQAV       0.4321       466.0        WB    32.00     Sequence
  DRB5_0101   89  QHGYRVGNAVVQVIG  YRVGNAVVQ       0.4203       529.7              32.00     Sequence
  DRB5_0101   88  TQHGYRVGNAVVQVI  YRVGNAVVQ       0.4203       529.7              32.00     Sequence
  DRB5_0101   74  VSGADMLRHVVVLIT  VSGADMLRH       0.4180       543.1              32.00     Sequence
  DRB5_0101   87  ITQHGYRVGNAVVQV  GYRVGNAVV       0.4052       623.4              50.00     Sequence
  DRB5_0101   90  HGYRVGNAVVQVIGN  YRVGNAVVQ       0.4031       638.2              50.00     Sequence
  DRB5_0101   77  ADMLRHVVVLITQHG  RHVVVLITQ       0.3998       661.1              50.00     Sequence
  DRB5_0101  120  SRLLNAPVSVSATTT  RLLNAPVSV       0.3985       670.4              50.00     Sequence
  DRB5_0101  100  QVIGNRPKIGWRRLE  VIGNRPKIG       0.3906       730.6              50.00     Sequence
  DRB5_0101   76  GADMLRHVVVLITQH  LRHVVVLIT       0.3783       834.0              50.00     Sequence
  DRB5_0101   75  SGADMLRHVVVLITQ  LRHVVVLIT       0.3579      1040.9              50.00     Sequence
  DRB5_0101   45  HALCDAVLSAAGLGD  VLSAAGLGD       0.3520      1108.8              50.00     Sequence
  DRB5_0101  101  VIGNRPKIGWRRLEA  VIGNRPKIG       0.3511      1120.0              50.00     Sequence
  DRB5_0101   41  DVAVHALCDAVLSAA  AVHALCDAV       0.3365      1311.3              50.00     Sequence
  DRB5_0101   46  ALCDAVLSAAGLGDI  VLSAAGLGD       0.3288      1425.4              50.00     Sequence
  DRB5_0101   67  DDPRWQGVSGADMLR  WQGVSGADM       0.3285      1430.2              50.00     Sequence
  DRB5_0101   43  AVHALCDAVLSAAGL  AVHALCDAV       0.3276      1443.4              50.00     Sequence
  DRB5_0101  121  RLLNAPVSVSATTTD  RLLNAPVSV       0.3241      1499.2              50.00     Sequence
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DRB5_0101   40  GDVAVHALCDAVLSA  AVHALCDAV       0.3235      1509.1              50.00     Sequence
DRB5_0101   42  VAVHALCDAVLSAAG  HALCDAVLS       0.3227      1522.0              50.00     Sequence
DRB5_0101   44  VHALCDAVLSAAGLG  HALCDAVLS       0.3181      1600.8              50.00     Sequence
DRB5_0101   47  LCDAVLSAAGLGDIG  VLSAAGLGD       0.3167      1624.1              50.00     Sequence
DRB5_0101   39  DGDVAVHALCDAVLS  AVHALCDAV       0.2950      2054.5              50.00     Sequence
DRB5_0101   19  RPCWLVGLLFPSADG  WLVGLLFPS       0.2928      2105.4              50.00     Sequence
DRB5_0101  102  IGNRPKIGWRRLEAQ  NRPKIGWRR       0.2907      2153.2              50.00     Sequence
DRB5_0101   48  CDAVLSAAGLGDIGE  AVLSAAGLG       0.2878      2220.2              50.00     Sequence
DRB5_0101    9  GTDVHPIEPGRPCWL  VHPIEPGRP       0.2865      2251.9              50.00     Sequence
DRB5_0101  103  GNRPKIGWRRLEAQA  NRPKIGWRR       0.2753      2544.1              50.00     Sequence
DRB5_0101   10  TDVHPIEPGRPCWLV  VHPIEPGRP       0.2740      2579.2              50.00     Sequence
DRB5_0101   20  PCWLVGLLFPSADGC  WLVGLLFPS       0.2735      2594.3              50.00     Sequence
DRB5_0101   49  DAVLSAAGLGDIGEV  AVLSAAGLG       0.2687      2730.0              50.00     Sequence
DRB5_0101   11  DVHPIEPGRPCWLVG  VHPIEPGRP       0.2619      2941.0              50.00     Sequence
DRB5_0101    8  LGTDVHPIEPGRPCW  VHPIEPGRP       0.2601      2997.8              50.00     Sequence
DRB5_0101   66  VDDPRWQGVSGADML  WQGVSGADM       0.2575      3084.2              50.00     Sequence
DRB5_0101   21  CWLVGLLFPSADGCA  WLVGLLFPS       0.2542      3193.6              50.00     Sequence
DRB5_0101  144  EGLAAIATALVVSLR  GLAAIATAL       0.2513      3297.4              50.00     Sequence
DRB5_0101   18  GRPCWLVGLLFPSAD  WLVGLLFPS       0.2512      3300.7              50.00     Sequence
DRB5_0101   22  WLVGLLFPSADGCAG  WLVGLLFPS       0.2505      3324.4              50.00     Sequence
DRB5_0101  141  GRGEGLAAIATALVV  GLAAIATAL       0.2412      3678.0              50.00     Sequence
DRB5_0101   17  PGRPCWLVGLLFPSA  WLVGLLFPS       0.2375      3827.8              50.00     Sequence
DRB5_0101    7  GLGTDVHPIEPGRPC  VHPIEPGRP       0.2354      3915.0              50.00     Sequence
DRB5_0101   50  AVLSAAGLGDIGEVF  AVLSAAGLG       0.2344      3960.0              50.00     Sequence
DRB5_0101  143  GEGLAAIATALVVSL  GLAAIATAL       0.2327      4031.9              50.00     Sequence
DRB5_0101  142  RGEGLAAIATALVVS  GLAAIATAL       0.2309      4112.8              50.00     Sequence
DRB5_0101   12  VHPIEPGRPCWLVGL  VHPIEPGRP       0.2294      4177.9              50.00     Sequence
DRB5_0101   16  EPGRPCWLVGLLFPS  WLVGLLFPS       0.2272      4278.2              50.00     Sequence
DRB5_0101    6  VGLGTDVHPIEPGRP  VHPIEPGRP       0.2258      4342.4              50.00     Sequence
DRB5_0101   65  GVDDPRWQGVSGADM  WQGVSGADM       0.2251      4378.1              50.00     Sequence
DRB5_0101   23  LVGLLFPSADGCAGH  GLLFPSADG       0.2244      4412.5              50.00     Sequence
DRB5_0101   24  VGLLFPSADGCAGHS  GLLFPSADG       0.2226      4499.2              50.00     Sequence
DRB5_0101   63  VFGVDDPRWQGVSGA  VFGVDDPRW       0.2158      4841.4              50.00     Sequence
DRB5_0101   62  EVFGVDDPRWQGVSG  VFGVDDPRW       0.2104      5130.5              50.00     Sequence
DRB5_0101   61  GEVFGVDDPRWQGVS  VFGVDDPRW       0.2007      5702.9              50.00     Sequence
DRB5_0101  140  TGRGEGLAAIATALV  GLAAIATAL       0.1976      5894.8              50.00     Sequence
DRB5_0101   60  IGEVFGVDDPRWQGV  VFGVDDPRW       0.1966      5957.3              50.00     Sequence
DRB5_0101   38  SDGDVAVHALCDAVL  AVHALCDAV       0.1961      5994.1              50.00     Sequence
DRB5_0101   15  IEPGRPCWLVGLLFP  PCWLVGLLF       0.1911      6324.4              50.00     Sequence
DRB5_0101   25  GLLFPSADGCAGHSD  GLLFPSADG       0.1904      6373.9              50.00     Sequence
DRB5_0101   59  DIGEVFGVDDPRWQG  VFGVDDPRW       0.1803      7104.8              50.00     Sequence
DRB5_0101  139  LTGRGEGLAAIATAL  GRGEGLAAI       0.1743      7586.5              50.00     Sequence
DRB5_0101   14  PIEPGRPCWLVGLLF  PCWLVGLLF       0.1741      7603.5              50.00     Sequence
DRB5_0101   58  GDIGEVFGVDDPRWQ  VFGVDDPRW       0.1728      7712.1              50.00     Sequence
DRB5_0101    3  LPRVGLGTDVHPIEP  RVGLGTDVH       0.1674      8171.9              50.00     Sequence
DRB5_0101  135  DGLGLTGRGEGLAAI  GLGLTGRGE       0.1617      8690.6              50.00     Sequence
DRB5_0101    2  QLPRVGLGTDVHPIE  RVGLGTDVH       0.1615      8711.5              50.00     Sequence
DRB5_0101   64  FGVDDPRWQGVSGAD  FGVDDPRWQ       0.1579      9061.7              50.00     Sequence
DRB5_0101   51  VLSAAGLGDIGEVFG  VLSAAGLGD       0.1543      9413.4              50.00     Sequence
DRB5_0101  122  LLNAPVSVSATTTDG  LNAPVSVSA       0.1526      9592.4              50.00     Sequence
DRB5_0101    1  NQLPRVGLGTDVHPI  RVGLGTDVH       0.1518      9679.3              50.00     Sequence
DRB5_0101  134  TDGLGLTGRGEGLAA  DGLGLTGRG       0.1504      9827.6              50.00     Sequence
DRB5_0101   37  HSDGDVAVHALCDAV  AVHALCDAV       0.1489      9988.2              50.00     Sequence
DRB5_0101  133  TTDGLGLTGRGEGLA  DGLGLTGRG       0.1486      10011.9             50.00     Sequence
DRB5_0101  136  GLGLTGRGEGLAAIA  GRGEGLAAI       0.1465      10250.5             50.00     Sequence
DRB5_0101    5  RVGLGTDVHPIEPGR  DVHPIEPGR       0.1448      10436.9             50.00     Sequence
DRB5_0101  123  LNAPVSVSATTTDGL  PVSVSATTT       0.1423      10717.3             50.00     Sequence
DRB5_0101  137  LGLTGRGEGLAAIAT  GRGEGLAAI       0.1423      10719.9             50.00     Sequence
DRB5_0101  138  GLTGRGEGLAAIATA  GRGEGLAAI       0.1408      10896.8             50.00     Sequence
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  DRB5_0101   0  VNQLPRVGLGTDVHP  VNQLPRVGL       0.1364     11427.6             50.00    Sequence
  DRB5_0101   57  LGDIGEVFGVDDPRW  VFGVDDPRW       0.1359     11486.0             50.00    Sequence
  DRB5_0101  132  TTTDGLGLTGRGEGL  DGLGLTGRG       0.1347     11635.8             50.00    Sequence
  DRB5_0101  125  APVSVSATTTDGLGL  PVSVSATTT      0.1329     11864.4             50.00    Sequence
  DRB5_0101   4  PRVGLGTDVHPIEPG  RVGLGTDVH       0.1317     12025.1             50.00    Sequence
  DRB5_0101   13  HPIEPGRPCWLVGLL  IEPGRPCWL       0.1305     12182.6             50.00    Sequence
  DRB5_0101  124  NAPVSVSATTTDGLG  PVSVSATTT      0.1263     12753.8             50.00    Sequence
  DRB5_0101  126  PVSVSATTTDGLGLT  PVSVSATTT      0.1211     13480.4             50.00    Sequence
  DRB5_0101  127  VSVSATTTDGLGLTG  VSVSATTTD      0.1132     14697.7             50.00    Sequence
  DRB5_0101  131  ATTTDGLGLTGRGEG  DGLGLTGRG       0.1124     14816.3             50.00    Sequence
  DRB5_0101  130  SATTTDGLGLTGRGE  DGLGLTGRG       0.1122     14848.4             50.00    Sequence
  DRB5_0101   26  LLFPSADGCAGHSDG  LLFPSADGC       0.1096     15278.8             50.00    Sequence
  DRB5_0101  129  VSATTTDGLGLTGRG  DGLGLTGRG       0.1039     16237.8             50.00    Sequence
  DRB5_0101   27  LFPSADGCAGHSDGD  FPSADGCAG       0.0914     18594.9             50.00    Sequence
  DRB5_0101   56  GLGDIGEVFGVDDPR  IGEVFGVDD       0.0904     18809.8             50.00    Sequence
  DRB5_0101  128  SVSATTTDGLGLTGR  ATTTDGLGL       0.0892     19038.3             50.00    Sequence
  DRB5_0101   52  LSAAGLGDIGEVFGV  GLGDIGEVF      0.0824     20507.9             50.00    Sequence
  DRB5_0101   53  SAAGLGDIGEVFGVD  GLGDIGEVF      0.0750     22216.7             50.00    Sequence
  DRB5_0101   55  AGLGDIGEVFGVDDP  GLGDIGEVF      0.0749     22227.5             50.00    Sequence
  DRB5_0101   54  AAGLGDIGEVFGVDD  GLGDIGEVF      0.0745     22333.1             50.00    Sequence
  DRB5_0101   36  GHSDGDVAVHALCDA  DVAVHALCD      0.0706     23298.2             50.00    Sequence
  DRB5_0101   28  FPSADGCAGHSDGDV  FPSADGCAG       0.0654     24629.7             50.00    Sequence
  DRB5_0101   35  AGHSDGDVAVHALCD  DVAVHALCD      0.0622     25501.9             50.00    Sequence
  DRB5_0101   34  CAGHSDGDVAVHALC  GDVAVHALC      0.0456     30527.9             50.00    Sequence
  DRB5_0101   32  DGCAGHSDGDVAVHA  GHSDGDVAV       0.0406     32231.9             50.00    Sequence
  DRB5_0101   30  SADGCAGHSDGDVAV  SADGCAGHS       0.0396     32562.8             50.00    Sequence
  DRB5_0101   29  PSADGCAGHSDGDVA  SADGCAGHS       0.0396     32568.8             50.00    Sequence
  DRB5_0101   33  GCAGHSDGDVAVHAL  GCAGHSDGD       0.0350     34233.7             50.00    Sequence
  DRB5_0101   31  ADGCAGHSDGDVAVH  ADGCAGHSD       0.0331     34946.3             50.00    Sequence
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Allele: DRB5_0101. Number of high binders 7. Number of weak binders 33. Number of peptides 145

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     Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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        IAb  119  LSRLLNAPVSVSATT  RLLNAPVSV      0.6148       64.5       WB    2.00    Sequence
        IAb  120  SRLLNAPVSVSATTT  RLLNAPVSV      0.6148       64.6       WB    2.00    Sequence
        IAb  118  VLSRLLNAPVSVSAT  RLLNAPVSV      0.6066       70.6       WB    2.00    Sequence
        IAb  117  AVLSRLLNAPVSVSA  RLLNAPVSV      0.5734      101.0       WB    4.00    Sequence
        IAb  121  RLLNAPVSVSATTTD  RLLNAPVSV      0.5340      154.7       WB    4.00    Sequence
        IAb  116  QAVLSRLLNAPVSVS  RLLNAPVSV      0.5092      202.4       WB    8.00    Sequence
        IAb   89  QHGYRVGNAVVQVIG  YRVGNAVVQ      0.5054      211.0       WB    8.00    Sequence
        IAb   90  HGYRVGNAVVQVIGN  YRVGNAVVQ      0.4928      241.6       WB    8.00    Sequence
        IAb   88  TQHGYRVGNAVVQVI  YRVGNAVVQ      0.4882      254.1       WB    8.00    Sequence
        IAb   23  LVGLLFPSADGCAGH  VGLLFPSAD      0.4737      297.2       WB    8.00    Sequence
        IAb   22  WLVGLLFPSADGCAG  VGLLFPSAD      0.4686      313.9       WB    8.00    Sequence
        IAb   24  VGLLFPSADGCAGHS  VGLLFPSAD      0.4580      352.2       WB    8.00    Sequence
        IAb   87  ITQHGYRVGNAVVQV  HGYRVGNAV      0.4556      361.7       WB    8.00    Sequence
        IAb   21  CWLVGLLFPSADGCA  VGLLFPSAD      0.4490      388.3       WB    8.00    Sequence
        IAb  142  RGEGLAAIATALVVS  GLAAIATAL      0.4438      410.8       WB    8.00    Sequence
        IAb  143  GEGLAAIATALVVSL  GLAAIATAL      0.4425      416.5       WB    8.00    Sequence
        IAb  115  AQAVLSRLLNAPVSV  RLLNAPVSV      0.4390      432.6       WB    8.00    Sequence
        IAb  141  GRGEGLAAIATALVV  GLAAIATAL      0.4335      459.4       WB   16.00    Sequence
        IAb  144  EGLAAIATALVVSLR  GLAAIATAL      0.4321      466.0       WB   16.00    Sequence
        IAb  140  TGRGEGLAAIATALV  GLAAIATAL      0.4167      550.5            16.00    Sequence
        IAb   91  GYRVGNAVVQVIGNR  YRVGNAVVQ      0.4166      551.4            16.00    Sequence
        IAb   86  LITQHGYRVGNAVVQ  HGYRVGNAV      0.4155      557.9            16.00    Sequence
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IAb	20	PCWLVGLLFPSADGC	VGLLFPSAD	0.4127	574.8	16.00	Sequence
IAb	122	LLNAPVSVSATTTDG	NAPVSVSAT	0.4005	656.1	16.00	Sequence
IAb	123	LNAPVSVSATTTDGL	NAPVSVSAT	0.3907	729.3	16.00	Sequence
IAb	19	RPCWLVGLLFPSADG	VGLLFPSAD	0.3814	806.5	16.00	Sequence
IAb	107	KIGWRRLEAQAVLSR	WRRLEAQAV	0.3756	859.1	16.00	Sequence
IAb	139	LTGRGEGLAAIATAL	GLAAIATAL	0.3712	901.3	16.00	Sequence
IAb	98	VVQVIGNRPKIGWRR	VQVIGNRPK	0.3711	902.1	16.00	Sequence
IAb	108	IGWRRLEAQAVLSRL	WRRLEAQAV	0.3704	908.6	16.00	Sequence
IAb	106	PKIGWRRLEAQAVLS	WRRLEAQAV	0.3640	974.2	16.00	Sequence
IAb	92	YRVGNAVVQVIGNRP	YRVGNAVVQ	0.3588	1030.3	16.00	Sequence
IAb	97	AVVQVIGNRPKIGWR	VQVIGNRPK	0.3528	1098.9	16.00	Sequence
IAb	124	NAPVSVSATTTDGLG	NAPVSVSAT	0.3522	1106.8	16.00	Sequence
IAb	99	VQVIGNRPKIGWRRL	VQVIGNRPK	0.3487	1149.9	16.00	Sequence
IAb	105	RPKIGWRRLEAQAVL	WRRLEAQAV	0.3365	1311.7	32.00	Sequence
IAb	85	VLITQHGYRVGNAVV	HGYRVGNAV	0.3357	1322.4	32.00	Sequence
IAb	18	GRPCWLVGLLFPSAD	VGLLFPSAD	0.3333	1357.7	32.00	Sequence
IAb	96	NAVVQVIGNRPKIGW	VQVIGNRPK	0.3309	1393.6	32.00	Sequence
IAb	125	APVSVSATTTDGLGL	PVSVSATTT	0.3181	1600.7	32.00	Sequence
IAb	104	NRPKIGWRRLEAQAV	WRRLEAQAV	0.3055	1834.2	32.00	Sequence
IAb	69	PRWQGVSGADMLRHV	PRWQGVSGA	0.2997	1952.5	32.00	Sequence
IAb	110	WRRLEAQAVLSRLLN	WRRLEAQAV	0.2975	1999.7	32.00	Sequence
IAb	109	GWRRLEAQAVLSRLL	WRRLEAQAV	0.2967	2018.0	32.00	Sequence
IAb	95	GNAVVQVIGNRPKIG	VQVIGNRPK	0.2950	2055.0	32.00	Sequence
IAb	68	DPRWQGVSGADMLRH	PRWQGVSGA	0.2949	2056.2	32.00	Sequence
IAb	12	VHPIEPGRPCWLVGL	VHPIEPGRP	0.2939	2080.4	32.00	Sequence
IAb	67	DDPRWQGVSGADMLR	PRWQGVSGA	0.2901	2165.6	32.00	Sequence
IAb	11	DVHPIEPGRPCWLVG	VHPIEPGRP	0.2900	2168.2	32.00	Sequence
IAb	10	TDVHPIEPGRPCWLV	VHPIEPGRP	0.2892	2187.2	32.00	Sequence
IAb	126	PVSVSATTTDGLGLT	PVSVSATTT	0.2867	2247.5	32.00	Sequence
IAb	114	EAQAVLSRLLNAPVS	SRLLNAPVS	0.2854	2279.9	32.00	Sequence
IAb	9	GTDVHPIEPGRPCWL	VHPIEPGRP	0.2823	2357.5	32.00	Sequence
IAb	66	VDDPRWQGVSGADML	PRWQGVSGA	0.2792	2439.1	32.00	Sequence
IAb	138	GLTGRGEGLAAIATA	GEGLAAIAT	0.2595	3017.4	32.00	Sequence
IAb	65	GVDDPRWQGVSGADM	PRWQGVSGA	0.2514	3295.1	32.00	Sequence
IAb	84	VVLITQHGYRVGNAV	HGYRVGNAV	0.2472	3445.9	32.00	Sequence
IAb	41	DVAVHALCDAVLSAA	DVAVHALCD	0.2467	3464.1	32.00	Sequence
IAb	8	LGTDVHPIEPGRPCW	VHPIEPGRP	0.2355	3913.7	50.00	Sequence
IAb	94	VGNAVVQVIGNRPKI	VQVIGNRPK	0.2352	3926.1	50.00	Sequence
IAb	49	DAVLSAAGLGDIGEV	AVLSAAGLG	0.2336	3991.5	50.00	Sequence
IAb	48	CDAVLSAAGLGDIGE	AVLSAAGLG	0.2230	4480.0	50.00	Sequence
IAb	113	LEAQAVLSRLLNAPV	LEAQAVLSR	0.2217	4543.7	50.00	Sequence
IAb	112	RLEAQAVLSRLLNAP	RLEAQAVLS	0.2183	4711.9	50.00	Sequence
IAb	127	VSVSATTTDGLGLTG	VSVSATTTD	0.2147	4899.9	50.00	Sequence
IAb	47	LCDAVLSAAGLGDIG	AVLSAAGLG	0.2138	4946.4	50.00	Sequence
IAb	111	RRLEAQAVLSRLLNA	RLEAQAVLS	0.2113	5082.2	50.00	Sequence
IAb	7	GLGTDVHPIEPGRPC	VHPIEPGRP	0.2100	5156.5	50.00	Sequence
IAb	137	LGLTGRGEGLAAIAT	GEGLAAIAT	0.2073	5309.0	50.00	Sequence
IAb	93	RVGNAVVQVIGNRPK	VQVIGNRPK	0.2072	5312.9	50.00	Sequence
IAb	70	RWQGVSGADMLRHVV	QGVSGADML	0.2071	5321.5	50.00	Sequence
IAb	100	QVIGNRPKIGWRRLE	VIGNRPKIG	0.2044	5475.0	50.00	Sequence
IAb	25	GLLFPSADGCAGHSD	GLLFPSADG	0.2043	5481.3	50.00	Sequence
IAb	40	GDVAVHALCDAVLSA	DVAVHALCD	0.2034	5538.7	50.00	Sequence
IAb	64	FGVDDPRWQGVSGAD	PRWQGVSGA	0.1988	5816.8	50.00	Sequence
IAb	50	AVLSAAGLGDIGEVF	AVLSAAGLG	0.1987	5823.5	50.00	Sequence
IAb	46	ALCDAVLSAAGLGDI	AVLSAAGLG	0.1968	5945.9	50.00	Sequence
IAb	39	DGDVAVHALCDAVLS	DVAVHALCD	0.1890	6467.7	50.00	Sequence
IAb	6	VGLGTDVHPIEPGRP	VHPIEPGRP	0.1873	6587.5	50.00	Sequence
IAb	42	VAVHALCDAVLSAAG	HALCDAVLS	0.1865	6649.0	50.00	Sequence
IAb	43	AVHALCDAVLSAAGL	HALCDAVLS	0.1832	6887.7	50.00	Sequence

IAb	103	GNRPKIGWRRLEAQA	IGWRRLEAQ	0.1820	6979.0	50.00	Sequence
IAb	71	WQGVSGADMLRHVVV	QGVSGADML	0.1815	7012.9	50.00	Sequence
IAb	63	VFGVDDPRWQGVSGA	PRWQGVSGA	0.1809	7063.6	50.00	Sequence
IAb	13	HPIEPGRPCWLVGLL	IEPGRPCWL	0.1787	7235.6	50.00	Sequence
IAb	44	VHALCDAVLSAAGLG	HALCDAVLS	0.1784	7252.7	50.00	Sequence
IAb	101	VIGNRPKIGWRRLEA	VIGNRPKIG	0.1755	7489.1	50.00	Sequence
IAb	2	QLPRVGLGTDVHPIE	RVGLGTDVH	0.1749	7535.1	50.00	Sequence
IAb	38	SDGDVAVHALCDAVL	DVAVHALCD	0.1718	7793.0	50.00	Sequence
IAb	26	LLFPSADGCAGHSDG	LFPSADGCA	0.1710	7861.9	50.00	Sequence
IAb	45	HALCDAVLSAAGLGD	DAVLSAAGL	0.1691	8020.4	50.00	Sequence
IAb	3	LPRVGLGTDVHPIEP	RVGLGTDVH	0.1689	8037.8	50.00	Sequence
IAb	1	NQLPRVGLGTDVHPI	RVGLGTDVH	0.1636	8512.9	50.00	Sequence
IAb	136	GLGLTGRGEGLAAIA	GRGEGLAAI	0.1612	8735.6	50.00	Sequence
IAb	5	RVGLGTDVHPIEPGR	RVGLGTDVH	0.1562	9225.0	50.00	Sequence
IAb	4	PRVGLGTDVHPIEPG	RVGLGTDVH	0.1547	9380.3	50.00	Sequence
IAb	17	PGRPCWLVGLLFPSA	WLVGLLFPS	0.1537	9483.1	50.00	Sequence
IAb	27	LFPSADGCAGHSDGD	LFPSADGCA	0.1527	9586.4	50.00	Sequence
IAb	72	QGVSGADMLRHVVVL	QGVSGADML	0.1493	9944.0	50.00	Sequence
IAb	0	VNQLPRVGLGTDVHP	RVGLGTDVH	0.1491	9966.2	50.00	Sequence
IAb	102	IGNRPKIGWRRLEAQ	IGWRRLEAQ	0.1489	9979.9	50.00	Sequence
IAb	37	HSDGDVAVHALCDAV	DVAVHALCD	0.1368	11385.5	50.00	Sequence
IAb	51	VLSAAGLGDIGEVFG	VLSAAGLGD	0.1344	11685.4	50.00	Sequence
IAb	15	IEPGRPCWLVGLLFP	IEPGRPCWL	0.1310	12119.9	50.00	Sequence
IAb	14	PIEPGRPCWLVGLLF	IEPGRPCWL	0.1304	12197.2	50.00	Sequence
IAb	16	EPGRPCWLVGLLFPS	WLVGLLFPS	0.1244	13020.0	50.00	Sequence
IAb	135	DGLGLTGRGEGLAAI	TGRGEGLAA	0.1194	13743.6	50.00	Sequence
IAb	28	FPSADGCAGHSDGDV	FPSADGCAG	0.1123	14830.3	50.00	Sequence
IAb	83	VVVLITQHGYRVGNA	QHGYRVGNA	0.1096	15274.9	50.00	Sequence
IAb	61	GEVFGVDDPRWQGVS	EVFGVDDPR	0.1093	15325.3	50.00	Sequence
IAb	78	DMLRHVVVLITQHGY	LRHVVVLIT	0.1008	16793.5	50.00	Sequence
IAb	77	ADMLRHVVVLITQHG	LRHVVVLIT	0.0990	17129.3	50.00	Sequence
IAb	73	GVSGADMLRHVVVLI	GVSGADMLR	0.0988	17171.0	50.00	Sequence
IAb	62	EVFGVDDPRWQGVSG	EVFGVDDPR	0.0970	17510.1	50.00	Sequence
IAb	79	MLRHVVVLITQHGYR	LRHVVVLIT	0.0969	17519.1	50.00	Sequence
IAb	60	IGEVFGVDDPRWQGV	FGVDDPRWQ	0.0960	17691.7	50.00	Sequence
IAb	80	LRHVVVLITQHGYRV	LRHVVVLIT	0.0925	18369.8	50.00	Sequence
IAb	134	TDGLGLTGRGEGLAA	TGRGEGLAA	0.0921	18466.8	50.00	Sequence
IAb	76	GADMLRHVVVLITQH	LRHVVVLIT	0.0894	19009.5	50.00	Sequence
IAb	36	GHSDGDVAVHALCDA	DVAVHALCD	0.0888	19136.4	50.00	Sequence
IAb	59	DIGEVFGVDDPRWQG	FGVDDPRWQ	0.0869	19536.7	50.00	Sequence
IAb	74	VSGADMLRHVVVLIT	LRHVVVLIT	0.0842	20109.9	50.00	Sequence
IAb	75	SGADMLRHVVVLITQ	LRHVVVLIT	0.0834	20286.5	50.00	Sequence
IAb	81	RHVVVLITQHGYRVG	RHVVVLITQ	0.0803	20970.8	50.00	Sequence
IAb	35	AGHSDGDVAVHALCD	DVAVHALCD	0.0795	21143.2	50.00	Sequence
IAb	52	LSAAGLGDIGEVFGV	LSAAGLGDI	0.0787	21337.7	50.00	Sequence
IAb	128	SVSATTTDGLGLTGR	SVSATTTDG	0.0732	22658.0	50.00	Sequence
IAb	58	GDIGEVFGVDDPRWQ	FGVDDPRWQ	0.0716	23039.7	50.00	Sequence
IAb	82	HVVVLITQHGYRVGN	HVVVLITQH	0.0708	23229.9	50.00	Sequence
IAb	133	TTDGLGLTGRGEGLA	GLGLTGRGE	0.0608	25896.7	50.00	Sequence
IAb	34	CAGHSDGDVAVHALC	AGHSDGDVA	0.0596	26234.3	50.00	Sequence
IAb	29	PSADGCAGHSDGDVA	PSADGCAGH	0.0588	26457.2	50.00	Sequence
IAb	33	GCAGHSDGDVAVHAL	AGHSDGDVA	0.0561	27261.5	50.00	Sequence
IAb	129	VSATTTDGLGLTGRG	VSATTTDGL	0.0546	27690.5	50.00	Sequence
IAb	132	TTTDGLGLTGRGEGL	GLGLTGRGE	0.0535	28018.4	50.00	Sequence
IAb	131	ATTTDGLGLTGRGEG	ATTTDGLGL	0.0515	28645.3	50.00	Sequence
IAb	130	SATTTDGLGLTGRGE	ATTTDGLGL	0.0497	29198.8	50.00	Sequence
IAb	54	AAGLGDIGEVFGVDD	AAGLGDIGE	0.0490	29419.9	50.00	Sequence
IAb	32	DGCAGHSDGDVAVHA	AGHSDGDVA	0.0478	29795.0	50.00	Sequence
IAb	57	LGDIGEVFGVDDPRW	GEVFGVDDP	0.0478	29803.7	50.00	Sequence

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     IAb  30  SADGCAGHSDGDVAV  ADGCAGHSD      0.0471     30033.2            50.00    Sequence
     IAb  53  SAAGLGDIGEVFGVD  AAGLGDIGE      0.0466     30185.7            50.00    Sequence
     IAb  31  ADGCAGHSDGDVAVH  AGHSDGDVA      0.0456     30541.5            50.00    Sequence
     IAb  56  GLGDIGEVFGVDDPR  EVFGVDDPR      0.0416     31889.5            50.00    Sequence
     IAb  55  AGLGDIGEVFGVDDP  AGLGDIGEV      0.0396     32571.9            50.00    Sequence
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Allele: IAb. Number of high binders 0. Number of weak binders 19. Number of peptides 145

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   Allele  pos       peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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     IAd  109  GWRRLEAQAVLSRLL  LEAQAVLSR      0.6115       66.9       WB    0.05    Sequence
     IAd  108  IGWRRLEAQAVLSRL  LEAQAVLSR      0.6052       71.6       WB    0.10    Sequence
     IAd  110  WRRLEAQAVLSRLLN  LEAQAVLSR      0.5966       78.6       WB    0.10    Sequence
     IAd  111  RRLEAQAVLSRLLNA  LEAQAVLSR      0.5466      135.0       WB    0.20    Sequence
     IAd  112  RLEAQAVLSRLLNAP  LEAQAVLSR      0.5304      160.9       WB    0.30    Sequence
     IAd  113  LEAQAVLSRLLNAPV  LEAQAVLSR      0.5135      193.2       WB    0.40    Sequence
     IAd  107  KIGWRRLEAQAVLSR  LEAQAVLSR      0.4558      360.6       WB    1.00    Sequence
     IAd   75  SGADMLRHVVVLITQ  LRHVVVLIT      0.4144      564.4             2.00    Sequence
     IAd   76  GADMLRHVVVLITQH  LRHVVVLIT      0.4119      580.2             2.00    Sequence
     IAd   77  ADMLRHVVVLITQHG  LRHVVVLIT      0.4035      634.9             2.00    Sequence
     IAd   78  DMLRHVVVLITQHGY  LRHVVVLIT      0.3869      760.0             4.00    Sequence
     IAd  143  GEGLAAIATALVVSL  IATALVVSL      0.3678      935.0             4.00    Sequence
     IAd   41  DVAVHALCDAVLSAA  VHALCDAVL      0.3644      970.1             4.00    Sequence
     IAd  114  EAQAVLSRLLNAPVS  EAQAVLSRL      0.3624      991.1             4.00    Sequence
     IAd   42  VAVHALCDAVLSAAG  VHALCDAVL      0.3577     1043.1             4.00    Sequence
     IAd  144  EGLAAIATALVVSLR  IATALVVSL      0.3511     1120.1             8.00    Sequence
     IAd   79  MLRHVVVLITQHGYR  LRHVVVLIT      0.3486     1150.5             8.00    Sequence
     IAd   43  AVHALCDAVLSAAGL  VHALCDAVL      0.3286     1427.9             8.00    Sequence
     IAd   80  LRHVVVLITQHGYRV  RHVVVLITQ      0.3270     1454.2             8.00    Sequence
     IAd   74  VSGADMLRHVVVLIT  LRHVVVLIT      0.3223     1529.6             8.00    Sequence
     IAd  119  LSRLLNAPVSVSATT  NAPVSVSAT      0.3154     1647.5             8.00    Sequence
     IAd  104  NRPKIGWRRLEAQAV  WRRLEAQAV      0.3116     1717.8             8.00    Sequence
     IAd  106  PKIGWRRLEAQAVLS  WRRLEAQAV      0.3066     1812.9             8.00    Sequence
     IAd  118  VLSRLLNAPVSVSAT  SRLLNAPVS      0.2996     1954.9            16.00    Sequence
     IAd   69  PRWQGVSGADMLRHV  PRWQGVSGA      0.2986     1975.9            16.00    Sequence
     IAd  105  RPKIGWRRLEAQAVL  WRRLEAQAV      0.2918     2128.0            16.00    Sequence
     IAd  142  RGEGLAAIATALVVS  EGLAAIATA      0.2899     2170.6            16.00    Sequence
     IAd   40  GDVAVHALCDAVLSA  VAVHALCDA      0.2896     2177.5            16.00    Sequence
     IAd   68  DPRWQGVSGADMLRH  VSGADMLRH      0.2880     2216.4            16.00    Sequence
     IAd  141  GRGEGLAAIATALVV  EGLAAIATA      0.2763     2514.9            16.00    Sequence
     IAd  120  SRLLNAPVSVSATTT  LNAPVSVSA      0.2719     2638.9            16.00    Sequence
     IAd   44  VHALCDAVLSAAGLG  LCDAVLSAA      0.2693     2712.5            16.00    Sequence
     IAd  117  AVLSRLLNAPVSVSA  SRLLNAPVS      0.2670     2780.4            16.00    Sequence
     IAd   39  DGDVAVHALCDAVLS  HALCDAVLS      0.2615     2952.5            16.00    Sequence
     IAd  140  TGRGEGLAAIATALV  EGLAAIATA      0.2537     3213.1            16.00    Sequence
     IAd   46  ALCDAVLSAAGLGDI  ALCDAVLSA      0.2443     3556.8            16.00    Sequence
     IAd  121  RLLNAPVSVSATTTD  NAPVSVSAT      0.2434     3591.6            32.00    Sequence
     IAd  122  LLNAPVSVSATTTDG  NAPVSVSAT      0.2392     3756.6            32.00    Sequence
     IAd   33  GCAGHSDGDVAVHAL  GHSDGDVAV      0.2384     3792.8            32.00    Sequence
     IAd   34  CAGHSDGDVAVHALC  DGDVAVHAL      0.2357     3905.2            32.00    Sequence
     IAd  123  LNAPVSVSATTTDGL  LNAPVSVSA      0.2336     3992.1            32.00    Sequence
     IAd   45  HALCDAVLSAAGLGD  ALCDAVLSA      0.2334     4002.5            32.00    Sequence
     IAd   38  SDGDVAVHALCDAVL  VHALCDAVL      0.2330     4019.8            32.00    Sequence
     IAd   67  DDPRWQGVSGADMLR  PRWQGVSGA      0.2314     4090.3            32.00    Sequence
     IAd  103  GNRPKIGWRRLEAQA  RPKIGWRRL      0.2311     4102.3            32.00    Sequence
     IAd   99  VQVIGNRPKIGWRRL  RPKIGWRRL      0.2220     4526.1            32.00    Sequence
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IAd	102	IGNRPKIGWRRLEAQ	RPKIGWRRL	0.2191	4673.7	32.00	Sequence
IAd	81	RHVVVLITQHGYRVG	RHVVVLITQ	0.2174	4758.0	32.00	Sequence
IAd	101	VIGNRPKIGWRRLEA	RPKIGWRRL	0.2161	4827.0	32.00	Sequence
IAd	100	QVIGNRPKIGWRRLE	RPKIGWRRL	0.2149	4890.1	32.00	Sequence
IAd	66	VDDPRWQGVSGADML	PRWQGVSGA	0.2146	4902.4	32.00	Sequence
IAd	115	AQAVLSRLLNAPVSV	SRLLNAPVS	0.2068	5333.7	32.00	Sequence
IAd	35	AGHSDGDVAVHALCD	DGDVAVHAL	0.2067	5343.0	32.00	Sequence
IAd	47	LCDAVLSAAGLGDIG	LCDAVLSAA	0.2060	5384.8	32.00	Sequence
IAd	116	QAVLSRLLNAPVSVS	SRLLNAPVS	0.2028	5571.2	32.00	Sequence
IAd	139	LTGRGEGLAAIATAL	EGLAAIATA	0.2009	5689.6	32.00	Sequence
IAd	36	GHSDGDVAVHALCDA	HSDGDVAVH	0.1999	5749.8	32.00	Sequence
IAd	37	HSDGDVAVHALCDAV	SDGDVAVHA	0.1996	5770.2	32.00	Sequence
IAd	65	GVDDPRWQGVSGADM	PRWQGVSGA	0.1965	5962.3	32.00	Sequence
IAd	32	DGCAGHSDGDVAVHA	GHSDGDVAV	0.1950	6065.8	32.00	Sequence
IAd	138	GLTGRGEGLAAIATA	EGLAAIATA	0.1863	6664.1	32.00	Sequence
IAd	49	DAVLSAAGLGDIGEV	VLSAAGLGD	0.1734	7660.8	50.00	Sequence
IAd	89	QHGYRVGNAVVQVIG	QHGYRVGNA	0.1703	7922.9	50.00	Sequence
IAd	70	RWQGVSGADMLRHVV	WQGVSGADM	0.1693	8007.0	50.00	Sequence
IAd	88	TQHGYRVGNAVVQVI	RVGNAVVQV	0.1610	8758.0	50.00	Sequence
IAd	73	GVSGADMLRHVVVLI	MLRHVVVLI	0.1605	8804.7	50.00	Sequence
IAd	71	WQGVSGADMLRHVVV	VSGADMLRH	0.1562	9230.3	50.00	Sequence
IAd	17	PGRPCWLVGLLFPSA	WLVGLLFPS	0.1545	9400.3	50.00	Sequence
IAd	19	RPCWLVGLLFPSADG	WLVGLLFPS	0.1523	9622.6	50.00	Sequence
IAd	18	GRPCWLVGLLFPSAD	WLVGLLFPS	0.1517	9690.2	50.00	Sequence
IAd	124	NAPVSVSATTTDGLG	NAPVSVSAT	0.1493	9936.3	50.00	Sequence
IAd	31	ADGCAGHSDGDVAVH	GHSDGDVAV	0.1484	10039.5	50.00	Sequence
IAd	48	CDAVLSAAGLGDIGE	VLSAAGLGD	0.1436	10569.4	50.00	Sequence
IAd	50	AVLSAAGLGDIGEVF	VLSAAGLGD	0.1397	11029.2	50.00	Sequence
IAd	52	LSAAGLGDIGEVFGV	LSAAGLGDI	0.1381	11216.4	50.00	Sequence
IAd	64	FGVDDPRWQGVSGAD	PRWQGVSGA	0.1379	11243.3	50.00	Sequence
IAd	51	VLSAAGLGDIGEVFG	LSAAGLGDI	0.1362	11456.2	50.00	Sequence
IAd	93	RVGNAVVQVIGNRPK	AVVQVIGNR	0.1319	11996.5	50.00	Sequence
IAd	98	VVQVIGNRPKIGWRR	VQVIGNRPK	0.1278	12546.5	50.00	Sequence
IAd	87	ITQHGYRVGNAVVQV	RVGNAVVQV	0.1276	12577.1	50.00	Sequence
IAd	63	VFGVDDPRWQGVSGA	PRWQGVSGA	0.1266	12712.1	50.00	Sequence
IAd	72	QGVSGADMLRHVVVL	VSGADMLRH	0.1257	12825.8	50.00	Sequence
IAd	97	AVVQVIGNRPKIGWR	AVVQVIGNR	0.1257	12826.5	50.00	Sequence
IAd	86	LITQHGYRVGNAVVQ	QHGYRVGNA	0.1204	13588.8	50.00	Sequence
IAd	30	SADGCAGHSDGDVAV	GHSDGDVAV	0.1187	13846.0	50.00	Sequence
IAd	16	EPGRPCWLVGLLFPS	WLVGLLFPS	0.1169	14114.5	50.00	Sequence
IAd	22	WLVGLLFPSADGCAG	WLVGLLFPS	0.1149	14427.3	50.00	Sequence
IAd	137	LGLTGRGEGLAAIAT	GEGLAAIAT	0.1136	14634.7	50.00	Sequence
IAd	94	VGNAVVQVIGNRPKI	VGNAVVQVI	0.1130	14716.9	50.00	Sequence
IAd	92	YRVGNAVVQVIGNRP	RVGNAVVQV	0.1088	15400.0	50.00	Sequence
IAd	83	VVVLITQHGYRVGNA	VVVLITQHG	0.1084	15472.1	50.00	Sequence
IAd	20	PCWLVGLLFPSADGC	WLVGLLFPS	0.1052	16016.5	50.00	Sequence
IAd	91	GYRVGNAVVQVIGNR	RVGNAVVQV	0.1033	16349.0	50.00	Sequence
IAd	1	NQLPRVGLGTDVHPI	VGLGTDVHP	0.1032	16366.9	50.00	Sequence
IAd	24	VGLLFPSADGCAGHS	FPSADGCAG	0.1021	16571.6	50.00	Sequence
IAd	0	VNQLPRVGLGTDVHP	VNQLPRVGL	0.1019	16601.9	50.00	Sequence
IAd	53	SAAGLGDIGEVFGVD	AGLGDIGEV	0.0907	18744.4	50.00	Sequence
IAd	25	GLLFPSADGCAGHSD	FPSADGCAG	0.0904	18807.4	50.00	Sequence
IAd	96	NAVVQVIGNRPKIGW	AVVQVIGNR	0.0897	18936.0	50.00	Sequence
IAd	85	VLITQHGYRVGNAVV	QHGYRVGNA	0.0897	18949.8	50.00	Sequence
IAd	95	GNAVVQVIGNRPKIG	AVVQVIGNR	0.0889	19115.3	50.00	Sequence
IAd	82	HVVVLITQHGYRVGN	HVVVLITQH	0.0887	19151.6	50.00	Sequence
IAd	55	AGLGDIGEVFGVDDP	AGLGDIGEV	0.0885	19201.4	50.00	Sequence
IAd	84	VVLITQHGYRVGNAV	LITQHGYRV	0.0879	19322.0	50.00	Sequence
IAd	90	HGYRVGNAVVQVIGN	RVGNAVVQV	0.0867	19572.6	50.00	Sequence

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    IAd   6  VGLGTDVHPIEPGRP  VHPIEPGRP     0.0860    19719.1          50.00   Sequence
    IAd  125  APVSVSATTTDGLGL  PVSVSATTT     0.0857    19790.9          50.00   Sequence
    IAd   21  CWLVGLLFPSADGCA  WLVGLLFPS     0.0829    20395.5          50.00   Sequence
    IAd   23  LVGLLFPSADGCAGH  LVGLLFPSA     0.0819    20619.8          50.00   Sequence
    IAd   54  AAGLGDIGEVFGVDD  AGLGDIGEV     0.0819    20621.8          50.00   Sequence
    IAd   15  IEPGRPCWLVGLLFP  RPCWLVGLL     0.0788    21320.1          50.00   Sequence
    IAd   26  LLFPSADGCAGHSDG  FPSADGCAG     0.0755    22096.1          50.00   Sequence
    IAd    7  GLGTDVHPIEPGRPC  VHPIEPGRP     0.0740    22452.3          50.00   Sequence
    IAd    4  PRVGLGTDVHPIEPG  VGLGTDVHP     0.0733    22619.5          50.00   Sequence
    IAd    2  QLPRVGLGTDVHPIE  GLGTDVHPI     0.0731    22659.7          50.00   Sequence
    IAd    3  LPRVGLGTDVHPIEP  PRVGLGTDV     0.0719    22967.3          50.00   Sequence
    IAd    5  RVGLGTDVHPIEPGR  VGLGTDVHP     0.0718    22992.9          50.00   Sequence
    IAd   14  PIEPGRPCWLVGLLF  RPCWLVGLL     0.0710    23195.8          50.00   Sequence
    IAd   27  LFPSADGCAGHSDGD  FPSADGCAG     0.0662    24422.5          50.00   Sequence
    IAd   57  LGDIGEVFGVDDPRW  GDIGEVFGV     0.0651    24709.3          50.00   Sequence
    IAd   58  GDIGEVFGVDDPRWQ  GDIGEVFGV     0.0628    25354.1          50.00   Sequence
    IAd  136  GLGLTGRGEGLAAIA  RGEGLAAIA     0.0603    26043.1          50.00   Sequence
    IAd   28  FPSADGCAGHSDGDV  FPSADGCAG     0.0601    26091.0          50.00   Sequence
    IAd   13  HPIEPGRPCWLVGLL  RPCWLVGLL     0.0583    26609.1          50.00   Sequence
    IAd    8  LGTDVHPIEPGRPCW  VHPIEPGRP     0.0567    27073.7          50.00   Sequence
    IAd   56  GLGDIGEVFGVDDPR  GDIGEVFGV     0.0562    27211.7          50.00   Sequence
    IAd    9  GTDVHPIEPGRPCWL  VHPIEPGRP     0.0546    27698.6          50.00   Sequence
    IAd   10  TDVHPIEPGRPCWLV  VHPIEPGRP     0.0543    27784.5          50.00   Sequence
    IAd  126  PVSVSATTTDGLGLT  PVSVSATTT     0.0529    28220.4          50.00   Sequence
    IAd   11  DVHPIEPGRPCWLVG  VHPIEPGRP     0.0504    28977.3          50.00   Sequence
    IAd   29  PSADGCAGHSDGDVA  AGHSDGDVA     0.0474    29952.4          50.00   Sequence
    IAd   59  DIGEVFGVDDPRWQG  IGEVFGVDD     0.0408    32168.1          50.00   Sequence
    IAd   60  IGEVFGVDDPRWQGV  IGEVFGVDD     0.0383    33046.9          50.00   Sequence
    IAd  127  VSVSATTTDGLGLTG  VSVSATTTD     0.0363    33769.1          50.00   Sequence
    IAd   12  VHPIEPGRPCWLVGL  GRPCWLVGL     0.0356    34011.1          50.00   Sequence
    IAd  128  SVSATTTDGLGLTGR  VSATTTDGL     0.0350    34243.7          50.00   Sequence
    IAd  129  VSATTTDGLGLTGRG  VSATTTDGL     0.0340    34605.4          50.00   Sequence
    IAd   61  GEVFGVDDPRWQGVS  VDDPRWQGV     0.0338    34698.0          50.00   Sequence
    IAd   62  EVFGVDDPRWQGVSG  VDDPRWQGV     0.0277    37034.5          50.00   Sequence
    IAd  135  DGLGLTGRGEGLAAI  GRGEGLAAI     0.0247    38257.6          50.00   Sequence
    IAd  134  TDGLGLTGRGEGLAA  TGRGEGLAA     0.0186    40893.0          50.00   Sequence
    IAd  130  SATTTDGLGLTGRGE  ATTTDGLGL     0.0160    42041.5          50.00   Sequence
    IAd  131  ATTTDGLGLTGRGEG  ATTTDGLGL     0.0135    43207.8          50.00   Sequence
    IAd  133  TTDGLGLTGRGEGLA  TTDGLGLTG     0.0098    44974.6          50.00   Sequence
    IAd  132  TTTDGLGLTGRGEGL  DGLGLTGRG     0.0096    45068.6          50.00   Sequence
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Allele: IAd. Number of high binders 0. Number of weak binders 7. Number of peptides 145

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  Allele  pos       peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
-----------------------------------------------------------------------------------------------
    IAs   66  VDDPRWQGVSGADML  QGVSGADML     0.3052     1839.3           4.00   Sequence
    IAs   67  DDPRWQGVSGADMLR  QGVSGADML     0.2850     2289.5           4.00   Sequence
    IAs    7  GLGTDVHPIEPGRPC  GLGTDVHPI     0.2726     2617.3           4.00   Sequence
    IAs   68  DPRWQGVSGADMLRH  QGVSGADML     0.2667     2791.0           4.00   Sequence
    IAs   71  WQGVSGADMLRHVVV  QGVSGADML     0.2609     2973.0           8.00   Sequence
    IAs   70  RWQGVSGADMLRHVV  QGVSGADML     0.2561     3131.2           8.00   Sequence
    IAs   69  PRWQGVSGADMLRHV  QGVSGADML     0.2531     3234.6           8.00   Sequence
    IAs  115  AQAVLSRLLNAPVSV  RLLNAPVSV     0.2477     3429.1           8.00   Sequence
    IAs    6  VGLGTDVHPIEPGRP  GLGTDVHPI     0.2388     3776.1           8.00   Sequence
    IAs  116  QAVLSRLLNAPVSVS  RLLNAPVSV     0.2363     3876.9           8.00   Sequence
    IAs  117  AVLSRLLNAPVSVSA  RLLNAPVSV     0.2280     4241.6           8.00   Sequence
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IAs	118	VLSRLLNAPVSVSAT	RLLNAPVSV	0.2203	4611.3	8.00	Sequence
IAs	72	QGVSGADMLRHVVVL	QGVSGADML	0.2088	5224.4	16.00	Sequence
IAs	95	GNAVVQVIGNRPKIG	VIGNRPKIG	0.1958	6007.8	16.00	Sequence
IAs	58	GDIGEVFGVDDPRWQ	FGVDDPRWQ	0.1955	6027.9	16.00	Sequence
IAs	8	LGTDVHPIEPGRPCW	VHPIEPGRP	0.1920	6266.1	16.00	Sequence
IAs	96	NAVVQVIGNRPKIGW	VIGNRPKIG	0.1887	6488.1	16.00	Sequence
IAs	9	GTDVHPIEPGRPCWL	VHPIEPGRP	0.1876	6568.6	16.00	Sequence
IAs	59	DIGEVFGVDDPRWQG	FGVDDPRWQ	0.1819	6983.0	16.00	Sequence
IAs	4	PRVGLGTDVHPIEPG	GLGTDVHPI	0.1812	7035.7	16.00	Sequence
IAs	5	RVGLGTDVHPIEPGR	GLGTDVHPI	0.1760	7450.4	16.00	Sequence
IAs	97	AVVQVIGNRPKIGWR	VIGNRPKIG	0.1748	7547.6	16.00	Sequence
IAs	12	VHPIEPGRPCWLVGL	HPIEPGRPC	0.1716	7807.4	16.00	Sequence
IAs	98	VVQVIGNRPKIGWRR	VIGNRPKIG	0.1694	8000.9	16.00	Sequence
IAs	60	IGEVFGVDDPRWQGV	FGVDDPRWQ	0.1693	8006.7	16.00	Sequence
IAs	61	GEVFGVDDPRWQGVS	FGVDDPRWQ	0.1633	8542.3	16.00	Sequence
IAs	10	TDVHPIEPGRPCWLV	VHPIEPGRP	0.1632	8552.9	16.00	Sequence
IAs	114	EAQAVLSRLLNAPVS	SRLLNAPVS	0.1588	8966.9	32.00	Sequence
IAs	11	DVHPIEPGRPCWLVG	VHPIEPGRP	0.1555	9295.4	32.00	Sequence
IAs	120	SRLLNAPVSVSATTT	RLLNAPVSV	0.1535	9497.7	32.00	Sequence
IAs	119	LSRLLNAPVSVSATT	RLLNAPVSV	0.1519	9666.2	32.00	Sequence
IAs	1	NQLPRVGLGTDVHPI	GLGTDVHPI	0.1458	10319.6	32.00	Sequence
IAs	2	QLPRVGLGTDVHPIE	GLGTDVHPI	0.1439	10542.4	32.00	Sequence
IAs	94	VGNAVVQVIGNRPKI	QVIGNRPKI	0.1433	10601.7	32.00	Sequence
IAs	105	RPKIGWRRLEAQAVL	RRLEAQAVL	0.1420	10753.2	32.00	Sequence
IAs	3	LPRVGLGTDVHPIEP	GLGTDVHPI	0.1416	10799.4	32.00	Sequence
IAs	62	EVFGVDDPRWQGVSG	FGVDDPRWQ	0.1401	10985.1	32.00	Sequence
IAs	13	HPIEPGRPCWLVGLL	HPIEPGRPC	0.1354	11549.3	32.00	Sequence
IAs	100	QVIGNRPKIGWRRLE	VIGNRPKIG	0.1346	11656.9	32.00	Sequence
IAs	99	VQVIGNRPKIGWRRL	VIGNRPKIG	0.1337	11769.3	32.00	Sequence
IAs	141	GRGEGLAAIATALVV	AAIATALVV	0.1330	11863.5	32.00	Sequence
IAs	47	LCDAVLSAAGLGDIG	AVLSAAGLG	0.1290	12387.0	32.00	Sequence
IAs	106	PKIGWRRLEAQAVLS	RRLEAQAVL	0.1287	12423.8	32.00	Sequence
IAs	44	VHALCDAVLSAAGLG	AVLSAAGLG	0.1279	12531.0	32.00	Sequence
IAs	121	RLLNAPVSVSATTTD	RLLNAPVSV	0.1263	12752.4	32.00	Sequence
IAs	63	VFGVDDPRWQGVSGA	FGVDDPRWQ	0.1224	13296.6	32.00	Sequence
IAs	110	WRRLEAQAVLSRLLN	RRLEAQAVL	0.1203	13605.9	32.00	Sequence
IAs	107	KIGWRRLEAQAVLSR	RRLEAQAVL	0.1169	14120.3	32.00	Sequence
IAs	45	HALCDAVLSAAGLGD	AVLSAAGLG	0.1164	14185.5	32.00	Sequence
IAs	79	MLRHVVVLITQHGYR	VLITQHGYR	0.1141	14548.6	32.00	Sequence
IAs	46	ALCDAVLSAAGLGDI	AVLSAAGLG	0.1124	14813.9	32.00	Sequence
IAs	113	LEAQAVLSRLLNAPV	VLSRLLNAP	0.1124	14818.6	32.00	Sequence
IAs	80	LRHVVVLITQHGYRV	VLITQHGYR	0.1101	15187.3	50.00	Sequence
IAs	111	RRLEAQAVLSRLLNA	RRLEAQAVL	0.1088	15414.0	50.00	Sequence
IAs	109	GWRRLEAQAVLSRLL	RRLEAQAVL	0.1087	15427.7	50.00	Sequence
IAs	65	GVDDPRWQGVSGADM	RWQGVSGAD	0.1087	15429.0	50.00	Sequence
IAs	18	GRPCWLVGLLFPSAD	LVGLLFPSA	0.1084	15475.8	50.00	Sequence
IAs	64	FGVDDPRWQGVSGAD	FGVDDPRWQ	0.1078	15571.4	50.00	Sequence
IAs	108	IGWRRLEAQAVLSRL	RRLEAQAVL	0.1077	15585.2	50.00	Sequence
IAs	14	PIEPGRPCWLVGLLF	RPCWLVGLL	0.1075	15618.1	50.00	Sequence
IAs	50	AVLSAAGLGDIGEVF	AVLSAAGLG	0.1067	15755.9	50.00	Sequence
IAs	19	RPCWLVGLLFPSADG	LVGLLFPSA	0.1054	15977.6	50.00	Sequence
IAs	57	LGDIGEVFGVDDPRW	EVFGVDDPR	0.1035	16317.7	50.00	Sequence
IAs	56	GLGDIGEVFGVDDPR	GEVFGVDDP	0.1024	16506.8	50.00	Sequence
IAs	48	CDAVLSAAGLGDIGE	AVLSAAGLG	0.1023	16536.3	50.00	Sequence
IAs	49	DAVLSAAGLGDIGEV	AVLSAAGLG	0.1020	16574.5	50.00	Sequence
IAs	15	IEPGRPCWLVGLLFP	RPCWLVGLL	0.1002	16909.6	50.00	Sequence
IAs	142	RGEGLAAIATALVVS	AAIATALVV	0.0988	17175.3	50.00	Sequence
IAs	81	RHVVVLITQHGYRVG	RHVVVLITQ	0.0963	17637.2	50.00	Sequence
IAs	17	PGRPCWLVGLLFPSA	RPCWLVGLL	0.0950	17888.8	50.00	Sequence

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IAs  93  RVGNAVVQVIGNRPK  AVVQVIGNR   0.0946  17965.3  50.00  Sequence
IAs 101  VIGNRPKIGWRRLEA  VIGNRPKIG   0.0937  18140.7  50.00  Sequence
IAs  91  GYRVGNAVVQVIGNR  AVVQVIGNR   0.0932  18233.3  50.00  Sequence
IAs  92  YRVGNAVVQVIGNRP  AVVQVIGNR   0.0923  18408.8  50.00  Sequence
IAs 144  EGLAAIATALVVSLR  AAIATALVV   0.0915  18577.7  50.00  Sequence
IAs  85  VLITQHGYRVGNAVV  VLITQHGYR   0.0912  18642.7  50.00  Sequence
IAs 143  GEGLAAIATALVVSL  AAIATALVV   0.0911  18657.2  50.00  Sequence
IAs  84  VVLITQHGYRVGNAV  QHGYRVGNA   0.0870  19498.9  50.00  Sequence
IAs 123  LNAPVSVSATTTDGL  APVSVSATT   0.0848  19971.6  50.00  Sequence
IAs 140  TGRGEGLAAIATALV  GRGEGLAAI   0.0835  20260.2  50.00  Sequence
IAs 112  RLEAQAVLSRLLNAP  VLSRLLNAP   0.0828  20404.3  50.00  Sequence
IAs 139  LTGRGEGLAAIATAL  EGLAAIATA   0.0810  20817.5  50.00  Sequence
IAs  83  VVVLITQHGYRVGNA  QHGYRVGNA   0.0805  20933.8  50.00  Sequence
IAs  52  LSAAGLGDIGEVFGV  SAAGLGDIG   0.0802  21003.7  50.00  Sequence
IAs  82  HVVVLITQHGYRVGN  HVVVLITQH   0.0799  21067.0  50.00  Sequence
IAs  74  VSGADMLRHVVVLIT  SGADMLRHV   0.0798  21095.3  50.00  Sequence
IAs  16  EPGRPCWLVGLLFPS  RPCWLVGLL   0.0783  21423.7  50.00  Sequence
IAs  51  VLSAAGLGDIGEVFG  SAAGLGDIG   0.0780  21502.7  50.00  Sequence
IAs 138  GLTGRGEGLAAIATA  EGLAAIATA   0.0776  21600.8  50.00  Sequence
IAs  75  SGADMLRHVVVLITQ  RHVVVLITQ   0.0775  21620.5  50.00  Sequence
IAs  88  TQHGYRVGNAVVQVI  RVGNAVVQV   0.0770  21733.8  50.00  Sequence
IAs  73  GVSGADMLRHVVVLI  SGADMLRHV   0.0767  21808.7  50.00  Sequence
IAs  89  QHGYRVGNAVVQVIG  RVGNAVVQV   0.0763  21888.6  50.00  Sequence
IAs  23  LVGLLFPSADGCAGH  VGLLFPSAD   0.0751  22180.9  50.00  Sequence
IAs  76  GADMLRHVVVLITQH  RHVVVLITQ   0.0750  22212.8  50.00  Sequence
IAs 124  NAPVSVSATTTDGLG  APVSVSATT   0.0748  22267.4  50.00  Sequence
IAs  20  PCWLVGLLFPSADGC  LVGLLFPSA   0.0742  22398.4  50.00  Sequence
IAs 122  LLNAPVSVSATTTDG  APVSVSATT   0.0732  22639.6  50.00  Sequence
IAs  87  ITQHGYRVGNAVVQV  RVGNAVVQV   0.0731  22670.5  50.00  Sequence
IAs  22  WLVGLLFPSADGCAG  VGLLFPSAD   0.0721  22906.7  50.00  Sequence
IAs  21  CWLVGLLFPSADGCA  LVGLLFPSA   0.0709  23218.9  50.00  Sequence
IAs   0  VNQLPRVGLGTDVHP  RVGLGTDVH   0.0702  23400.0  50.00  Sequence
IAs  90  HGYRVGNAVVQVIGN  VGNAVVQVI   0.0689  23715.5  50.00  Sequence
IAs 136  GLGLTGRGEGLAAIA  RGEGLAAIA   0.0682  23908.2  50.00  Sequence
IAs 137  LGLTGRGEGLAAIAT  RGEGLAAIA   0.0675  24100.2  50.00  Sequence
IAs  55  AGLGDIGEVFGVDDP  GEVFGVDDP   0.0668  24260.5  50.00  Sequence
IAs  43  AVHALCDAVLSAAGL  DAVLSAAGL   0.0640  25011.1  50.00  Sequence
IAs  77  ADMLRHVVVLITQHG  RHVVVLITQ   0.0639  25056.3  50.00  Sequence
IAs  78  DMLRHVVVLITQHGY  RHVVVLITQ   0.0606  25950.8  50.00  Sequence
IAs  53  SAAGLGDIGEVFGVD  SAAGLGDIG   0.0603  26044.8  50.00  Sequence
IAs  38  SDGDVAVHALCDAVL  VAVHALCDA   0.0587  26497.6  50.00  Sequence
IAs  37  HSDGDVAVHALCDAV  VAVHALCDA   0.0562  27225.9  50.00  Sequence
IAs 135  DGLGLTGRGEGLAAI  GRGEGLAAI   0.0561  27257.4  50.00  Sequence
IAs  86  LITQHGYRVGNAVVQ  YRVGNAVVQ   0.0544  27743.9  50.00  Sequence
IAs  36  GHSDGDVAVHALCDA  VAVHALCDA   0.0539  27902.8  50.00  Sequence
IAs 104  NRPKIGWRRLEAQAV  IGWRRLEAQ   0.0532  28126.9  50.00  Sequence
IAs 125  APVSVSATTTDGLGL  APVSVSATT   0.0515  28649.6  50.00  Sequence
IAs  42  VAVHALCDAVLSAAG  VAVHALCDA   0.0491  29377.9  50.00  Sequence
IAs  30  SADGCAGHSDGDVAV  AGHSDGDVA   0.0470  30060.8  50.00  Sequence
IAs  29  PSADGCAGHSDGDVA  AGHSDGDVA   0.0470  30076.4  50.00  Sequence
IAs 102  IGNRPKIGWRRLEAQ  IGWRRLEAQ   0.0458  30453.7  50.00  Sequence
IAs  41  DVAVHALCDAVLSAA  HALCDAVLS   0.0454  30607.3  50.00  Sequence
IAs  39  DGDVAVHALCDAVLS  HALCDAVLS   0.0453  30639.4  50.00  Sequence
IAs  34  CAGHSDGDVAVHALC  GDVAVHALC   0.0442  30994.2  50.00  Sequence
IAs  40  GDVAVHALCDAVLSA  HALCDAVLS   0.0431  31350.4  50.00  Sequence
IAs  24  VGLLFPSADGCAGHS  VGLLFPSAD   0.0430  31394.5  50.00  Sequence
IAs 127  VSVSATTTDGLGLTG  VSVSATTTD   0.0427  31484.6  50.00  Sequence
IAs 103  GNRPKIGWRRLEAQA  IGWRRLEAQ   0.0427  31492.1  50.00  Sequence
IAs 128  SVSATTTDGLGLTGR  VSATTTDGL   0.0417  31847.5  50.00  Sequence
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    IAs  126  PVSVSATTTDGLGLT  VSVSATTTD       0.0415      31899.5             50.00     Sequence
    IAs   54  AAGLGDIGEVFGVDD  AGLGDIGEV       0.0415      31920.2             50.00     Sequence
    IAs   28  FPSADGCAGHSDGDV  CAGHSDGDV       0.0412      32007.1             50.00     Sequence
    IAs   35  AGHSDGDVAVHALCD  GDVAVHALC       0.0396      32565.3             50.00     Sequence
    IAs   25  GLLFPSADGCAGHSD  ADGCAGHSD       0.0374      33359.8             50.00     Sequence
    IAs   31  ADGCAGHSDGDVAVH  AGHSDGDVA       0.0368      33577.5             50.00     Sequence
    IAs  129  VSATTTDGLGLTGRG  VSATTTDGL       0.0365      33685.9             50.00     Sequence
    IAs   26  LLFPSADGCAGHSDG  ADGCAGHSD       0.0359      33906.0             50.00     Sequence
    IAs   33  GCAGHSDGDVAVHAL  SDGDVAVHA       0.0353      34142.4             50.00     Sequence
    IAs   27  LFPSADGCAGHSDGD  ADGCAGHSD       0.0334      34825.1             50.00     Sequence
    IAs   32  DGCAGHSDGDVAVHA  SDGDVAVHA       0.0330      34983.8             50.00     Sequence
    IAs  130  SATTTDGLGLTGRGE  GLGLTGRGE       0.0304      35972.1             50.00     Sequence
    IAs  134  TDGLGLTGRGEGLAA  GLGLTGRGE       0.0304      35988.1             50.00     Sequence
    IAs  133  TTDGLGLTGRGEGLA  GLGLTGRGE       0.0293      36419.0             50.00     Sequence
    IAs  131  ATTTDGLGLTGRGEG  GLGLTGRGE       0.0283      36817.2             50.00     Sequence
    IAs  132  TTTDGLGLTGRGEGL  GLGLTGRGE       0.0280      36935.3             50.00     Sequence
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Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 145

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Explain the output. Go **back**.