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  220  AFLYLVLGGMGVWAK  YLVLGGMGV        0.8906          3.3         SB     0.20     Sequence
   DRB1_0101  219  VAFLYLVLGGMGVWA  YLVLGGMGV        0.8906          3.3         SB     0.20     Sequence
   DRB1_0101   81  LNRFISGASAPVTGP  FISGASAPV        0.8888          3.3         SB     0.30     Sequence
   DRB1_0101   80  RLNRFISGASAPVTG  FISGASAPV        0.8884          3.3         SB     0.30     Sequence
   DRB1_0101  218  TVAFLYLVLGGMGVW  YLVLGGMGV        0.8854          3.5         SB     0.40     Sequence
   DRB1_0101  217  ITVAFLYLVLGGMGV  YLVLGGMGV        0.8811          3.6         SB     0.80     Sequence
   DRB1_0101   79  ARLNRFISGASAPVT  FISGASAPV        0.8800          3.7         SB     0.80     Sequence
   DRB1_0101  221  FLYLVLGGMGVWAKL  YLVLGGMGV        0.8798          3.7         SB     0.80     Sequence
   DRB1_0101   82  NRFISGASAPVTGPA  FISGASAPV        0.8744          3.9         SB     0.80     Sequence
   DRB1_0101  271  IVLMTALATIGAFVY  MTALATIGA        0.8690          4.1         SB     1.00     Sequence
   DRB1_0101  222  LYLVLGGMGVWAKLN  YLVLGGMGV        0.8673          4.2         SB     1.00     Sequence
   DRB1_0101   78  DARLNRFISGASAPV  FISGASAPV        0.8609          4.5         SB     2.00     Sequence
   DRB1_0101   83  RFISGASAPVTGPAA  FISGASAPV        0.8592          4.6         SB     2.00     Sequence
   DRB1_0101  270  NIVLMTALATIGAFV  MTALATIGA        0.8569          4.7         SB     2.00     Sequence
   DRB1_0101  272  VLMTALATIGAFVYN  MTALATIGA        0.8485          5.2         SB     4.00     Sequence
   DRB1_0101  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.8455          5.3         SB     4.00     Sequence
   DRB1_0101  269  VNIVLMTALATIGAF  IVLMTALAT        0.8418          5.5         SB     4.00     Sequence
   DRB1_0101  268  LVNIVLMTALATIGA  IVLMTALAT        0.8384          5.7         SB     4.00     Sequence
   DRB1_0101  273  LMTALATIGAFVYNL  MTALATIGA        0.8253          6.6         SB     4.00     Sequence
   DRB1_0101  189  SMQIRRIDPWSTLKV  IRRIDPWST        0.8222          6.9         SB     4.00     Sequence
   DRB1_0101   84  FISGASAPVTGPAAA  FISGASAPV        0.8218          6.9         SB     8.00     Sequence
   DRB1_0101  267  GLVNIVLMTALATIG  IVLMTALAT        0.8175          7.2         SB     8.00     Sequence
   DRB1_0101  266  IGLVNIVLMTALATI  IVLMTALAT        0.8003          8.7         SB     8.00     Sequence
   DRB1_0101  171  RDARVQLSARRSRGP  RVQLSARRS        0.7933          9.4         SB     8.00     Sequence
   DRB1_0101  170  SRDARVQLSARRSRG  RVQLSARRS        0.7928          9.4         SB     8.00     Sequence
   DRB1_0101  265  LIGLVNIVLMTALAT  IVLMTALAT        0.7921          9.5         SB     8.00     Sequence
   DRB1_0101  190  MQIRRIDPWSTLKVS  IRRIDPWST        0.7865         10.1         SB     8.00     Sequence
   DRB1_0101  274  MTALATIGAFVYNLI  MTALATIGA        0.7737         11.6         SB    16.00     Sequence
   DRB1_0101  197  PWSTLKVSLLLSVAL  VSLLLSVAL        0.7727         11.7         SB    16.00     Sequence
   DRB1_0101  280  IGAFVYNLITDLIGG  FVYNLITDL        0.7711         11.9         SB    16.00     Sequence
   DRB1_0101  198  WSTLKVSLLLSVALF  VSLLLSVAL        0.7696         12.1         SB    16.00     Sequence
   DRB1_0101  281  GAFVYNLITDLIGGI  FVYNLITDL        0.7689         12.2         SB    16.00     Sequence
   DRB1_0101  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.7638         12.9         SB    16.00     Sequence
   DRB1_0101  282  AFVYNLITDLIGGIE  YNLITDLIG        0.7614         13.2         SB    16.00     Sequence
   DRB1_0101  169  ESRDARVQLSARRSR  RVQLSARRS        0.7608         13.3         SB    16.00     Sequence
   DRB1_0101  192  IRRIDPWSTLKVSLL  WSTLKVSLL        0.7601         13.4         SB    16.00     Sequence
   DRB1_0101  199  STLKVSLLLSVALFF  VSLLLSVAL        0.7594         13.5         SB    16.00     Sequence
   DRB1_0101  195  IDPWSTLKVSLLLSV  WSTLKVSLL        0.7544         14.3         SB    16.00     Sequence
   DRB1_0101  188  ASMQIRRIDPWSTLK  IRRIDPWST        0.7480         15.3         SB    16.00     Sequence
   DRB1_0101  229  MGVWAKLNSNVGDLL  WAKLNSNVG        0.7457         15.7         SB    16.00     Sequence
   DRB1_0101  279  TIGAFVYNLITDLIG  FVYNLITDL        0.7410         16.5         SB    16.00     Sequence
   DRB1_0101  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.7405         16.6         SB    16.00     Sequence
   DRB1_0101  191  QIRRIDPWSTLKVSL  IRRIDPWST        0.7342         17.7         SB    16.00     Sequence
   DRB1_0101  172  DARVQLSARRSRGPV  RVQLSARRS        0.7333         17.9         SB    16.00     Sequence
   DRB1_0101  196  DPWSTLKVSLLLSVA  WSTLKVSLL        0.7279         19.0         SB    16.00     Sequence
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DRB1_0101  193  RRIDPWSTLKVSLLL  WSTLKVSLL        0.7268         19.2        SB    16.00     Sequence
DRB1_0101  173  ARVQLSARRSRGPVR  RVQLSARRS        0.7146         21.9        SB    16.00     Sequence
DRB1_0101  201  LKVSLLLSVALFFVW  VSLLLSVAL        0.7122         22.5        SB    16.00     Sequence
DRB1_0101  278  ATIGAFVYNLITDLI  FVYNLITDL        0.7072         23.8        SB    32.00     Sequence
DRB1_0101  209  VALFFVWMITVAFLY  FVWMITVAF        0.6976         26.4        SB    32.00     Sequence
DRB1_0101  232  WAKLNSNVGDLLNNA  LNSNVGDLL        0.6976         26.4        SB    32.00     Sequence
DRB1_0101  210  ALFFVWMITVAFLYL  FVWMITVAF        0.6970         26.5        SB    32.00     Sequence
DRB1_0101  208  SVALFFVWMITVAFL  FVWMITVAF        0.6970         26.5        SB    32.00     Sequence
DRB1_0101  283  FVYNLITDLIGGIEV  YNLITDLIG        0.6957         26.9        SB    32.00     Sequence
DRB1_0101  168  AESRDARVQLSARRS  RVQLSARRS        0.6896         28.7        SB    32.00     Sequence
DRB1_0101  216  MITVAFLYLVLGGMG  FLYLVLGGM        0.6883         29.2        SB    32.00     Sequence
DRB1_0101   18  DGLVDRGGAHRAATG  VDRGGAHRA        0.6847         30.3        SB    32.00     Sequence
DRB1_0101  211  LFFVWMITVAFLYLV  FVWMITVAF        0.6807         31.6        SB    32.00     Sequence
DRB1_0101  187  RASMQIRRIDPWSTL  IRRIDPWST        0.6795         32.0        SB    32.00     Sequence
DRB1_0101  286  NLITDLIGGIEVTLA  TDLIGGIEV        0.6778         32.7        SB    32.00     Sequence
DRB1_0101  230  GVWAKLNSNVGDLLN  WAKLNSNVG        0.6775         32.8        SB    32.00     Sequence
DRB1_0101   19  GLVDRGGAHRAATGP  VDRGGAHRA        0.6760         33.3        SB    32.00     Sequence
DRB1_0101   77  ADARLNRFISGASAP  NRFISGASA        0.6752         33.6        SB    32.00     Sequence
DRB1_0101  212  FFVWMITVAFLYLVL  FVWMITVAF        0.6711         35.1        SB    32.00     Sequence
DRB1_0101   76  AADARLNRFISGASA  NRFISGASA        0.6703         35.4        SB    32.00     Sequence
DRB1_0101  259  IFGGAFLIGLVNIVL  FLIGLVNIV        0.6690         35.9        SB    32.00     Sequence
DRB1_0101  207  LSVALFFVWMITVAF  FVWMITVAF        0.6664         36.9        SB    32.00     Sequence
DRB1_0101  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.6625         38.5        SB    32.00     Sequence
DRB1_0101  215  WMITVAFLYLVLGGM  FLYLVLGGM        0.6587         40.2        SB    32.00     Sequence
DRB1_0101  174  RVQLSARRSRGPVRA  RVQLSARRS        0.6575         40.7        SB    32.00     Sequence
DRB1_0101  260  FGGAFLIGLVNIVLM  FLIGLVNIV        0.6564         41.2        SB    32.00     Sequence
DRB1_0101  261  GGAFLIGLVNIVLMT  FLIGLVNIV        0.6525         43.0        SB    32.00     Sequence
DRB1_0101  231  VWAKLNSNVGDLLNN  WAKLNSNVG        0.6501         44.1        SB    32.00     Sequence
DRB1_0101  258  TIFGGAFLIGLVNIV  FLIGLVNIV        0.6443         46.9        SB    32.00     Sequence
DRB1_0101  118  AEAYASELPDLSGPT  YASELPDLS        0.6437         47.2        SB    32.00     Sequence
DRB1_0101  233  AKLNSNVGDLLNNAS  LNSNVGDLL        0.6412         48.5        SB    32.00     Sequence
DRB1_0101   17  ADGLVDRGGAHRAAT  VDRGGAHRA        0.6371         50.7        WB    32.00     Sequence
DRB1_0101  213  FVWMITVAFLYLVLG  FVWMITVAF        0.6348         52.0        WB    32.00     Sequence
DRB1_0101  262  GAFLIGLVNIVLMTA  FLIGLVNIV        0.6343         52.3        WB    32.00     Sequence
DRB1_0101  277  LATIGAFVYNLITDL  FVYNLITDL        0.6337         52.6        WB    32.00     Sequence
DRB1_0101  228  GMGVWAKLNSNVGDL  WAKLNSNVG        0.6329         53.1        WB    32.00     Sequence
DRB1_0101  264  FLIGLVNIVLMTALA  NIVLMTALA        0.6304         54.5        WB    32.00     Sequence
DRB1_0101  240  GDLLNNASGSSAELV  LNNASGSSA        0.6299         54.8        WB    32.00     Sequence
DRB1_0101   20  LVDRGGAHRAATGPG  VDRGGAHRA        0.6293         55.2        WB    32.00     Sequence
DRB1_0101  285  YNLITDLIGGIEVTL  TDLIGGIEV        0.6270         56.6        WB    32.00     Sequence
DRB1_0101   87  GASAPVTGPAAAVRT  PVTGPAAAV        0.6247         58.0        WB    32.00     Sequence
DRB1_0101   88  ASAPVTGPAAAVRTP  PVTGPAAAV        0.6244         58.2        WB    32.00     Sequence
DRB1_0101  255  SSGTIFGGAFLIGLV  TIFGGAFLI        0.6244         58.2        WB    32.00     Sequence
DRB1_0101  254  VSSGTIFGGAFLIGL  TIFGGAFLI        0.6239         58.5        WB    32.00     Sequence
DRB1_0101  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.6181         62.3        WB    32.00     Sequence
DRB1_0101  287  LITDLIGGIEVTLAD  TDLIGGIEV        0.6171         63.0        WB    32.00     Sequence
DRB1_0101  257  GTIFGGAFLIGLVNI  TIFGGAFLI        0.6143         64.9        WB    32.00     Sequence
DRB1_0101  263  AFLIGLVNIVLMTAL  FLIGLVNIV        0.6079         69.6        WB    32.00     Sequence
DRB1_0101  256  SGTIFGGAFLIGLVN  TIFGGAFLI        0.6073         70.1        WB    32.00     Sequence
DRB1_0101  242  LLNNASGSSAELVSS  LNNASGSSA        0.6059         71.1        WB    32.00     Sequence
DRB1_0101  284  VYNLITDLIGGIEVT  YNLITDLIG        0.6051         71.7        WB    32.00     Sequence
DRB1_0101   86  SGASAPVTGPAAAVR  PVTGPAAAV        0.5995         76.2        WB    50.00     Sequence
DRB1_0101  275  TALATIGAFVYNLIT  LATIGAFVY        0.5963         78.9        WB    50.00     Sequence
DRB1_0101  253  LVSSGTIFGGAFLIG  TIFGGAFLI        0.5926         82.1        WB    50.00     Sequence
DRB1_0101  241  DLLNNASGSSAELVS  LNNASGSSA        0.5919         82.7        WB    50.00     Sequence
DRB1_0101  214  VWMITVAFLYLVLGG  ITVAFLYLV        0.5824         91.7        WB    50.00     Sequence
DRB1_0101  206  LLSVALFFVWMITVA  LFFVWMITV        0.5810         93.1        WB    50.00     Sequence
DRB1_0101  252  ELVSSGTIFGGAFLI  TIFGGAFLI        0.5740        100.4        WB    50.00     Sequence
DRB1_0101  288  ITDLIGGIEVTLADR  LIGGIEVTL        0.5736        100.9        WB    50.00     Sequence
DRB1_0101   89  SAPVTGPAAAVRTPQ  PVTGPAAAV        0.5710        103.7        WB    50.00     Sequence
DRB1_0101  224  LVLGGMGVWAKLNSN  VLGGMGVWA        0.5674        107.9        WB    50.00     Sequence
DRB1_0101  119  EAYASELPDLSGPTP  YASELPDLS        0.5665        108.9        WB    50.00     Sequence
DRB1_0101  234  KLNSNVGDLLNNASG  LNSNVGDLL        0.5616        114.8        WB    50.00     Sequence
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DRB1_0101  276  ALATIGAFVYNLITD  LATIGAFVY         0.5591         117.9          WB     50.00      Sequence
DRB1_0101  243  LNNASGSSAELVSSG  ASGSSAELV         0.5533         125.7          WB     50.00      Sequence
DRB1_0101  186  VRASMQIRRIDPWST  IRRIDPWST         0.5520         127.3          WB     50.00      Sequence
DRB1_0101   16  NADGLVDRGGAHRAA  VDRGGAHRA         0.5514         128.3          WB     50.00      Sequence
DRB1_0101  205  LLLSVALFFVWMITV  LFFVWMITV         0.5491         131.4          WB     50.00      Sequence
DRB1_0101  117  PAEAYASELPDLSGP  YASELPDLS         0.5459         136.1          WB     50.00      Sequence
DRB1_0101  225  VLGGMGVWAKLNSNV  VLGGMGVWA         0.5458         136.2          WB     50.00      Sequence
DRB1_0101  226  LGGMGVWAKLNSNVG  WAKLNSNVG         0.5439         139.1          WB     50.00      Sequence
DRB1_0101   85  ISGASAPVTGPAAAV  PVTGPAAAV         0.5396         145.6          WB     50.00      Sequence
DRB1_0101  116  SPAEAYASELPDLSG  YASELPDLS         0.5379         148.4          WB     50.00      Sequence
DRB1_0101   21  VDRGGAHRAATGPGR  VDRGGAHRA         0.5309         160.1          WB     50.00      Sequence
DRB1_0101  239  VGDLLNNASGSSAEL  LNNASGSSA         0.5255         169.8          WB     50.00      Sequence
DRB1_0101   90  APVTGPAAAVRTPQP  PVTGPAAAV         0.5186         182.9          WB     50.00      Sequence
DRB1_0101  227  GGMGVWAKLNSNVGD  WAKLNSNVG         0.5172         185.7          WB     50.00      Sequence
DRB1_0101  289  TDLIGGIEVTLADRD  LIGGIEVTL         0.5162         187.6          WB     50.00      Sequence
DRB1_0101  120  AYASELPDLSGPTPR  YASELPDLS         0.5128         194.8          WB     50.00      Sequence
DRB1_0101  236  NSNVGDLLNNASGSS  VGDLLNNAS         0.5097         201.3          WB     50.00      Sequence
DRB1_0101  204  SLLLSVALFFVWMIT  LLSVALFFV         0.5096         201.5          WB     50.00      Sequence
DRB1_0101  247  SGSSAELVSSGTIFG  SAELVSSGT         0.4900         249.2          WB     50.00      Sequence
DRB1_0101  248  GSSAELVSSGTIFGG  AELVSSGTI         0.4844         264.7          WB     50.00      Sequence
DRB1_0101  250  SAELVSSGTIFGGAF  LVSSGTIFG         0.4829         269.0          WB     50.00      Sequence
DRB1_0101  251  AELVSSGTIFGGAFL  VSSGTIFGG         0.4805         276.2          WB     50.00      Sequence
DRB1_0101  235  LNSNVGDLLNNASGS  LNSNVGDLL         0.4780         283.8          WB     50.00      Sequence
DRB1_0101  237  SNVGDLLNNASGSSA  VGDLLNNAS         0.4755         291.4          WB     50.00      Sequence
DRB1_0101  238  NVGDLLNNASGSSAE  DLLNNASGS         0.4739         296.7          WB     50.00      Sequence
DRB1_0101  181  RSRGPVRASMQIRRI  RASMQIRRI         0.4737         297.1          WB     50.00      Sequence
DRB1_0101  115  GSPAEAYASELPDLS  YASELPDLS         0.4682         315.4          WB     50.00      Sequence
DRB1_0101  184  GPVRASMQIRRIDPW  RASMQIRRI         0.4679         316.5          WB     50.00      Sequence
DRB1_0101  167  TAESRDARVQLSARR  SRDARVQLS         0.4641         329.8          WB     50.00      Sequence
DRB1_0101  162  GGRSITAESRDARVQ  SITAESRDA         0.4631         333.3          WB     50.00      Sequence
DRB1_0101   15  PNADGLVDRGGAHRA  VDRGGAHRA         0.4611         340.6          WB     50.00      Sequence
DRB1_0101  157  AAGSSGGRSITAESR  SSGGRSITA         0.4585         350.3          WB     50.00      Sequence
DRB1_0101  177  LSARRSRGPVRASMQ  RRSRGPVRA         0.4569         356.5          WB     50.00      Sequence
DRB1_0101  182  SRGPVRASMQIRRID  RASMQIRRI         0.4561         359.4          WB     50.00      Sequence
DRB1_0101  244  NNASGSSAELVSSGT  ASGSSAELV         0.4528         372.6          WB     50.00      Sequence
DRB1_0101  180  RRSRGPVRASMQIRR  RGPVRASMQ         0.4488         389.1          WB     50.00      Sequence
DRB1_0101   91  PVTGPAAAVRTPQPD  PVTGPAAAV         0.4473         395.5          WB     50.00      Sequence
DRB1_0101  183  RGPVRASMQIRRIDP  RASMQIRRI         0.4463         399.8          WB     50.00      Sequence
DRB1_0101  249  SSAELVSSGTIFGGA  AELVSSGTI         0.4455         403.3          WB     50.00      Sequence
DRB1_0101   42  PPPWQRAATRQSQAG  WQRAATRQS         0.4408         424.4          WB     50.00      Sequence
DRB1_0101  246  ASGSSAELVSSGTIF  SAELVSSGT         0.4343         455.4          WB     50.00      Sequence
DRB1_0101  178  SARRSRGPVRASMQI  RSRGPVRAS         0.4340         456.6          WB     50.00      Sequence
DRB1_0101  176  QLSARRSRGPVRASM  RRSRGPVRA         0.4257         499.7          WB     50.00      Sequence
DRB1_0101  185  PVRASMQIRRIDPWS  RASMQIRRI         0.4250         503.7                 50.00      Sequence
DRB1_0101  124  ELPDLSGPTPRAPQR  DLSGPTPRA         0.4247         504.9                 50.00      Sequence
DRB1_0101  179  ARRSRGPVRASMQIR  RGPVRASMQ         0.4240         508.7                 50.00      Sequence
DRB1_0101  121  YASELPDLSGPTPRA  YASELPDLS         0.4197         532.8                 50.00      Sequence
DRB1_0101   71  TNPPAAADARLNRFI  PAAADARLN         0.4150         561.2                 50.00      Sequence
DRB1_0101   43  PPWQRAATRQSQAGH  WQRAATRQS         0.4138         568.0                 50.00      Sequence
DRB1_0101  107  DASLGCGDGSPAEAY  LGCGDGSPA         0.4114         582.9                 50.00      Sequence
DRB1_0101  163  GRSITAESRDARVQL  SITAESRDA         0.4095         595.6                 50.00      Sequence
DRB1_0101  161  SGGRSITAESRDARV  SITAESRDA         0.4085         601.5                 50.00      Sequence
DRB1_0101  108  ASLGCGDGSPAEAYA  LGCGDGSPA         0.3990         666.9                 50.00      Sequence
DRB1_0101  245  NASGSSAELVSSGTI  ASGSSAELV         0.3989         667.3                 50.00      Sequence
DRB1_0101  125  LPDLSGPTPRAPQRN  DLSGPTPRA         0.3982         672.6                 50.00      Sequence
DRB1_0101   75  AAADARLNRFISGAS  LNRFISGAS         0.3978         675.6                 50.00      Sequence
DRB1_0101   41  DPPPWQRAATRQSQA  WQRAATRQS         0.3954         693.2                 50.00      Sequence
DRB1_0101  175  VQLSARRSRGPVRAS  LSARRSRGP         0.3952         694.8                 50.00      Sequence
DRB1_0101   44  PWQRAATRQSQAGHR  WQRAATRQS         0.3885         746.8                 50.00      Sequence
DRB1_0101  135  APQRNPAPARPAEGG  RNPAPARPA         0.3866         762.5                 50.00      Sequence
DRB1_0101  166  ITAESRDARVQLSAR  SRDARVQLS         0.3847         778.2                 50.00      Sequence
DRB1_0101  158  AGSSGGRSITAESRD  SSGGRSITA         0.3784         833.2                 50.00      Sequence
DRB1_0101    6  PGALSKGDGPNADGL  LSKGDGPNA         0.3695         918.0                 50.00      Sequence
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DRB1_0101  164  RSITAESRDARVQLS  SITAESRDA        0.3690         922.4                 50.00      Sequence
DRB1_0101   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.3667         945.5                 50.00      Sequence
DRB1_0101  160  SSGGRSITAESRDAR  SITAESRDA        0.3594        1023.2                 50.00      Sequence
DRB1_0101  109  SLGCGDGSPAEAYAS  LGCGDGSPA        0.3581        1038.2                 50.00      Sequence
DRB1_0101  156  SAAGSSGGRSITAES  SSGGRSITA        0.3578        1041.6                 50.00      Sequence
DRB1_0101   72  NPPAAADARLNRFIS  PAAADARLN        0.3559        1063.5                 50.00      Sequence
DRB1_0101   74  PAAADARLNRFISGA  ADARLNRFI        0.3513        1118.0                 50.00      Sequence
DRB1_0101  152  SRGDSAAGSSGGRSI  DSAAGSSGG        0.3468        1173.0                 50.00      Sequence
DRB1_0101  134  RAPQRNPAPARPAEG  RNPAPARPA        0.3436        1214.8                 50.00      Sequence
DRB1_0101  165  SITAESRDARVQLSA  SRDARVQLS        0.3434        1217.8                 50.00      Sequence
DRB1_0101  106  PDASLGCGDGSPAEA  LGCGDGSPA        0.3408        1251.5                 50.00      Sequence
DRB1_0101    7  GALSKGDGPNADGLV  LSKGDGPNA        0.3397        1266.3                 50.00      Sequence
DRB1_0101   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.3383        1286.9                 50.00      Sequence
DRB1_0101   73  PPAAADARLNRFISG  PAAADARLN        0.3349        1333.8                 50.00      Sequence
DRB1_0101  123  SELPDLSGPTPRAPQ  DLSGPTPRA        0.3333        1358.0                 50.00      Sequence
DRB1_0101  136  PQRNPAPARPAEGGA  RNPAPARPA        0.3330        1361.8                 50.00      Sequence
DRB1_0101  159  GSSGGRSITAESRDA  SSGGRSITA        0.3314        1386.4                 50.00      Sequence
DRB1_0101   22  DRGGAHRAATGPGRI  HRAATGPGR        0.3240        1501.9                 50.00      Sequence
DRB1_0101   70  PTNPPAAADARLNRF  PAAADARLN        0.3181        1600.5                 50.00      Sequence
DRB1_0101  110  LGCGDGSPAEAYASE  LGCGDGSPA        0.3172        1616.2                 50.00      Sequence
DRB1_0101   23  RGGAHRAATGPGRIP  AHRAATGPG        0.3134        1684.3                 50.00      Sequence
DRB1_0101  133  PRAPQRNPAPARPAE  RNPAPARPA        0.3098        1749.9                 50.00      Sequence
DRB1_0101  137  QRNPAPARPAEGGAG  RNPAPARPA        0.3087        1772.1                 50.00      Sequence
DRB1_0101   39  AGDPPPWQRAATRQS  WQRAATRQS        0.3075        1793.9                 50.00      Sequence
DRB1_0101   53  SQAGHRQPPPVSHPE  GHRQPPPVS        0.3074        1797.3                 50.00      Sequence
DRB1_0101   68  GRPTNPPAAADARLN  TNPPAAADA        0.3054        1836.0                 50.00      Sequence
DRB1_0101  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.3043        1857.1                 50.00      Sequence
DRB1_0101  153  RGDSAAGSSGGRSIT  DSAAGSSGG        0.3031        1881.8                 50.00      Sequence
DRB1_0101  155  DSAAGSSGGRSITAE  SSGGRSITA        0.3026        1892.9                 50.00      Sequence
DRB1_0101    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.3010        1924.8                 50.00      Sequence
DRB1_0101  151  GSRGDSAAGSSGGRS  DSAAGSSGG        0.2997        1953.0                 50.00      Sequence
DRB1_0101  154  GDSAAGSSGGRSITA  SSGGRSITA        0.2986        1977.0                 50.00      Sequence
DRB1_0101  105  DPDASLGCGDGSPAE  LGCGDGSPA        0.2969        2013.4                 50.00      Sequence
DRB1_0101    5  EPGALSKGDGPNADG  LSKGDGPNA        0.2941        2074.9                 50.00      Sequence
DRB1_0101   24  GGAHRAATGPGRIPD  HRAATGPGR        0.2940        2077.4                 50.00      Sequence
DRB1_0101  132  TPRAPQRNPAPARPA  RNPAPARPA        0.2922        2117.2                 50.00      Sequence
DRB1_0101  149  GAGSRGDSAAGSSGG  SRGDSAAGS        0.2922        2117.5                 50.00      Sequence
DRB1_0101   69  RPTNPPAAADARLNR  TNPPAAADA        0.2898        2174.6                 50.00      Sequence
DRB1_0101   52  QSQAGHRQPPPVSHP  GHRQPPPVS        0.2858        2269.7                 50.00      Sequence
DRB1_0101  104  PDPDASLGCGDGSPA  LGCGDGSPA        0.2852        2283.6                 50.00      Sequence
DRB1_0101  150  AGSRGDSAAGSSGGR  DSAAGSSGG        0.2847        2296.3                 50.00      Sequence
DRB1_0101   51  RQSQAGHRQPPPVSH  GHRQPPPVS        0.2831        2335.9                 50.00      Sequence
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DRB1_0101  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.2762        2519.2                 50.00      Sequence
DRB1_0101    3  PNEPGALSKGDGPNA  LSKGDGPNA        0.2739        2581.5                 50.00      Sequence
DRB1_0101    4  NEPGALSKGDGPNAD  LSKGDGPNA        0.2724        2625.3                 50.00      Sequence
DRB1_0101   67  EGRPTNPPAAADARL  TNPPAAADA        0.2721        2631.6                 50.00      Sequence
DRB1_0101  111  GCGDGSPAEAYASEL  GSPAEAYAS        0.2694        2709.4                 50.00      Sequence
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DRB1_0101    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.2656        2825.9                 50.00      Sequence
DRB1_0101  148  GGAGSRGDSAAGSSG  SRGDSAAGS        0.2625        2920.8                 50.00      Sequence
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DRB1_0101  143  ARPAEGGAGSRGDSA  AEGGAGSRG        0.2545        3184.5                 50.00      Sequence
DRB1_0101   65  HPEGRPTNPPAAADA  GRPTNPPAA        0.2541        3197.2                 50.00      Sequence
DRB1_0101   26  AHRAATGPGRIPDAG  AHRAATGPG        0.2539        3207.2                 50.00      Sequence
DRB1_0101   92  VTGPAAAVRTPQPDP  TGPAAAVRT        0.2513        3297.9                 50.00      Sequence
DRB1_0101   66  PEGRPTNPPAAADAR  TNPPAAADA        0.2511        3303.4                 50.00      Sequence
DRB1_0101   60  PPPVSHPEGRPTNPP  VSHPEGRPT        0.2497        3352.9                 50.00      Sequence
DRB1_0101   59  QPPPVSHPEGRPTNP  VSHPEGRPT        0.2465        3471.6                 50.00      Sequence
DRB1_0101   58  RQPPPVSHPEGRPTN  VSHPEGRPT        0.2463        3481.3                 50.00      Sequence
DRB1_0101  147  EGGAGSRGDSAAGSS  SRGDSAAGS        0.2452        3521.4                 50.00      Sequence
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   DRB1_0101   61  PPVSHPEGRPTNPPA  VSHPEGRPT        0.2430       3607.9               50.00     Sequence
   DRB1_0101   57  HRQPPPVSHPEGRPT  VSHPEGRPT        0.2416       3662.7               50.00     Sequence
   DRB1_0101   63  VSHPEGRPTNPPAAA  VSHPEGRPT        0.2415       3667.1               50.00     Sequence
   DRB1_0101   46  QRAATRQSQAGHRQP  TRQSQAGHR        0.2401       3722.4               50.00     Sequence
   DRB1_0101   62  PVSHPEGRPTNPPAA  VSHPEGRPT        0.2398       3733.0               50.00     Sequence
   DRB1_0101   96  AAAVRTPQPDPDASL  VRTPQPDPD        0.2394       3750.1               50.00     Sequence
   DRB1_0101  146  AEGGAGSRGDSAAGS  GAGSRGDSA        0.2393       3752.5               50.00     Sequence
   DRB1_0101   47  RAATRQSQAGHRQPP  TRQSQAGHR        0.2367       3862.6               50.00     Sequence
   DRB1_0101   97  AAVRTPQPDPDASLG  VRTPQPDPD        0.2329       4021.9               50.00     Sequence
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   DRB1_0101  113  GDGSPAEAYASELPD  GSPAEAYAS        0.2244       4410.6               50.00     Sequence
   DRB1_0101    0  VTAPNEPGALSKGDG  TAPNEPGAL        0.2236       4449.6               50.00     Sequence
   DRB1_0101  144  RPAEGGAGSRGDSAA  AEGGAGSRG        0.2229       4481.5               50.00     Sequence
   DRB1_0101   95  PAAAVRTPQPDPDAS  VRTPQPDPD        0.2229       4483.0               50.00     Sequence
   DRB1_0101  140  PAPARPAEGGAGSRG  AEGGAGSRG        0.2228       4489.3               50.00     Sequence
   DRB1_0101  145  PAEGGAGSRGDSAAG  GAGSRGDSA        0.2209       4579.2               50.00     Sequence
   DRB1_0101  128  LSGPTPRAPQRNPAP  LSGPTPRAP        0.2209       4579.9               50.00     Sequence
   DRB1_0101  142  PARPAEGGAGSRGDS  AEGGAGSRG        0.2206       4597.9               50.00     Sequence
   DRB1_0101   98  AVRTPQPDPDASLGC  VRTPQPDPD        0.2201       4618.8               50.00     Sequence
   DRB1_0101  131  PTPRAPQRNPAPARP  PQRNPAPAR        0.2171       4773.7               50.00     Sequence
   DRB1_0101   93  TGPAAAVRTPQPDPD  TGPAAAVRT        0.2163       4815.0               50.00     Sequence
   DRB1_0101   94  GPAAAVRTPQPDPDA  VRTPQPDPD        0.2161       4827.4               50.00     Sequence
   DRB1_0101   48  AATRQSQAGHRQPPP  RQSQAGHRQ        0.2157       4847.3               50.00     Sequence
   DRB1_0101  141  APARPAEGGAGSRGD  AEGGAGSRG        0.2130       4988.5               50.00     Sequence
   DRB1_0101  130  GPTPRAPQRNPAPAR  PQRNPAPAR        0.2106       5121.6               50.00     Sequence
   DRB1_0101   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.2105       5128.4               50.00     Sequence
   DRB1_0101   14  GPNADGLVDRGGAHR  ADGLVDRGG        0.2083       5250.9               50.00     Sequence
   DRB1_0101   64  SHPEGRPTNPPAAAD  GRPTNPPAA        0.2075       5293.3               50.00     Sequence
   DRB1_0101  139  NPAPARPAEGGAGSR  ARPAEGGAG        0.2048       5454.7               50.00     Sequence
   DRB1_0101   56  GHRQPPPVSHPEGRP  GHRQPPPVS        0.2013       5663.6               50.00     Sequence
   DRB1_0101   27  HRAATGPGRIPDAGD  RAATGPGRI        0.1961       5992.4               50.00     Sequence
   DRB1_0101   49  ATRQSQAGHRQPPPV  RQSQAGHRQ        0.1961       5993.8               50.00     Sequence
   DRB1_0101  114  DGSPAEAYASELPDL  GSPAEAYAS        0.1931       6188.1               50.00     Sequence
   DRB1_0101  129  SGPTPRAPQRNPAPA  RAPQRNPAP        0.1882       6522.6               50.00     Sequence
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   DRB1_0101   34  GRIPDAGDPPPWQRA  IPDAGDPPP        0.1668       8221.7               50.00     Sequence
   DRB1_0101   10  SKGDGPNADGLVDRG  DGPNADGLV        0.1649       8398.2               50.00     Sequence
   DRB1_0101  103  QPDPDASLGCGDGSP  ASLGCGDGS        0.1648       8406.6               50.00     Sequence
   DRB1_0101   32  GPGRIPDAGDPPPWQ  RIPDAGDPP        0.1645       8433.9               50.00     Sequence
   DRB1_0101   31  TGPGRIPDAGDPPPW  RIPDAGDPP        0.1633       8539.2               50.00     Sequence
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   DRB1_0101   35  RIPDAGDPPPWQRAA  IPDAGDPPP        0.1618       8681.1               50.00     Sequence
   DRB1_0101   33  PGRIPDAGDPPPWQR  RIPDAGDPP        0.1599       8862.1               50.00     Sequence
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   DRB1_0101   28  RAATGPGRIPDAGDP  RAATGPGRI        0.1524       9613.9               50.00     Sequence
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   DRB1_0101   29  AATGPGRIPDAGDPP  RIPDAGDPP        0.1489       9986.4               50.00     Sequence
   DRB1_0101    2  APNEPGALSKGDGPN  GALSKGDGP        0.1465      10248.5               50.00     Sequence
   DRB1_0101   11  KGDGPNADGLVDRGG  DGPNADGLV        0.1435      10588.7               50.00     Sequence
   DRB1_0101   38  DAGDPPPWQRAATRQ  GDPPPWQRA        0.1420      10753.0               50.00     Sequence
   DRB1_0101   37  PDAGDPPPWQRAATR  GDPPPWQRA        0.1400      10991.5               50.00     Sequence
   DRB1_0101   12  GDGPNADGLVDRGGA  ADGLVDRGG        0.1384      11182.2               50.00     Sequence
   DRB1_0101  101  TPQPDPDASLGCGDG  PQPDPDASL        0.1252      12901.5               50.00     Sequence
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Allele: DRB1_0101. Number of high binders 76. Number of weak binders 75. Number of peptides 290

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      Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0301  163  GRSITAESRDARVQL  ITAESRDAR         0.5216         177.0         WB     8.00      Sequence
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   DRB1_0301  283  FVYNLITDLIGGIEV  VYNLITDLI         0.4889         252.2         WB     8.00      Sequence
   DRB1_0301  173  ARVQLSARRSRGPVR  RVQLSARRS         0.4710         305.9         WB    16.00      Sequence
   DRB1_0301  282  AFVYNLITDLIGGIE  VYNLITDLI         0.4702         308.5         WB    16.00      Sequence
   DRB1_0301  172  DARVQLSARRSRGPV  VQLSARRSR         0.4672         318.8         WB    16.00      Sequence
   DRB1_0301  174  RVQLSARRSRGPVRA  RVQLSARRS         0.4637         331.0         WB    16.00      Sequence
   DRB1_0301  281  GAFVYNLITDLIGGI  VYNLITDLI         0.4556         361.4         WB    16.00      Sequence
   DRB1_0301  162  GGRSITAESRDARVQ  GRSITAESR         0.4487         389.6         WB    16.00      Sequence
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   DRB1_0301  164  RSITAESRDARVQLS  ITAESRDAR         0.4336         458.9         WB    16.00      Sequence
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   DRB1_0301  165  SITAESRDARVQLSA  ITAESRDAR         0.4170         548.8               16.00      Sequence
   DRB1_0301  166  ITAESRDARVQLSAR  ITAESRDAR         0.4153         558.8               16.00      Sequence
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   DRB1_0301  186  VRASMQIRRIDPWST  VRASMQIRR         0.3781         835.9               32.00      Sequence
   DRB1_0301  185  PVRASMQIRRIDPWS  VRASMQIRR         0.3726         887.9               32.00      Sequence
   DRB1_0301  160  SSGGRSITAESRDAR  GRSITAESR         0.3668         944.9               32.00      Sequence
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   DRB1_0301  285  YNLITDLIGGIEVTL  LITDLIGGI         0.3114        1720.9               32.00      Sequence
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   DRB1_0301  265  LIGLVNIVLMTALAT  IGLVNIVLM         0.2837        2321.5               50.00      Sequence
   DRB1_0301  200  TLKVSLLLSVALFFV  VSLLLSVAL         0.2831        2336.2               50.00      Sequence
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   DRB1_0301   74  PAAADARLNRFISGA  AAADARLNR         0.2784        2458.7               50.00      Sequence
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   DRB1_0301  277  LATIGAFVYNLITDL  IGAFVYNLI         0.2720        2635.0               50.00      Sequence
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DRB1_0301   78  DARLNRFISGASAPV  LNRFISGAS         0.2643        2864.9              50.00      Sequence
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DRB1_0301  189  SMQIRRIDPWSTLKV  SMQIRRIDP         0.2201        4620.5              50.00      Sequence
DRB1_0301  203  VSLLLSVALFFVWMI  VSLLLSVAL         0.2184        4707.0              50.00      Sequence
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DRB1_0301  240  GDLLNNASGSSAELV  LLNNASGSS         0.2147        4898.7              50.00      Sequence
DRB1_0301  267  GLVNIVLMTALATIG  GLVNIVLMT         0.2143        4921.6              50.00      Sequence
DRB1_0301  236  NSNVGDLLNNASGSS  VGDLLNNAS         0.2115        5069.4              50.00      Sequence
DRB1_0301  251  AELVSSGTIFGGAFL  AELVSSGTI         0.2113        5085.3              50.00      Sequence
DRB1_0301  192  IRRIDPWSTLKVSLL  IRRIDPWST         0.2100        5155.3              50.00      Sequence
DRB1_0301  231  VWAKLNSNVGDLLNN  KLNSNVGDL         0.2098        5164.6              50.00      Sequence
DRB1_0301  119  EAYASELPDLSGPTP  YASELPDLS         0.2030        5558.1              50.00      Sequence
DRB1_0301  261  GGAFLIGLVNIVLMT  FLIGLVNIV         0.2028        5573.8              50.00      Sequence
DRB1_0301  188  ASMQIRRIDPWSTLK  SMQIRRIDP         0.2017        5636.5              50.00      Sequence
DRB1_0301   69  RPTNPPAAADARLNR  NPPAAADAR         0.2014        5655.7              50.00      Sequence
DRB1_0301  241  DLLNNASGSSAELVS  LLNNASGSS         0.1980        5868.2              50.00      Sequence
DRB1_0301   77  ADARLNRFISGASAP  DARLNRFIS         0.1976        5894.3              50.00      Sequence
DRB1_0301  179  ARRSRGPVRASMQIR  RRSRGPVRA         0.1972        5919.9              50.00      Sequence
DRB1_0301  271  IVLMTALATIGAFVY  VLMTALATI         0.1971        5926.0              50.00      Sequence
DRB1_0301   14  GPNADGLVDRGGAHR  GLVDRGGAH         0.1947        6085.4              50.00      Sequence
DRB1_0301  219  VAFLYLVLGGMGVWA  LYLVLGGMG         0.1935        6162.3              50.00      Sequence
DRB1_0301  270  NIVLMTALATIGAFV  VLMTALATI         0.1934        6171.6              50.00      Sequence
DRB1_0301  272  VLMTALATIGAFVYN  LMTALATIG         0.1904        6373.4              50.00      Sequence
DRB1_0301   20  LVDRGGAHRAATGPG  LVDRGGAHR         0.1858        6696.2              50.00      Sequence
DRB1_0301  190  MQIRRIDPWSTLKVS  MQIRRIDPW         0.1849        6763.3              50.00      Sequence
DRB1_0301  269  VNIVLMTALATIGAF  VLMTALATI         0.1836        6855.3              50.00      Sequence
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DRB1_0301  230  GVWAKLNSNVGDLLN  WAKLNSNVG         0.1714        7825.3              50.00      Sequence
DRB1_0301  101  TPQPDPDASLGCGDG  TPQPDPDAS         0.1706        7893.9              50.00      Sequence
DRB1_0301  268  LVNIVLMTALATIGA  IVLMTALAT         0.1695        7992.7              50.00      Sequence
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DRB1_0301  191  QIRRIDPWSTLKVSL  IRRIDPWST         0.1692        8012.8            50.00      Sequence
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DRB1_0301  273  LMTALATIGAFVYNL  LMTALATIG         0.1625        8615.8            50.00      Sequence
DRB1_0301  213  FVWMITVAFLYLVLG  MITVAFLYL         0.1607        8784.9            50.00      Sequence
DRB1_0301  246  ASGSSAELVSSGTIF  SAELVSSGT         0.1604        8813.4            50.00      Sequence
DRB1_0301  117  PAEAYASELPDLSGP  AEAYASELP         0.1604        8817.1            50.00      Sequence
DRB1_0301   98  AVRTPQPDPDASLGC  TPQPDPDAS         0.1594        8913.4            50.00      Sequence
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DRB1_0301  252  ELVSSGTIFGGAFLI  ELVSSGTIF         0.1580        9046.3            50.00      Sequence
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DRB1_0301  158  AGSSGGRSITAESRD  GRSITAESR         0.1526        9596.7            50.00      Sequence
DRB1_0301  212  FFVWMITVAFLYLVL  VWMITVAFL         0.1513        9727.9            50.00      Sequence
DRB1_0301  211  LFFVWMITVAFLYLV  FVWMITVAF         0.1480       10081.5            50.00      Sequence
DRB1_0301   13  DGPNADGLVDRGGAH  PNADGLVDR         0.1475       10131.5            50.00      Sequence
DRB1_0301   12  GDGPNADGLVDRGGA  PNADGLVDR         0.1463       10263.3            50.00      Sequence
DRB1_0301    5  EPGALSKGDGPNADG  GALSKGDGP         0.1434       10592.8            50.00      Sequence
DRB1_0301  275  TALATIGAFVYNLIT  IGAFVYNLI         0.1432       10623.1            50.00      Sequence
DRB1_0301  218  TVAFLYLVLGGMGVW  LYLVLGGMG         0.1405       10934.1            50.00      Sequence
DRB1_0301  216  MITVAFLYLVLGGMG  MITVAFLYL         0.1400       10993.1            50.00      Sequence
DRB1_0301  115  GSPAEAYASELPDLS  AEAYASELP         0.1397       11024.0            50.00      Sequence
DRB1_0301  109  SLGCGDGSPAEAYAS  LGCGDGSPA         0.1381       11224.0            50.00      Sequence
DRB1_0301   27  HRAATGPGRIPDAGD  RAATGPGRI         0.1361       11470.2            50.00      Sequence
DRB1_0301  274  MTALATIGAFVYNLI  MTALATIGA         0.1349       11621.8            50.00      Sequence
DRB1_0301  126  PDLSGPTPRAPQRNP  PDLSGPTPR         0.1335       11791.7            50.00      Sequence
DRB1_0301  204  SLLLSVALFFVWMIT  SLLLSVALF         0.1332       11830.1            50.00      Sequence
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DRB1_0301   90  APVTGPAAAVRTPQP  APVTGPAAA         0.1296       12306.1            50.00      Sequence
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DRB1_0301  210  ALFFVWMITVAFLYL  FVWMITVAF         0.1284       12467.9            50.00      Sequence
DRB1_0301  215  WMITVAFLYLVLGGM  MITVAFLYL         0.1283       12481.1            50.00      Sequence
DRB1_0301  228  GMGVWAKLNSNVGDL  GMGVWAKLN         0.1276       12565.2            50.00      Sequence
DRB1_0301   11  KGDGPNADGLVDRGG  PNADGLVDR         0.1267       12701.2            50.00      Sequence
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DRB1_0301   96  AAAVRTPQPDPDASL  PQPDPDASL         0.1256       12846.1            50.00      Sequence
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DRB1_0301   84  FISGASAPVTGPAAA  FISGASAPV         0.1224       13301.6            50.00      Sequence
DRB1_0301  205  LLLSVALFFVWMITV  LLLSVALFF         0.1216       13408.1            50.00      Sequence
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DRB1_0301   91  PVTGPAAAVRTPQPD  VTGPAAAVR         0.1164       14191.7            50.00      Sequence
DRB1_0301  243  LNNASGSSAELVSSG  LNNASGSSA         0.1147       14460.1            50.00      Sequence
DRB1_0301  245  NASGSSAELVSSGTI  SGSSAELVS         0.1126       14782.8            50.00      Sequence
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DRB1_0301  107  DASLGCGDGSPAEAY  LGCGDGSPA         0.1090       15374.5            50.00      Sequence
DRB1_0301  209  VALFFVWMITVAFLY  FVWMITVAF         0.1063       15823.1            50.00      Sequence
DRB1_0301  226  LGGMGVWAKLNSNVG  GGMGVWAKL         0.1061       15868.0            50.00      Sequence
DRB1_0301   25  GAHRAATGPGRIPDA  RAATGPGRI         0.1058       15920.1            50.00      Sequence
DRB1_0301  217  ITVAFLYLVLGGMGV  LYLVLGGMG         0.1039       16253.2            50.00      Sequence
DRB1_0301  149  GAGSRGDSAAGSSGG  GAGSRGDSA         0.1027       16453.0            50.00      Sequence
DRB1_0301  114  DGSPAEAYASELPDL  AYASELPDL         0.1024       16515.4            50.00      Sequence
DRB1_0301  111  GCGDGSPAEAYASEL  CGDGSPAEA         0.1018       16627.7            50.00      Sequence
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DRB1_0301  156  SAAGSSGGRSITAES  SAAGSSGGR        0.1013      16712.4                  50.00      Sequence
DRB1_0301    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.1011      16749.5                  50.00      Sequence
DRB1_0301  244  NNASGSSAELVSSGT  SGSSAELVS        0.1008      16800.5                  50.00      Sequence
DRB1_0301  257  GTIFGGAFLIGLVNI  FGGAFLIGL        0.1001      16934.9                  50.00      Sequence
DRB1_0301    3  PNEPGALSKGDGPNA  GALSKGDGP        0.0999      16973.2                  50.00      Sequence
DRB1_0301   47  RAATRQSQAGHRQPP  RAATRQSQA        0.0988      17171.0                  50.00      Sequence
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   DRB1_0301   38  DAGDPPPWQRAATRQ  PPWQRAATR         0.0264      37575.4               50.00     Sequence
   DRB1_0301  141  APARPAEGGAGSRGD  RPAEGGAGS         0.0249      38188.1               50.00     Sequence
   DRB1_0301  140  PAPARPAEGGAGSRG  RPAEGGAGS         0.0222      39333.4               50.00     Sequence
   DRB1_0301  139  NPAPARPAEGGAGSR  PAPARPAEG         0.0220      39416.0               50.00     Sequence
   DRB1_0301  138  RNPAPARPAEGGAGS  PAPARPAEG         0.0206      40025.0               50.00     Sequence
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Allele: DRB1_0301. Number of high binders 0. Number of weak binders 12. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0401  270  NIVLMTALATIGAFV  IVLMTALAT         0.6173         62.9         WB     8.00     Sequence
   DRB1_0401  268  LVNIVLMTALATIGA  IVLMTALAT         0.6165         63.4         WB     8.00     Sequence
   DRB1_0401  269  VNIVLMTALATIGAF  IVLMTALAT         0.6097         68.3         WB     8.00     Sequence
   DRB1_0401  271  IVLMTALATIGAFVY  IVLMTALAT         0.6050         71.8         WB     8.00     Sequence
   DRB1_0401  267  GLVNIVLMTALATIG  IVLMTALAT         0.5954         79.7         WB     8.00     Sequence
   DRB1_0401   80  RLNRFISGASAPVTG  NRFISGASA         0.5893         85.1         WB     8.00     Sequence
   DRB1_0401   81  LNRFISGASAPVTGP  NRFISGASA         0.5799         94.2         WB     8.00     Sequence
   DRB1_0401   79  ARLNRFISGASAPVT  NRFISGASA         0.5799         94.2         WB     8.00     Sequence
   DRB1_0401   82  NRFISGASAPVTGPA  NRFISGASA         0.5703        104.5         WB     8.00     Sequence
   DRB1_0401  229  MGVWAKLNSNVGDLL  MGVWAKLNS         0.5649        110.8         WB    16.00     Sequence
   DRB1_0401  228  GMGVWAKLNSNVGDL  MGVWAKLNS         0.5614        115.1         WB    16.00     Sequence
   DRB1_0401  266  IGLVNIVLMTALATI  IVLMTALAT         0.5595        117.5         WB    16.00     Sequence
   DRB1_0401  262  GAFLIGLVNIVLMTA  AFLIGLVNI         0.5490        131.5         WB    16.00     Sequence
   DRB1_0401  279  TIGAFVYNLITDLIG  AFVYNLITD         0.5456        136.5         WB    16.00     Sequence
   DRB1_0401  280  IGAFVYNLITDLIGG  AFVYNLITD         0.5438        139.2         WB    16.00     Sequence
   DRB1_0401  281  GAFVYNLITDLIGGI  AFVYNLITD         0.5436        139.4         WB    16.00     Sequence
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DRB1_0401  210  ALFFVWMITVAFLYL  FFVWMITVA        0.5415       142.7        WB    16.00      Sequence
DRB1_0401  227  GGMGVWAKLNSNVGD  MGVWAKLNS        0.5361       151.4        WB    16.00      Sequence
DRB1_0401  209  VALFFVWMITVAFLY  LFFVWMITV        0.5350       153.1        WB    16.00      Sequence
DRB1_0401  261  GGAFLIGLVNIVLMT  AFLIGLVNI        0.5313       159.4        WB    16.00      Sequence
DRB1_0401   78  DARLNRFISGASAPV  NRFISGASA        0.5298       161.9        WB    16.00      Sequence
DRB1_0401  265  LIGLVNIVLMTALAT  IVLMTALAT        0.5292       163.1        WB    16.00      Sequence
DRB1_0401  278  ATIGAFVYNLITDLI  GAFVYNLIT        0.5213       177.6        WB    16.00      Sequence
DRB1_0401  226  LGGMGVWAKLNSNVG  MGVWAKLNS        0.5208       178.6        WB    16.00      Sequence
DRB1_0401  263  AFLIGLVNIVLMTAL  AFLIGLVNI        0.5173       185.4        WB    16.00      Sequence
DRB1_0401  211  LFFVWMITVAFLYLV  LFFVWMITV        0.5075       206.1        WB    16.00      Sequence
DRB1_0401  208  SVALFFVWMITVAFL  LFFVWMITV        0.4968       231.6        WB    16.00      Sequence
DRB1_0401  260  FGGAFLIGLVNIVLM  AFLIGLVNI        0.4963       232.7        WB    16.00      Sequence
DRB1_0401  272  VLMTALATIGAFVYN  MTALATIGA        0.4940       238.6        WB    16.00      Sequence
DRB1_0401  259  IFGGAFLIGLVNIVL  AFLIGLVNI        0.4760       289.9        WB    32.00      Sequence
DRB1_0401   77  ADARLNRFISGASAP  NRFISGASA        0.4752       292.5        WB    32.00      Sequence
DRB1_0401  277  LATIGAFVYNLITDL  GAFVYNLIT        0.4740       296.1        WB    32.00      Sequence
DRB1_0401  264  FLIGLVNIVLMTALA  LIGLVNIVL        0.4700       309.2        WB    32.00      Sequence
DRB1_0401  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.4663       321.8        WB    32.00      Sequence
DRB1_0401  207  LSVALFFVWMITVAF  LFFVWMITV        0.4615       339.2        WB    32.00      Sequence
DRB1_0401  198  WSTLKVSLLLSVALF  WSTLKVSLL        0.4577       353.5        WB    32.00      Sequence
DRB1_0401  282  AFVYNLITDLIGGIE  AFVYNLITD        0.4573       354.8        WB    32.00      Sequence
DRB1_0401  212  FFVWMITVAFLYLVL  FFVWMITVA        0.4458       402.0        WB    32.00      Sequence
DRB1_0401  230  GVWAKLNSNVGDLLN  WAKLNSNVG        0.4450       405.6        WB    32.00      Sequence
DRB1_0401  199  STLKVSLLLSVALFF  VSLLLSVAL        0.4393       431.1        WB    32.00      Sequence
DRB1_0401  201  LKVSLLLSVALFFVW  VSLLLSVAL        0.4377       438.9        WB    32.00      Sequence
DRB1_0401  225  VLGGMGVWAKLNSNV  MGVWAKLNS        0.4374       440.4        WB    32.00      Sequence
DRB1_0401  197  PWSTLKVSLLLSVAL  WSTLKVSLL        0.4314       469.5        WB    32.00      Sequence
DRB1_0401   83  RFISGASAPVTGPAA  RFISGASAP        0.4313       470.4        WB    32.00      Sequence
DRB1_0401  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.4229       514.9              32.00      Sequence
DRB1_0401  192  IRRIDPWSTLKVSLL  IRRIDPWST        0.4200       531.3              32.00      Sequence
DRB1_0401  276  ALATIGAFVYNLITD  GAFVYNLIT        0.4199       532.1              32.00      Sequence
DRB1_0401  273  LMTALATIGAFVYNL  MTALATIGA        0.4183       541.3              32.00      Sequence
DRB1_0401  190  MQIRRIDPWSTLKVS  IRRIDPWST        0.4135       570.1              32.00      Sequence
DRB1_0401  191  QIRRIDPWSTLKVSL  IRRIDPWST        0.4130       573.2              32.00      Sequence
DRB1_0401  258  TIFGGAFLIGLVNIV  GAFLIGLVN        0.4027       640.7              32.00      Sequence
DRB1_0401  189  SMQIRRIDPWSTLKV  IRRIDPWST        0.4024       643.1              32.00      Sequence
DRB1_0401  196  DPWSTLKVSLLLSVA  WSTLKVSLL        0.3926       715.0              32.00      Sequence
DRB1_0401  171  RDARVQLSARRSRGP  RVQLSARRS        0.3922       718.0              32.00      Sequence
DRB1_0401  215  WMITVAFLYLVLGGM  WMITVAFLY        0.3899       735.7              32.00      Sequence
DRB1_0401  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.3858       769.5              50.00      Sequence
DRB1_0401  213  FVWMITVAFLYLVLG  WMITVAFLY        0.3854       773.1              50.00      Sequence
DRB1_0401  224  LVLGGMGVWAKLNSN  MGVWAKLNS        0.3827       795.6              50.00      Sequence
DRB1_0401  170  SRDARVQLSARRSRG  RVQLSARRS        0.3777       839.7              50.00      Sequence
DRB1_0401  193  RRIDPWSTLKVSLLL  WSTLKVSLL        0.3773       843.7              50.00      Sequence
DRB1_0401  195  IDPWSTLKVSLLLSV  WSTLKVSLL        0.3723       890.6              50.00      Sequence
DRB1_0401   76  AADARLNRFISGASA  NRFISGASA        0.3718       895.6              50.00      Sequence
DRB1_0401  206  LLSVALFFVWMITVA  FFVWMITVA        0.3690       922.4              50.00      Sequence
DRB1_0401  214  VWMITVAFLYLVLGG  WMITVAFLY        0.3648       965.5              50.00      Sequence
DRB1_0401  274  MTALATIGAFVYNLI  MTALATIGA        0.3611      1004.6              50.00      Sequence
DRB1_0401  231  VWAKLNSNVGDLLNN  WAKLNSNVG        0.3534      1092.5              50.00      Sequence
DRB1_0401  172  DARVQLSARRSRGPV  RVQLSARRS        0.3524      1104.8              50.00      Sequence
DRB1_0401  283  FVYNLITDLIGGIEV  YNLITDLIG        0.3494      1140.3              50.00      Sequence
DRB1_0401  169  ESRDARVQLSARRSR  RVQLSARRS        0.3491      1144.6              50.00      Sequence
DRB1_0401  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.3490      1145.0              50.00      Sequence
DRB1_0401  159  GSSGGRSITAESRDA  SSGGRSITA        0.3473      1166.3              50.00      Sequence
DRB1_0401  160  SSGGRSITAESRDAR  SSGGRSITA        0.3453      1192.6              50.00      Sequence
DRB1_0401  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.3448      1198.2              50.00      Sequence
DRB1_0401  186  VRASMQIRRIDPWST  VRASMQIRR        0.3432      1219.7              50.00      Sequence
DRB1_0401  188  ASMQIRRIDPWSTLK  IRRIDPWST        0.3371      1302.6              50.00      Sequence
DRB1_0401  257  GTIFGGAFLIGLVNI  GAFLIGLVN        0.3359      1320.7              50.00      Sequence
DRB1_0401  284  VYNLITDLIGGIEVT  YNLITDLIG        0.3277      1443.2              50.00      Sequence
DRB1_0401  158  AGSSGGRSITAESRD  SSGGRSITA        0.3272      1450.7              50.00      Sequence
DRB1_0401  184  GPVRASMQIRRIDPW  VRASMQIRR        0.3250      1484.5              50.00      Sequence
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DRB1_0401  185  PVRASMQIRRIDPWS  VRASMQIRR        0.3236       1507.8                50.00      Sequence
DRB1_0401  173  ARVQLSARRSRGPVR  RVQLSARRS        0.3231       1516.3                50.00      Sequence
DRB1_0401  232  WAKLNSNVGDLLNNA  WAKLNSNVG        0.3211       1549.7                50.00      Sequence
DRB1_0401  275  TALATIGAFVYNLIT  GAFVYNLIT        0.3116       1717.0                50.00      Sequence
DRB1_0401  187  RASMQIRRIDPWSTL  IRRIDPWST        0.3058       1828.1                50.00      Sequence
DRB1_0401  174  RVQLSARRSRGPVRA  RVQLSARRS        0.3048       1849.0                50.00      Sequence
DRB1_0401  168  AESRDARVQLSARRS  RDARVQLSA        0.3041       1862.0                50.00      Sequence
DRB1_0401  183  RGPVRASMQIRRIDP  VRASMQIRR        0.3019       1906.6                50.00      Sequence
DRB1_0401  205  LLLSVALFFVWMITV  LFFVWMITV        0.3017       1910.9                50.00      Sequence
DRB1_0401  222  LYLVLGGMGVWAKLN  YLVLGGMGV        0.3002       1943.2                50.00      Sequence
DRB1_0401  157  AAGSSGGRSITAESR  SSGGRSITA        0.2993       1961.6                50.00      Sequence
DRB1_0401  220  AFLYLVLGGMGVWAK  YLVLGGMGV        0.2943       2070.2                50.00      Sequence
DRB1_0401  221  FLYLVLGGMGVWAKL  YLVLGGMGV        0.2942       2071.9                50.00      Sequence
DRB1_0401  285  YNLITDLIGGIEVTL  YNLITDLIG        0.2894       2183.3                50.00      Sequence
DRB1_0401  237  SNVGDLLNNASGSSA  VGDLLNNAS        0.2890       2192.7                50.00      Sequence
DRB1_0401  236  NSNVGDLLNNASGSS  VGDLLNNAS        0.2855       2276.7                50.00      Sequence
DRB1_0401  180  RRSRGPVRASMQIRR  RRSRGPVRA        0.2795       2430.6                50.00      Sequence
DRB1_0401  238  NVGDLLNNASGSSAE  VGDLLNNAS        0.2753       2542.3                50.00      Sequence
DRB1_0401   84  FISGASAPVTGPAAA  ISGASAPVT        0.2739       2581.5                50.00      Sequence
DRB1_0401  219  VAFLYLVLGGMGVWA  YLVLGGMGV        0.2701       2690.4                50.00      Sequence
DRB1_0401   42  PPPWQRAATRQSQAG  WQRAATRQS        0.2698       2697.4                50.00      Sequence
DRB1_0401   43  PPWQRAATRQSQAGH  WQRAATRQS        0.2681       2748.9                50.00      Sequence
DRB1_0401  204  SLLLSVALFFVWMIT  SLLLSVALF        0.2635       2889.1                50.00      Sequence
DRB1_0401  250  SAELVSSGTIFGGAF  ELVSSGTIF        0.2634       2891.8                50.00      Sequence
DRB1_0401  108  ASLGCGDGSPAEAYA  LGCGDGSPA        0.2609       2972.3                50.00      Sequence
DRB1_0401  239  VGDLLNNASGSSAEL  LLNNASGSS        0.2596       3014.3                50.00      Sequence
DRB1_0401  218  TVAFLYLVLGGMGVW  YLVLGGMGV        0.2576       3080.0                50.00      Sequence
DRB1_0401  181  RSRGPVRASMQIRRI  VRASMQIRR        0.2570       3098.3                50.00      Sequence
DRB1_0401  217  ITVAFLYLVLGGMGV  AFLYLVLGG        0.2562       3127.0                50.00      Sequence
DRB1_0401  178  SARRSRGPVRASMQI  RRSRGPVRA        0.2551       3163.1                50.00      Sequence
DRB1_0401  251  AELVSSGTIFGGAFL  ELVSSGTIF        0.2550       3168.9                50.00      Sequence
DRB1_0401  109  SLGCGDGSPAEAYAS  LGCGDGSPA        0.2542       3193.8                50.00      Sequence
DRB1_0401  182  SRGPVRASMQIRRID  VRASMQIRR        0.2530       3238.3                50.00      Sequence
DRB1_0401   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.2498       3351.2                50.00      Sequence
DRB1_0401  107  DASLGCGDGSPAEAY  LGCGDGSPA        0.2497       3353.3                50.00      Sequence
DRB1_0401  177  LSARRSRGPVRASMQ  RRSRGPVRA        0.2486       3393.0                50.00      Sequence
DRB1_0401  249  SSAELVSSGTIFGGA  ELVSSGTIF        0.2480       3417.6                50.00      Sequence
DRB1_0401   44  PWQRAATRQSQAGHR  WQRAATRQS        0.2476       3433.3                50.00      Sequence
DRB1_0401   75  AAADARLNRFISGAS  ARLNRFISG        0.2474       3439.0                50.00      Sequence
DRB1_0401  156  SAAGSSGGRSITAES  SSGGRSITA        0.2451       3526.7                50.00      Sequence
DRB1_0401  235  LNSNVGDLLNNASGS  NSNVGDLLN        0.2432       3598.5                50.00      Sequence
DRB1_0401  149  GAGSRGDSAAGSSGG  SRGDSAAGS        0.2419       3649.2                50.00      Sequence
DRB1_0401  179  ARRSRGPVRASMQIR  RRSRGPVRA        0.2414       3671.4                50.00      Sequence
DRB1_0401   41  DPPPWQRAATRQSQA  WQRAATRQS        0.2393       3754.8                50.00      Sequence
DRB1_0401  248  GSSAELVSSGTIFGG  GSSAELVSS        0.2380       3809.3                50.00      Sequence
DRB1_0401  256  SGTIFGGAFLIGLVN  IFGGAFLIG        0.2362       3883.8                50.00      Sequence
DRB1_0401  216  MITVAFLYLVLGGMG  VAFLYLVLG        0.2358       3898.9                50.00      Sequence
DRB1_0401   54  QAGHRQPPPVSHPEG  GHRQPPPVS        0.2351       3926.8                50.00      Sequence
DRB1_0401  161  SGGRSITAESRDARV  SGGRSITAE        0.2313       4094.5                50.00      Sequence
DRB1_0401  148  GGAGSRGDSAAGSSG  SRGDSAAGS        0.2264       4314.9                50.00      Sequence
DRB1_0401   53  SQAGHRQPPPVSHPE  GHRQPPPVS        0.2251       4378.8                50.00      Sequence
DRB1_0401  106  PDASLGCGDGSPAEA  SLGCGDGSP        0.2233       4463.2                50.00      Sequence
DRB1_0401  234  KLNSNVGDLLNNASG  SNVGDLLNN        0.2228       4485.7                50.00      Sequence
DRB1_0401  150  AGSRGDSAAGSSGGR  SRGDSAAGS        0.2221       4522.3                50.00      Sequence
DRB1_0401  240  GDLLNNASGSSAELV  LLNNASGSS        0.2207       4591.8                50.00      Sequence
DRB1_0401  121  YASELPDLSGPTPRA  YASELPDLS        0.2161       4826.5                50.00      Sequence
DRB1_0401  119  EAYASELPDLSGPTP  YASELPDLS        0.2142       4922.9                50.00      Sequence
DRB1_0401  252  ELVSSGTIFGGAFLI  ELVSSGTIF        0.2142       4925.0                50.00      Sequence
DRB1_0401  286  NLITDLIGGIEVTLA  NLITDLIGG        0.2136       4955.5                50.00      Sequence
DRB1_0401  162  GGRSITAESRDARVQ  GRSITAESR        0.2131       4985.2                50.00      Sequence
DRB1_0401  176  QLSARRSRGPVRASM  RRSRGPVRA        0.2117       5061.9                50.00      Sequence
DRB1_0401  151  GSRGDSAAGSSGGRS  SRGDSAAGS        0.2111       5092.8                50.00      Sequence
DRB1_0401  167  TAESRDARVQLSARR  SRDARVQLS        0.2107       5114.2                50.00      Sequence
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DRB1_0401   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.2101       5151.2               50.00      Sequence
DRB1_0401   85  ISGASAPVTGPAAAV  ISGASAPVT        0.2087       5228.1               50.00      Sequence
DRB1_0401  247  SGSSAELVSSGTIFG  GSSAELVSS        0.2075       5297.3               50.00      Sequence
DRB1_0401  118  AEAYASELPDLSGPT  YASELPDLS        0.2055       5413.5               50.00      Sequence
DRB1_0401  289  TDLIGGIEVTLADRD  LIGGIEVTL        0.2040       5500.7               50.00      Sequence
DRB1_0401  241  DLLNNASGSSAELVS  LLNNASGSS        0.2027       5579.5               50.00      Sequence
DRB1_0401  233  AKLNSNVGDLLNNAS  NSNVGDLLN        0.2008       5692.8               50.00      Sequence
DRB1_0401   55  AGHRQPPPVSHPEGR  GHRQPPPVS        0.2006       5706.0               50.00      Sequence
DRB1_0401  147  EGGAGSRGDSAAGSS  SRGDSAAGS        0.2003       5722.8               50.00      Sequence
DRB1_0401  120  AYASELPDLSGPTPR  YASELPDLS        0.1998       5758.1               50.00      Sequence
DRB1_0401   52  QSQAGHRQPPPVSHP  GHRQPPPVS        0.1935       6162.6               50.00      Sequence
DRB1_0401  105  DPDASLGCGDGSPAE  SLGCGDGSP        0.1930       6195.4               50.00      Sequence
DRB1_0401  155  DSAAGSSGGRSITAE  SSGGRSITA        0.1913       6312.9               50.00      Sequence
DRB1_0401  242  LLNNASGSSAELVSS  LLNNASGSS        0.1909       6336.3               50.00      Sequence
DRB1_0401  175  VQLSARRSRGPVRAS  RRSRGPVRA        0.1905       6363.5               50.00      Sequence
DRB1_0401  166  ITAESRDARVQLSAR  ITAESRDAR        0.1896       6429.4               50.00      Sequence
DRB1_0401  163  GRSITAESRDARVQL  GRSITAESR        0.1871       6603.8               50.00      Sequence
DRB1_0401  124  ELPDLSGPTPRAPQR  ELPDLSGPT        0.1854       6728.9               50.00      Sequence
DRB1_0401  110  LGCGDGSPAEAYASE  LGCGDGSPA        0.1837       6851.6               50.00      Sequence
DRB1_0401  117  PAEAYASELPDLSGP  EAYASELPD        0.1818       6990.3               50.00      Sequence
DRB1_0401  133  PRAPQRNPAPARPAE  RAPQRNPAP        0.1812       7040.3               50.00      Sequence
DRB1_0401  288  ITDLIGGIEVTLADR  LIGGIEVTL        0.1791       7202.8               50.00      Sequence
DRB1_0401  123  SELPDLSGPTPRAPQ  ELPDLSGPT        0.1767       7393.3               50.00      Sequence
DRB1_0401   19  GLVDRGGAHRAATGP  LVDRGGAHR        0.1745       7564.2               50.00      Sequence
DRB1_0401  134  RAPQRNPAPARPAEG  RAPQRNPAP        0.1743       7582.9               50.00      Sequence
DRB1_0401  165  SITAESRDARVQLSA  ITAESRDAR        0.1740       7611.8               50.00      Sequence
DRB1_0401  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.1702       7925.2               50.00      Sequence
DRB1_0401  132  TPRAPQRNPAPARPA  RAPQRNPAP        0.1699       7951.0               50.00      Sequence
DRB1_0401   56  GHRQPPPVSHPEGRP  GHRQPPPVS        0.1696       7982.7               50.00      Sequence
DRB1_0401  131  PTPRAPQRNPAPARP  RAPQRNPAP        0.1690       8031.2               50.00      Sequence
DRB1_0401  122  ASELPDLSGPTPRAP  LPDLSGPTP        0.1689       8039.0               50.00      Sequence
DRB1_0401   18  DGLVDRGGAHRAATG  GLVDRGGAH        0.1680       8115.9               50.00      Sequence
DRB1_0401   74  PAAADARLNRFISGA  ARLNRFISG        0.1668       8221.6               50.00      Sequence
DRB1_0401   51  RQSQAGHRQPPPVSH  GHRQPPPVS        0.1635       8528.7               50.00      Sequence
DRB1_0401   39  AGDPPPWQRAATRQS  WQRAATRQS        0.1629       8580.4               50.00      Sequence
DRB1_0401  146  AEGGAGSRGDSAAGS  AGSRGDSAA        0.1604       8818.3               50.00      Sequence
DRB1_0401  116  SPAEAYASELPDLSG  EAYASELPD        0.1590       8954.4               50.00      Sequence
DRB1_0401  246  ASGSSAELVSSGTIF  GSSAELVSS        0.1585       9001.3               50.00      Sequence
DRB1_0401   50  TRQSQAGHRQPPPVS  GHRQPPPVS        0.1584       9004.4               50.00      Sequence
DRB1_0401  104  PDPDASLGCGDGSPA  SLGCGDGSP        0.1582       9023.8               50.00      Sequence
DRB1_0401  125  LPDLSGPTPRAPQRN  DLSGPTPRA        0.1572       9128.1               50.00      Sequence
DRB1_0401  164  RSITAESRDARVQLS  ITAESRDAR        0.1566       9185.9               50.00      Sequence
DRB1_0401  154  GDSAAGSSGGRSITA  SSGGRSITA        0.1560       9246.4               50.00      Sequence
DRB1_0401  152  SRGDSAAGSSGGRSI  SRGDSAAGS        0.1529       9561.9               50.00      Sequence
DRB1_0401  115  GSPAEAYASELPDLS  YASELPDLS        0.1527       9581.5               50.00      Sequence
DRB1_0401  255  SSGTIFGGAFLIGLV  IFGGAFLIG        0.1492       9950.0               50.00      Sequence
DRB1_0401   17  ADGLVDRGGAHRAAT  GLVDRGGAH        0.1481      10071.4               50.00      Sequence
DRB1_0401   49  ATRQSQAGHRQPPPV  TRQSQAGHR        0.1478      10102.4               50.00      Sequence
DRB1_0401  287  LITDLIGGIEVTLAD  DLIGGIEVT        0.1465      10242.0               50.00      Sequence
DRB1_0401   23  RGGAHRAATGPGRIP  RGGAHRAAT        0.1455      10357.3               50.00      Sequence
DRB1_0401  130  GPTPRAPQRNPAPAR  RAPQRNPAP        0.1430      10639.4               50.00      Sequence
DRB1_0401   20  LVDRGGAHRAATGPG  LVDRGGAHR        0.1422      10737.3               50.00      Sequence
DRB1_0401   22  DRGGAHRAATGPGRI  RGGAHRAAT        0.1401      10983.4               50.00      Sequence
DRB1_0401   47  RAATRQSQAGHRQPP  TRQSQAGHR        0.1387      11149.9               50.00      Sequence
DRB1_0401   48  AATRQSQAGHRQPPP  TRQSQAGHR        0.1361      11473.0               50.00      Sequence
DRB1_0401   46  QRAATRQSQAGHRQP  TRQSQAGHR        0.1353      11567.8               50.00      Sequence
DRB1_0401  245  NASGSSAELVSSGTI  GSSAELVSS        0.1292      12360.4               50.00      Sequence
DRB1_0401  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.1262      12768.9               50.00      Sequence
DRB1_0401   21  VDRGGAHRAATGPGR  RGGAHRAAT        0.1241      13053.0               50.00      Sequence
DRB1_0401  254  VSSGTIFGGAFLIGL  IFGGAFLIG        0.1221      13344.3               50.00      Sequence
DRB1_0401   95  PAAAVRTPQPDPDAS  AAVRTPQPD        0.1220      13358.6               50.00      Sequence
DRB1_0401   73  PPAAADARLNRFISG  ARLNRFISG        0.1220      13361.8               50.00      Sequence
DRB1_0401   64  SHPEGRPTNPPAAAD  PEGRPTNPP        0.1212      13477.7               50.00      Sequence
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DRB1_0401   16  NADGLVDRGGAHRAA  GLVDRGGAH        0.1202      13613.1                 50.00       Sequence
DRB1_0401   96  AAAVRTPQPDPDASL  AAVRTPQPD        0.1197      13694.3                 50.00       Sequence
DRB1_0401   94  GPAAAVRTPQPDPDA  AAVRTPQPD        0.1192      13773.5                 50.00       Sequence
DRB1_0401  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.1176      14011.0                 50.00       Sequence
DRB1_0401  129  SGPTPRAPQRNPAPA  RAPQRNPAP        0.1175      14029.2                 50.00       Sequence
DRB1_0401   93  TGPAAAVRTPQPDPD  AAAVRTPQP        0.1167      14148.4                 50.00       Sequence
DRB1_0401   97  AAVRTPQPDPDASLG  AAVRTPQPD        0.1164      14197.7                 50.00       Sequence
DRB1_0401   66  PEGRPTNPPAAADAR  PEGRPTNPP        0.1156      14321.2                 50.00       Sequence
DRB1_0401   91  PVTGPAAAVRTPQPD  AAVRTPQPD        0.1151      14391.8                 50.00       Sequence
DRB1_0401   65  HPEGRPTNPPAAADA  PEGRPTNPP        0.1136      14625.7                 50.00       Sequence
DRB1_0401   24  GGAHRAATGPGRIPD  HRAATGPGR        0.1135      14648.1                 50.00       Sequence
DRB1_0401   63  VSHPEGRPTNPPAAA  PEGRPTNPP        0.1129      14742.0                 50.00       Sequence
DRB1_0401    7  GALSKGDGPNADGLV  LSKGDGPNA        0.1112      15008.5                 50.00       Sequence
DRB1_0401    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.1106      15115.0                 50.00       Sequence
DRB1_0401   92  VTGPAAAVRTPQPDP  VTGPAAAVR        0.1105      15124.5                 50.00       Sequence
DRB1_0401    6  PGALSKGDGPNADGL  LSKGDGPNA        0.1093      15319.9                 50.00       Sequence
DRB1_0401  135  APQRNPAPARPAEGG  PQRNPAPAR        0.1071      15691.8                 50.00       Sequence
DRB1_0401   25  GAHRAATGPGRIPDA  HRAATGPGR        0.1067      15755.1                 50.00       Sequence
DRB1_0401  114  DGSPAEAYASELPDL  GSPAEAYAS        0.1035      16316.5                 50.00       Sequence
DRB1_0401   90  APVTGPAAAVRTPQP  PVTGPAAAV        0.1030      16397.9                 50.00       Sequence
DRB1_0401  128  LSGPTPRAPQRNPAP  RAPQRNPAP        0.1027      16466.5                 50.00       Sequence
DRB1_0401  136  PQRNPAPARPAEGGA  PQRNPAPAR        0.1019      16603.9                 50.00       Sequence
DRB1_0401   62  PVSHPEGRPTNPPAA  HPEGRPTNP        0.1008      16796.2                 50.00       Sequence
DRB1_0401  113  GDGSPAEAYASELPD  GSPAEAYAS        0.1000      16950.8                 50.00       Sequence
DRB1_0401    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.0999      16964.4                 50.00       Sequence
DRB1_0401  244  NNASGSSAELVSSGT  GSSAELVSS        0.0988      17158.6                 50.00       Sequence
DRB1_0401  103  QPDPDASLGCGDGSP  SLGCGDGSP        0.0969      17530.3                 50.00       Sequence
DRB1_0401  145  PAEGGAGSRGDSAAG  GAGSRGDSA        0.0927      18336.8                 50.00       Sequence
DRB1_0401   15  PNADGLVDRGGAHRA  GLVDRGGAH        0.0914      18588.9                 50.00       Sequence
DRB1_0401  243  LNNASGSSAELVSSG  LNNASGSSA        0.0902      18847.7                 50.00       Sequence
DRB1_0401    5  EPGALSKGDGPNADG  LSKGDGPNA        0.0893      19030.5                 50.00       Sequence
DRB1_0401  144  RPAEGGAGSRGDSAA  GAGSRGDSA        0.0893      19034.6                 50.00       Sequence
DRB1_0401   61  PPVSHPEGRPTNPPA  SHPEGRPTN        0.0887      19151.8                 50.00       Sequence
DRB1_0401   26  AHRAATGPGRIPDAG  HRAATGPGR        0.0868      19557.6                 50.00       Sequence
DRB1_0401   57  HRQPPPVSHPEGRPT  HRQPPPVSH        0.0864      19623.5                 50.00       Sequence
DRB1_0401   89  SAPVTGPAAAVRTPQ  PVTGPAAAV        0.0861      19696.3                 50.00       Sequence
DRB1_0401   68  GRPTNPPAAADARLN  RPTNPPAAA        0.0853      19873.5                 50.00       Sequence
DRB1_0401   67  EGRPTNPPAAADARL  RPTNPPAAA        0.0852      19886.2                 50.00       Sequence
DRB1_0401   34  GRIPDAGDPPPWQRA  RIPDAGDPP        0.0849      19960.8                 50.00       Sequence
DRB1_0401   98  AVRTPQPDPDASLGC  RTPQPDPDA        0.0841      20137.2                 50.00       Sequence
DRB1_0401  112  CGDGSPAEAYASELP  GSPAEAYAS        0.0823      20520.7                 50.00       Sequence
DRB1_0401   33  PGRIPDAGDPPPWQR  RIPDAGDPP        0.0823      20522.3                 50.00       Sequence
DRB1_0401   35  RIPDAGDPPPWQRAA  RIPDAGDPP        0.0817      20659.8                 50.00       Sequence
DRB1_0401   69  RPTNPPAAADARLNR  RPTNPPAAA        0.0807      20872.3                 50.00       Sequence
DRB1_0401  111  GCGDGSPAEAYASEL  GCGDGSPAE        0.0796      21136.6                 50.00       Sequence
DRB1_0401   72  NPPAAADARLNRFIS  PAAADARLN        0.0765      21855.2                 50.00       Sequence
DRB1_0401   32  GPGRIPDAGDPPPWQ  RIPDAGDPP        0.0759      21988.3                 50.00       Sequence
DRB1_0401   60  PPPVSHPEGRPTNPP  VSHPEGRPT        0.0758      22016.6                 50.00       Sequence
DRB1_0401  143  ARPAEGGAGSRGDSA  GAGSRGDSA        0.0757      22052.1                 50.00       Sequence
DRB1_0401    0  VTAPNEPGALSKGDG  APNEPGALS        0.0751      22191.7                 50.00       Sequence
DRB1_0401   38  DAGDPPPWQRAATRQ  PPWQRAATR        0.0746      22301.9                 50.00       Sequence
DRB1_0401   88  ASAPVTGPAAAVRTP  PVTGPAAAV        0.0742      22414.4                 50.00       Sequence
DRB1_0401  137  QRNPAPARPAEGGAG  QRNPAPARP        0.0733      22624.7                 50.00       Sequence
DRB1_0401    4  NEPGALSKGDGPNAD  LSKGDGPNA        0.0723      22871.3                 50.00       Sequence
DRB1_0401   27  HRAATGPGRIPDAGD  HRAATGPGR        0.0717      23021.8                 50.00       Sequence
DRB1_0401   14  GPNADGLVDRGGAHR  GLVDRGGAH        0.0716      23036.2                 50.00       Sequence
DRB1_0401   31  TGPGRIPDAGDPPPW  RIPDAGDPP        0.0679      23975.6                 50.00       Sequence
DRB1_0401   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.0676      24071.2                 50.00       Sequence
DRB1_0401   86  SGASAPVTGPAAAVR  SGASAPVTG        0.0648      24799.3                 50.00       Sequence
DRB1_0401   87  GASAPVTGPAAAVRT  PVTGPAAAV        0.0621      25532.8                 50.00       Sequence
DRB1_0401   71  TNPPAAADARLNRFI  PAAADARLN        0.0619      25599.2                 50.00       Sequence
DRB1_0401    3  PNEPGALSKGDGPNA  LSKGDGPNA        0.0613      25759.8                 50.00       Sequence
DRB1_0401   59  QPPPVSHPEGRPTNP  PVSHPEGRP        0.0610      25839.6                 50.00       Sequence
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   DRB1_0401  100  RTPQPDPDASLGCGD  RTPQPDPDA        0.0600      26119.6               50.00     Sequence
   DRB1_0401   30  ATGPGRIPDAGDPPP  RIPDAGDPP        0.0596      26248.5               50.00     Sequence
   DRB1_0401   58  RQPPPVSHPEGRPTN  PVSHPEGRP        0.0590      26409.4               50.00     Sequence
   DRB1_0401   37  PDAGDPPPWQRAATR  DAGDPPPWQ        0.0590      26418.9               50.00     Sequence
   DRB1_0401   28  RAATGPGRIPDAGDP  RAATGPGRI        0.0582      26631.8               50.00     Sequence
   DRB1_0401    1  TAPNEPGALSKGDGP  APNEPGALS        0.0573      26908.7               50.00     Sequence
   DRB1_0401   10  SKGDGPNADGLVDRG  SKGDGPNAD        0.0566      27101.3               50.00     Sequence
   DRB1_0401  142  PARPAEGGAGSRGDS  RPAEGGAGS        0.0554      27467.3               50.00     Sequence
   DRB1_0401  138  RNPAPARPAEGGAGS  RNPAPARPA        0.0553      27486.6               50.00     Sequence
   DRB1_0401  153  RGDSAAGSSGGRSIT  RGDSAAGSS        0.0538      27934.3               50.00     Sequence
   DRB1_0401    2  APNEPGALSKGDGPN  GALSKGDGP        0.0527      28260.5               50.00     Sequence
   DRB1_0401   13  DGPNADGLVDRGGAH  GLVDRGGAH        0.0523      28400.2               50.00     Sequence
   DRB1_0401   29  AATGPGRIPDAGDPP  RIPDAGDPP        0.0515      28636.0               50.00     Sequence
   DRB1_0401  102  PQPDPDASLGCGDGS  PQPDPDASL        0.0515      28655.2               50.00     Sequence
   DRB1_0401   36  IPDAGDPPPWQRAAT  IPDAGDPPP        0.0509      28830.9               50.00     Sequence
   DRB1_0401  141  APARPAEGGAGSRGD  RPAEGGAGS        0.0509      28839.3               50.00     Sequence
   DRB1_0401   70  PTNPPAAADARLNRF  PAAADARLN        0.0499      29141.1               50.00     Sequence
   DRB1_0401   11  KGDGPNADGLVDRGG  KGDGPNADG        0.0469      30093.0               50.00     Sequence
   DRB1_0401  101  TPQPDPDASLGCGDG  PQPDPDASL        0.0414      31943.7               50.00     Sequence
   DRB1_0401  140  PAPARPAEGGAGSRG  RPAEGGAGS        0.0404      32309.0               50.00     Sequence
   DRB1_0401   12  GDGPNADGLVDRGGA  GPNADGLVD        0.0398      32508.9               50.00     Sequence
   DRB1_0401  139  NPAPARPAEGGAGSR  RPAEGGAGS        0.0303      36028.2               50.00     Sequence
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Allele: DRB1_0401. Number of high binders 0. Number of weak binders 44. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404  269  VNIVLMTALATIGAF  IVLMTALAT        0.7462         15.6         SB     2.00     Sequence
   DRB1_0404  270  NIVLMTALATIGAFV  IVLMTALAT        0.7362         17.4         SB     2.00     Sequence
   DRB1_0404  268  LVNIVLMTALATIGA  IVLMTALAT        0.7309         18.4         SB     2.00     Sequence
   DRB1_0404  267  GLVNIVLMTALATIG  NIVLMTALA        0.7079         23.6         SB     4.00     Sequence
   DRB1_0404  271  IVLMTALATIGAFVY  IVLMTALAT        0.6963         26.7         SB     4.00     Sequence
   DRB1_0404  282  AFVYNLITDLIGGIE  FVYNLITDL        0.6943         27.3         SB     4.00     Sequence
   DRB1_0404  281  GAFVYNLITDLIGGI  FVYNLITDL        0.6874         29.4         SB     4.00     Sequence
   DRB1_0404  283  FVYNLITDLIGGIEV  FVYNLITDL        0.6737         34.2         SB     4.00     Sequence
   DRB1_0404  280  IGAFVYNLITDLIGG  FVYNLITDL        0.6639         38.0         SB     8.00     Sequence
   DRB1_0404  266  IGLVNIVLMTALATI  NIVLMTALA        0.6588         40.1         SB     8.00     Sequence
   DRB1_0404  279  TIGAFVYNLITDLIG  FVYNLITDL        0.6532         42.6         SB     8.00     Sequence
   DRB1_0404  272  VLMTALATIGAFVYN  VLMTALATI        0.6416         48.3         SB     8.00     Sequence
   DRB1_0404  200  TLKVSLLLSVALFFV  LKVSLLLSV        0.6406         48.8         SB     8.00     Sequence
   DRB1_0404  201  LKVSLLLSVALFFVW  LKVSLLLSV        0.6382         50.1         WB     8.00     Sequence
   DRB1_0404  199  STLKVSLLLSVALFF  LKVSLLLSV        0.6278         56.1         WB     8.00     Sequence
   DRB1_0404  273  LMTALATIGAFVYNL  TALATIGAF        0.6145         64.8         WB     8.00     Sequence
   DRB1_0404  265  LIGLVNIVLMTALAT  NIVLMTALA        0.6097         68.2         WB     8.00     Sequence
   DRB1_0404  278  ATIGAFVYNLITDLI  TIGAFVYNL        0.6074         69.9         WB    16.00     Sequence
   DRB1_0404   79  ARLNRFISGASAPVT  RFISGASAP        0.6017         74.4         WB    16.00     Sequence
   DRB1_0404  198  WSTLKVSLLLSVALF  LKVSLLLSV        0.6012         74.8         WB    16.00     Sequence
   DRB1_0404   80  RLNRFISGASAPVTG  RFISGASAP        0.5997         76.1         WB    16.00     Sequence
   DRB1_0404  274  MTALATIGAFVYNLI  TALATIGAF        0.5987         76.9         WB    16.00     Sequence
   DRB1_0404   78  DARLNRFISGASAPV  RFISGASAP        0.5869         87.3         WB    16.00     Sequence
   DRB1_0404   81  LNRFISGASAPVTGP  RFISGASAP        0.5866         87.6         WB    16.00     Sequence
   DRB1_0404   82  NRFISGASAPVTGPA  RFISGASAP        0.5831         91.0         WB    16.00     Sequence
   DRB1_0404  263  AFLIGLVNIVLMTAL  FLIGLVNIV        0.5804         93.7         WB    16.00     Sequence
   DRB1_0404  262  GAFLIGLVNIVLMTA  FLIGLVNIV        0.5797         94.4         WB    16.00     Sequence
   DRB1_0404  264  FLIGLVNIVLMTALA  FLIGLVNIV        0.5746         99.7         WB    16.00     Sequence
   DRB1_0404  275  TALATIGAFVYNLIT  TALATIGAF        0.5742        100.1         WB    16.00     Sequence
   DRB1_0404  261  GGAFLIGLVNIVLMT  FLIGLVNIV        0.5742        100.1         WB    16.00     Sequence
   DRB1_0404  197  PWSTLKVSLLLSVAL  LKVSLLLSV        0.5670        108.3         WB    16.00     Sequence
   DRB1_0404  210  ALFFVWMITVAFLYL  FVWMITVAF        0.5657        109.8         WB    16.00     Sequence
   DRB1_0404   83  RFISGASAPVTGPAA  RFISGASAP        0.5638        112.1         WB    16.00     Sequence
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DRB1_0404  218  TVAFLYLVLGGMGVW  FLYLVLGGM        0.5628        113.4         WB    16.00       Sequence
DRB1_0404  284  VYNLITDLIGGIEVT  NLITDLIGG        0.5588        118.4         WB    16.00       Sequence
DRB1_0404  219  VAFLYLVLGGMGVWA  FLYLVLGGM        0.5577        119.8         WB    16.00       Sequence
DRB1_0404  211  LFFVWMITVAFLYLV  FVWMITVAF        0.5565        121.4         WB    16.00       Sequence
DRB1_0404  277  LATIGAFVYNLITDL  TIGAFVYNL        0.5553        123.0         WB    16.00       Sequence
DRB1_0404  220  AFLYLVLGGMGVWAK  FLYLVLGGM        0.5543        124.3         WB    16.00       Sequence
DRB1_0404  260  FGGAFLIGLVNIVLM  FLIGLVNIV        0.5511        128.7         WB    16.00       Sequence
DRB1_0404  276  ALATIGAFVYNLITD  TIGAFVYNL        0.5497        130.6         WB    16.00       Sequence
DRB1_0404   77  ADARLNRFISGASAP  RLNRFISGA        0.5487        132.0         WB    16.00       Sequence
DRB1_0404  212  FFVWMITVAFLYLVL  FVWMITVAF        0.5433        140.0         WB    16.00       Sequence
DRB1_0404  209  VALFFVWMITVAFLY  FVWMITVAF        0.5394        145.9         WB    16.00       Sequence
DRB1_0404  221  FLYLVLGGMGVWAKL  YLVLGGMGV        0.5363        150.9         WB    16.00       Sequence
DRB1_0404  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.5305        160.7         WB    16.00       Sequence
DRB1_0404  217  ITVAFLYLVLGGMGV  FLYLVLGGM        0.5295        162.4         WB    16.00       Sequence
DRB1_0404  285  YNLITDLIGGIEVTL  NLITDLIGG        0.5211        178.0         WB    32.00       Sequence
DRB1_0404  208  SVALFFVWMITVAFL  FVWMITVAF        0.5172        185.6         WB    32.00       Sequence
DRB1_0404  213  FVWMITVAFLYLVLG  FVWMITVAF        0.5138        192.7         WB    32.00       Sequence
DRB1_0404  193  RRIDPWSTLKVSLLL  RRIDPWSTL        0.5079        205.4         WB    32.00       Sequence
DRB1_0404  286  NLITDLIGGIEVTLA  NLITDLIGG        0.5074        206.4         WB    32.00       Sequence
DRB1_0404  259  IFGGAFLIGLVNIVL  FLIGLVNIV        0.5042        213.6         WB    32.00       Sequence
DRB1_0404  192  IRRIDPWSTLKVSLL  RRIDPWSTL        0.4945        237.3         WB    32.00       Sequence
DRB1_0404  191  QIRRIDPWSTLKVSL  RRIDPWSTL        0.4921        243.5         WB    32.00       Sequence
DRB1_0404  289  TDLIGGIEVTLADRD  LIGGIEVTL        0.4921        243.6         WB    32.00       Sequence
DRB1_0404  196  DPWSTLKVSLLLSVA  LKVSLLLSV        0.4891        251.7         WB    32.00       Sequence
DRB1_0404  190  MQIRRIDPWSTLKVS  RRIDPWSTL        0.4881        254.5         WB    32.00       Sequence
DRB1_0404  207  LSVALFFVWMITVAF  FVWMITVAF        0.4822        271.2         WB    32.00       Sequence
DRB1_0404  189  SMQIRRIDPWSTLKV  RRIDPWSTL        0.4791        280.2         WB    32.00       Sequence
DRB1_0404  288  ITDLIGGIEVTLADR  LIGGIEVTL        0.4772        286.3         WB    32.00       Sequence
DRB1_0404  216  MITVAFLYLVLGGMG  FLYLVLGGM        0.4758        290.6         WB    32.00       Sequence
DRB1_0404  287  LITDLIGGIEVTLAD  LIGGIEVTL        0.4704        308.0         WB    32.00       Sequence
DRB1_0404  222  LYLVLGGMGVWAKLN  YLVLGGMGV        0.4654        325.1         WB    32.00       Sequence
DRB1_0404  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.4627        334.7         WB    32.00       Sequence
DRB1_0404  195  IDPWSTLKVSLLLSV  LKVSLLLSV        0.4515        377.9         WB    32.00       Sequence
DRB1_0404   76  AADARLNRFISGASA  RLNRFISGA        0.4456        403.0         WB    32.00       Sequence
DRB1_0404  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.4392        431.6         WB    32.00       Sequence
DRB1_0404  258  TIFGGAFLIGLVNIV  FLIGLVNIV        0.4385        435.1         WB    32.00       Sequence
DRB1_0404  229  MGVWAKLNSNVGDLL  VWAKLNSNV        0.4378        438.1         WB    32.00       Sequence
DRB1_0404  188  ASMQIRRIDPWSTLK  RRIDPWSTL        0.4348        452.6         WB    32.00       Sequence
DRB1_0404  228  GMGVWAKLNSNVGDL  VWAKLNSNV        0.4281        486.8         WB    32.00       Sequence
DRB1_0404  227  GGMGVWAKLNSNVGD  GVWAKLNSN        0.4260        498.0         WB    32.00       Sequence
DRB1_0404  194  RIDPWSTLKVSLLLS  PWSTLKVSL        0.4232        513.6               32.00       Sequence
DRB1_0404  230  GVWAKLNSNVGDLLN  VWAKLNSNV        0.4218        520.9               32.00       Sequence
DRB1_0404  215  WMITVAFLYLVLGGM  FLYLVLGGM        0.4133        571.1               32.00       Sequence
DRB1_0404  187  RASMQIRRIDPWSTL  MQIRRIDPW        0.3912        725.8               50.00       Sequence
DRB1_0404  250  SAELVSSGTIFGGAF  ELVSSGTIF        0.3846        779.4               50.00       Sequence
DRB1_0404  226  LGGMGVWAKLNSNVG  GVWAKLNSN        0.3822        799.6               50.00       Sequence
DRB1_0404  249  SSAELVSSGTIFGGA  ELVSSGTIF        0.3817        804.4               50.00       Sequence
DRB1_0404  224  LVLGGMGVWAKLNSN  VLGGMGVWA        0.3767        848.8               50.00       Sequence
DRB1_0404  251  AELVSSGTIFGGAFL  ELVSSGTIF        0.3735        879.3               50.00       Sequence
DRB1_0404   75  AAADARLNRFISGAS  RLNRFISGA        0.3696        916.8               50.00       Sequence
DRB1_0404  236  NSNVGDLLNNASGSS  NVGDLLNNA        0.3647        966.8               50.00       Sequence
DRB1_0404  237  SNVGDLLNNASGSSA  NVGDLLNNA        0.3611       1004.6               50.00       Sequence
DRB1_0404  214  VWMITVAFLYLVLGG  MITVAFLYL        0.3584       1034.3               50.00       Sequence
DRB1_0404  225  VLGGMGVWAKLNSNV  GVWAKLNSN        0.3583       1035.9               50.00       Sequence
DRB1_0404  231  VWAKLNSNVGDLLNN  VWAKLNSNV        0.3579       1040.3               50.00       Sequence
DRB1_0404  204  SLLLSVALFFVWMIT  SLLLSVALF        0.3562       1059.7               50.00       Sequence
DRB1_0404  248  GSSAELVSSGTIFGG  ELVSSGTIF        0.3553       1069.9               50.00       Sequence
DRB1_0404   84  FISGASAPVTGPAAA  FISGASAPV        0.3549       1074.6               50.00       Sequence
DRB1_0404  252  ELVSSGTIFGGAFLI  ELVSSGTIF        0.3548       1076.2               50.00       Sequence
DRB1_0404  238  NVGDLLNNASGSSAE  NVGDLLNNA        0.3533       1093.3               50.00       Sequence
DRB1_0404  206  LLSVALFFVWMITVA  FFVWMITVA        0.3479       1159.8               50.00       Sequence
DRB1_0404  235  LNSNVGDLLNNASGS  NVGDLLNNA        0.3453       1193.0               50.00       Sequence
DRB1_0404  234  KLNSNVGDLLNNASG  NVGDLLNNA        0.3323       1372.4               50.00       Sequence
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DRB1_0404  205  LLLSVALFFVWMITV  LLLSVALFF        0.3271       1451.5                 50.00      Sequence
DRB1_0404  247  SGSSAELVSSGTIFG  ELVSSGTIF        0.3115       1718.8                 50.00      Sequence
DRB1_0404  232  WAKLNSNVGDLLNNA  WAKLNSNVG        0.3109       1730.9                 50.00      Sequence
DRB1_0404   74  PAAADARLNRFISGA  RLNRFISGA        0.3024       1897.6                 50.00      Sequence
DRB1_0404  257  GTIFGGAFLIGLVNI  AFLIGLVNI        0.3019       1906.9                 50.00      Sequence
DRB1_0404  186  VRASMQIRRIDPWST  QIRRIDPWS        0.2990       1967.8                 50.00      Sequence
DRB1_0404  233  AKLNSNVGDLLNNAS  NVGDLLNNA        0.2846       2299.9                 50.00      Sequence
DRB1_0404  239  VGDLLNNASGSSAEL  LLNNASGSS        0.2819       2368.8                 50.00      Sequence
DRB1_0404  185  PVRASMQIRRIDPWS  PVRASMQIR        0.2581       3062.0                 50.00      Sequence
DRB1_0404  256  SGTIFGGAFLIGLVN  TIFGGAFLI        0.2572       3092.4                 50.00      Sequence
DRB1_0404  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.2548       3174.4                 50.00      Sequence
DRB1_0404  120  AYASELPDLSGPTPR  AYASELPDL        0.2487       3391.4                 50.00      Sequence
DRB1_0404  240  GDLLNNASGSSAELV  LLNNASGSS        0.2444       3554.1                 50.00      Sequence
DRB1_0404  255  SSGTIFGGAFLIGLV  TIFGGAFLI        0.2429       3611.0                 50.00      Sequence
DRB1_0404  121  YASELPDLSGPTPRA  ELPDLSGPT        0.2379       3812.7                 50.00      Sequence
DRB1_0404  184  GPVRASMQIRRIDPW  PVRASMQIR        0.2351       3926.9                 50.00      Sequence
DRB1_0404  119  EAYASELPDLSGPTP  AYASELPDL        0.2337       3986.9                 50.00      Sequence
DRB1_0404  171  RDARVQLSARRSRGP  DARVQLSAR        0.2335       3995.4                 50.00      Sequence
DRB1_0404  172  DARVQLSARRSRGPV  DARVQLSAR        0.2306       4124.0                 50.00      Sequence
DRB1_0404  254  VSSGTIFGGAFLIGL  TIFGGAFLI        0.2290       4196.9                 50.00      Sequence
DRB1_0404  118  AEAYASELPDLSGPT  YASELPDLS        0.2225       4500.3                 50.00      Sequence
DRB1_0404  122  ASELPDLSGPTPRAP  ELPDLSGPT        0.2214       4555.8                 50.00      Sequence
DRB1_0404  170  SRDARVQLSARRSRG  ARVQLSARR        0.2206       4594.4                 50.00      Sequence
DRB1_0404  241  DLLNNASGSSAELVS  LLNNASGSS        0.2197       4642.7                 50.00      Sequence
DRB1_0404  246  ASGSSAELVSSGTIF  ELVSSGTIF        0.2174       4760.2                 50.00      Sequence
DRB1_0404  123  SELPDLSGPTPRAPQ  ELPDLSGPT        0.2136       4958.2                 50.00      Sequence
DRB1_0404  182  SRGPVRASMQIRRID  PVRASMQIR        0.2130       4988.4                 50.00      Sequence
DRB1_0404  183  RGPVRASMQIRRIDP  PVRASMQIR        0.2128       5001.7                 50.00      Sequence
DRB1_0404  117  PAEAYASELPDLSGP  AYASELPDL        0.1991       5800.5                 50.00      Sequence
DRB1_0404   73  PPAAADARLNRFISG  ARLNRFISG        0.1959       6003.4                 50.00      Sequence
DRB1_0404  173  ARVQLSARRSRGPVR  ARVQLSARR        0.1934       6170.0                 50.00      Sequence
DRB1_0404  169  ESRDARVQLSARRSR  DARVQLSAR        0.1932       6182.7                 50.00      Sequence
DRB1_0404  242  LLNNASGSSAELVSS  LLNNASGSS        0.1910       6329.5                 50.00      Sequence
DRB1_0404  181  RSRGPVRASMQIRRI  GPVRASMQI        0.1880       6537.4                 50.00      Sequence
DRB1_0404  174  RVQLSARRSRGPVRA  VQLSARRSR        0.1783       7260.7                 50.00      Sequence
DRB1_0404   95  PAAAVRTPQPDPDAS  AVRTPQPDP        0.1763       7422.3                 50.00      Sequence
DRB1_0404  124  ELPDLSGPTPRAPQR  ELPDLSGPT        0.1705       7900.7                 50.00      Sequence
DRB1_0404   94  GPAAAVRTPQPDPDA  AAAVRTPQP        0.1702       7931.8                 50.00      Sequence
DRB1_0404   96  AAAVRTPQPDPDASL  AVRTPQPDP        0.1690       8035.2                 50.00      Sequence
DRB1_0404   93  TGPAAAVRTPQPDPD  AAAVRTPQP        0.1672       8189.3                 50.00      Sequence
DRB1_0404   55  AGHRQPPPVSHPEGR  AGHRQPPPV        0.1665       8252.8                 50.00      Sequence
DRB1_0404  107  DASLGCGDGSPAEAY  SLGCGDGSP        0.1659       8309.5                 50.00      Sequence
DRB1_0404   54  QAGHRQPPPVSHPEG  AGHRQPPPV        0.1601       8841.4                 50.00      Sequence
DRB1_0404  116  SPAEAYASELPDLSG  AYASELPDL        0.1590       8946.0                 50.00      Sequence
DRB1_0404  175  VQLSARRSRGPVRAS  VQLSARRSR        0.1579       9056.2                 50.00      Sequence
DRB1_0404  132  TPRAPQRNPAPARPA  RAPQRNPAP        0.1577       9080.0                 50.00      Sequence
DRB1_0404  131  PTPRAPQRNPAPARP  RAPQRNPAP        0.1558       9269.6                 50.00      Sequence
DRB1_0404  178  SARRSRGPVRASMQI  SARRSRGPV        0.1551       9332.9                 50.00      Sequence
DRB1_0404  109  SLGCGDGSPAEAYAS  LGCGDGSPA        0.1549       9360.7                 50.00      Sequence
DRB1_0404   53  SQAGHRQPPPVSHPE  AGHRQPPPV        0.1545       9396.4                 50.00      Sequence
DRB1_0404   91  PVTGPAAAVRTPQPD  PVTGPAAAV        0.1541       9440.5                 50.00      Sequence
DRB1_0404  106  PDASLGCGDGSPAEA  SLGCGDGSP        0.1533       9515.4                 50.00      Sequence
DRB1_0404  108  ASLGCGDGSPAEAYA  LGCGDGSPA        0.1516       9692.0                 50.00      Sequence
DRB1_0404  168  AESRDARVQLSARRS  DARVQLSAR        0.1490       9972.6                 50.00      Sequence
DRB1_0404  180  RRSRGPVRASMQIRR  GPVRASMQI        0.1479      10089.1                 50.00      Sequence
DRB1_0404   52  QSQAGHRQPPPVSHP  AGHRQPPPV        0.1463      10270.3                 50.00      Sequence
DRB1_0404   92  VTGPAAAVRTPQPDP  PAAAVRTPQ        0.1462      10277.0                 50.00      Sequence
DRB1_0404   97  AAVRTPQPDPDASLG  AVRTPQPDP        0.1453      10379.8                 50.00      Sequence
DRB1_0404   85  ISGASAPVTGPAAAV  ISGASAPVT        0.1446      10460.0                 50.00      Sequence
DRB1_0404  130  GPTPRAPQRNPAPAR  RAPQRNPAP        0.1434      10593.6                 50.00      Sequence
DRB1_0404  177  LSARRSRGPVRASMQ  SARRSRGPV        0.1429      10653.3                 50.00      Sequence
DRB1_0404   90  APVTGPAAAVRTPQP  PVTGPAAAV        0.1390      11108.3                 50.00      Sequence
DRB1_0404  115  GSPAEAYASELPDLS  YASELPDLS        0.1382      11209.1                 50.00      Sequence
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DRB1_0404  105  DPDASLGCGDGSPAE  SLGCGDGSP        0.1378      11253.6                 50.00      Sequence
DRB1_0404  129  SGPTPRAPQRNPAPA  TPRAPQRNP        0.1367      11396.2                 50.00      Sequence
DRB1_0404   42  PPPWQRAATRQSQAG  WQRAATRQS        0.1358      11504.2                 50.00      Sequence
DRB1_0404   56  GHRQPPPVSHPEGRP  HRQPPPVSH        0.1348      11628.8                 50.00      Sequence
DRB1_0404   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.1345      11669.6                 50.00      Sequence
DRB1_0404  179  ARRSRGPVRASMQIR  PVRASMQIR        0.1336      11783.4                 50.00      Sequence
DRB1_0404  176  QLSARRSRGPVRASM  SARRSRGPV        0.1334      11810.9                 50.00      Sequence
DRB1_0404   44  PWQRAATRQSQAGHR  WQRAATRQS        0.1324      11937.8                 50.00      Sequence
DRB1_0404  245  NASGSSAELVSSGTI  AELVSSGTI        0.1308      12148.8                 50.00      Sequence
DRB1_0404   31  TGPGRIPDAGDPPPW  TGPGRIPDA        0.1306      12174.7                 50.00      Sequence
DRB1_0404   41  DPPPWQRAATRQSQA  WQRAATRQS        0.1295      12322.1                 50.00      Sequence
DRB1_0404   89  SAPVTGPAAAVRTPQ  PVTGPAAAV        0.1293      12341.5                 50.00      Sequence
DRB1_0404  133  PRAPQRNPAPARPAE  RAPQRNPAP        0.1293      12347.2                 50.00      Sequence
DRB1_0404   43  PPWQRAATRQSQAGH  WQRAATRQS        0.1277      12560.2                 50.00      Sequence
DRB1_0404   98  AVRTPQPDPDASLGC  AVRTPQPDP        0.1268      12683.1                 50.00      Sequence
DRB1_0404   33  PGRIPDAGDPPPWQR  RIPDAGDPP        0.1267      12697.8                 50.00      Sequence
DRB1_0404  134  RAPQRNPAPARPAEG  RAPQRNPAP        0.1260      12790.0                 50.00      Sequence
DRB1_0404   87  GASAPVTGPAAAVRT  SAPVTGPAA        0.1250      12934.3                 50.00      Sequence
DRB1_0404   32  GPGRIPDAGDPPPWQ  RIPDAGDPP        0.1248      12963.9                 50.00      Sequence
DRB1_0404  128  LSGPTPRAPQRNPAP  RAPQRNPAP        0.1244      13014.2                 50.00      Sequence
DRB1_0404   34  GRIPDAGDPPPWQRA  RIPDAGDPP        0.1238      13095.0                 50.00      Sequence
DRB1_0404  104  PDPDASLGCGDGSPA  SLGCGDGSP        0.1230      13219.4                 50.00      Sequence
DRB1_0404   88  ASAPVTGPAAAVRTP  PVTGPAAAV        0.1222      13325.8                 50.00      Sequence
DRB1_0404   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.1204      13594.4                 50.00      Sequence
DRB1_0404   57  HRQPPPVSHPEGRPT  HRQPPPVSH        0.1200      13645.2                 50.00      Sequence
DRB1_0404   30  ATGPGRIPDAGDPPP  TGPGRIPDA        0.1194      13739.2                 50.00      Sequence
DRB1_0404   86  SGASAPVTGPAAAVR  SAPVTGPAA        0.1171      14081.7                 50.00      Sequence
DRB1_0404   51  RQSQAGHRQPPPVSH  AGHRQPPPV        0.1164      14185.4                 50.00      Sequence
DRB1_0404   39  AGDPPPWQRAATRQS  PPPWQRAAT        0.1140      14568.3                 50.00      Sequence
DRB1_0404  167  TAESRDARVQLSARR  DARVQLSAR        0.1103      15167.0                 50.00      Sequence
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DRB1_0404   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.1083      15484.5                 50.00      Sequence
DRB1_0404   64  SHPEGRPTNPPAAAD  PEGRPTNPP        0.1080      15536.7                 50.00      Sequence
DRB1_0404  243  LNNASGSSAELVSSG  LNNASGSSA        0.1077      15596.7                 50.00      Sequence
DRB1_0404   35  RIPDAGDPPPWQRAA  RIPDAGDPP        0.1069      15728.5                 50.00      Sequence
DRB1_0404   66  PEGRPTNPPAAADAR  PEGRPTNPP        0.1035      16310.3                 50.00      Sequence
DRB1_0404   63  VSHPEGRPTNPPAAA  HPEGRPTNP        0.1030      16405.3                 50.00      Sequence
DRB1_0404  110  LGCGDGSPAEAYASE  LGCGDGSPA        0.1027      16453.2                 50.00      Sequence
DRB1_0404   62  PVSHPEGRPTNPPAA  HPEGRPTNP        0.1027      16461.7                 50.00      Sequence
DRB1_0404   50  TRQSQAGHRQPPPVS  AGHRQPPPV        0.1025      16489.7                 50.00      Sequence
DRB1_0404  114  DGSPAEAYASELPDL  PAEAYASEL        0.1015      16677.9                 50.00      Sequence
DRB1_0404   16  NADGLVDRGGAHRAA  GLVDRGGAH        0.1011      16753.5                 50.00      Sequence
DRB1_0404   65  HPEGRPTNPPAAADA  PEGRPTNPP        0.1008      16805.4                 50.00      Sequence
DRB1_0404  125  LPDLSGPTPRAPQRN  LPDLSGPTP        0.1000      16953.0                 50.00      Sequence
DRB1_0404   58  RQPPPVSHPEGRPTN  RQPPPVSHP        0.0990      17126.1                 50.00      Sequence
DRB1_0404   15  PNADGLVDRGGAHRA  NADGLVDRG        0.0982      17270.9                 50.00      Sequence
DRB1_0404   61  PPVSHPEGRPTNPPA  SHPEGRPTN        0.0982      17277.1                 50.00      Sequence
DRB1_0404  103  QPDPDASLGCGDGSP  SLGCGDGSP        0.0979      17333.2                 50.00      Sequence
DRB1_0404   46  QRAATRQSQAGHRQP  RAATRQSQA        0.0968      17538.1                 50.00      Sequence
DRB1_0404  165  SITAESRDARVQLSA  SITAESRDA        0.0947      17953.6                 50.00      Sequence
DRB1_0404   14  GPNADGLVDRGGAHR  NADGLVDRG        0.0941      18067.0                 50.00      Sequence
DRB1_0404    7  GALSKGDGPNADGLV  ALSKGDGPN        0.0939      18099.1                 50.00      Sequence
DRB1_0404    6  PGALSKGDGPNADGL  ALSKGDGPN        0.0936      18160.9                 50.00      Sequence
DRB1_0404  164  RSITAESRDARVQLS  SITAESRDA        0.0927      18347.5                 50.00      Sequence
DRB1_0404  126  PDLSGPTPRAPQRNP  PDLSGPTPR        0.0926      18365.6                 50.00      Sequence
DRB1_0404   47  RAATRQSQAGHRQPP  ATRQSQAGH        0.0924      18392.6                 50.00      Sequence
DRB1_0404   25  GAHRAATGPGRIPDA  AHRAATGPG        0.0916      18563.4                 50.00      Sequence
DRB1_0404   18  DGLVDRGGAHRAATG  LVDRGGAHR        0.0914      18596.1                 50.00      Sequence
DRB1_0404  163  GRSITAESRDARVQL  SITAESRDA        0.0914      18608.4                 50.00      Sequence
DRB1_0404  162  GGRSITAESRDARVQ  SITAESRDA        0.0902      18850.8                 50.00      Sequence
DRB1_0404   13  DGPNADGLVDRGGAH  NADGLVDRG        0.0896      18965.6                 50.00      Sequence
DRB1_0404  166  ITAESRDARVQLSAR  DARVQLSAR        0.0894      19003.4                 50.00      Sequence
DRB1_0404   26  AHRAATGPGRIPDAG  AHRAATGPG        0.0893      19026.8                 50.00      Sequence
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DRB1_0404  136  PQRNPAPARPAEGGA  PQRNPAPAR        0.0891      19063.9                 50.00      Sequence
DRB1_0404  160  SSGGRSITAESRDAR  SSGGRSITA        0.0890      19085.2                 50.00      Sequence
DRB1_0404  135  APQRNPAPARPAEGG  PQRNPAPAR        0.0889      19103.8                 50.00      Sequence
DRB1_0404   24  GGAHRAATGPGRIPD  AHRAATGPG        0.0888      19124.6                 50.00      Sequence
DRB1_0404  127  DLSGPTPRAPQRNPA  TPRAPQRNP        0.0886      19169.6                 50.00      Sequence
DRB1_0404    5  EPGALSKGDGPNADG  ALSKGDGPN        0.0886      19180.8                 50.00      Sequence
DRB1_0404   49  ATRQSQAGHRQPPPV  ATRQSQAGH        0.0880      19294.2                 50.00      Sequence
DRB1_0404   17  ADGLVDRGGAHRAAT  LVDRGGAHR        0.0880      19297.0                 50.00      Sequence
DRB1_0404   72  NPPAAADARLNRFIS  NPPAAADAR        0.0872      19460.9                 50.00      Sequence
DRB1_0404  244  NNASGSSAELVSSGT  NASGSSAEL        0.0864      19631.8                 50.00      Sequence
DRB1_0404    8  ALSKGDGPNADGLVD  ALSKGDGPN        0.0863      19653.9                 50.00      Sequence
DRB1_0404   60  PPPVSHPEGRPTNPP  HPEGRPTNP        0.0857      19776.6                 50.00      Sequence
DRB1_0404  100  RTPQPDPDASLGCGD  RTPQPDPDA        0.0849      19952.2                 50.00      Sequence
DRB1_0404  159  GSSGGRSITAESRDA  SSGGRSITA        0.0848      19982.8                 50.00      Sequence
DRB1_0404  101  TPQPDPDASLGCGDG  PQPDPDASL        0.0842      20108.2                 50.00      Sequence
DRB1_0404   23  RGGAHRAATGPGRIP  AHRAATGPG        0.0841      20132.4                 50.00      Sequence
DRB1_0404  102  PQPDPDASLGCGDGS  PQPDPDASL        0.0839      20177.7                 50.00      Sequence
DRB1_0404   48  AATRQSQAGHRQPPP  ATRQSQAGH        0.0827      20432.3                 50.00      Sequence
DRB1_0404   28  RAATGPGRIPDAGDP  TGPGRIPDA        0.0817      20662.7                 50.00      Sequence
DRB1_0404  161  SGGRSITAESRDARV  SITAESRDA        0.0816      20682.3                 50.00      Sequence
DRB1_0404    1  TAPNEPGALSKGDGP  TAPNEPGAL        0.0816      20688.4                 50.00      Sequence
DRB1_0404   27  HRAATGPGRIPDAGD  TGPGRIPDA        0.0813      20752.5                 50.00      Sequence
DRB1_0404  158  AGSSGGRSITAESRD  SSGGRSITA        0.0811      20782.4                 50.00      Sequence
DRB1_0404    0  VTAPNEPGALSKGDG  TAPNEPGAL        0.0809      20843.4                 50.00      Sequence
DRB1_0404   59  QPPPVSHPEGRPTNP  HPEGRPTNP        0.0797      21097.5                 50.00      Sequence
DRB1_0404  113  GDGSPAEAYASELPD  PAEAYASEL        0.0796      21131.4                 50.00      Sequence
DRB1_0404   38  DAGDPPPWQRAATRQ  PPPWQRAAT        0.0793      21201.0                 50.00      Sequence
DRB1_0404   19  GLVDRGGAHRAATGP  GLVDRGGAH        0.0792      21214.3                 50.00      Sequence
DRB1_0404   67  EGRPTNPPAAADARL  EGRPTNPPA        0.0780      21501.3                 50.00      Sequence
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DRB1_0404   71  TNPPAAADARLNRFI  NPPAAADAR        0.0754      22106.4                 50.00      Sequence
DRB1_0404    4  NEPGALSKGDGPNAD  ALSKGDGPN        0.0753      22138.9                 50.00      Sequence
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DRB1_0404   12  GDGPNADGLVDRGGA  NADGLVDRG        0.0736      22541.1                 50.00      Sequence
DRB1_0404  156  SAAGSSGGRSITAES  SSGGRSITA        0.0725      22812.5                 50.00      Sequence
DRB1_0404   70  PTNPPAAADARLNRF  NPPAAADAR        0.0725      22813.2                 50.00      Sequence
DRB1_0404   22  DRGGAHRAATGPGRI  AHRAATGPG        0.0725      22827.8                 50.00      Sequence
DRB1_0404   36  IPDAGDPPPWQRAAT  IPDAGDPPP        0.0723      22862.6                 50.00      Sequence
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DRB1_0404   37  PDAGDPPPWQRAATR  PPPWQRAAT        0.0709      23223.7                 50.00      Sequence
DRB1_0404  137  QRNPAPARPAEGGAG  RNPAPARPA        0.0708      23244.5                 50.00      Sequence
DRB1_0404  155  DSAAGSSGGRSITAE  SAAGSSGGR        0.0691      23666.8                 50.00      Sequence
DRB1_0404    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.0682      23907.2                 50.00      Sequence
DRB1_0404   10  SKGDGPNADGLVDRG  SKGDGPNAD        0.0669      24256.1                 50.00      Sequence
DRB1_0404    3  PNEPGALSKGDGPNA  ALSKGDGPN        0.0661      24447.4                 50.00      Sequence
DRB1_0404  112  CGDGSPAEAYASELP  PAEAYASEL        0.0648      24798.8                 50.00      Sequence
DRB1_0404   20  LVDRGGAHRAATGPG  LVDRGGAHR        0.0638      25068.2                 50.00      Sequence
DRB1_0404  139  NPAPARPAEGGAGSR  PAPARPAEG        0.0623      25482.0                 50.00      Sequence
DRB1_0404   11  KGDGPNADGLVDRGG  NADGLVDRG        0.0621      25538.6                 50.00      Sequence
DRB1_0404   21  VDRGGAHRAATGPGR  AHRAATGPG        0.0618      25624.7                 50.00      Sequence
DRB1_0404  154  GDSAAGSSGGRSITA  SAAGSSGGR        0.0605      25993.8                 50.00      Sequence
DRB1_0404  111  GCGDGSPAEAYASEL  PAEAYASEL        0.0579      26738.1                 50.00      Sequence
DRB1_0404  140  PAPARPAEGGAGSRG  PAPARPAEG        0.0573      26910.8                 50.00      Sequence
DRB1_0404  153  RGDSAAGSSGGRSIT  RGDSAAGSS        0.0525      28345.6                 50.00      Sequence
DRB1_0404    2  APNEPGALSKGDGPN  ALSKGDGPN        0.0523      28382.4                 50.00      Sequence
DRB1_0404  151  GSRGDSAAGSSGGRS  GSRGDSAAG        0.0513      28692.4                 50.00      Sequence
DRB1_0404  152  SRGDSAAGSSGGRSI  RGDSAAGSS        0.0513      28694.9                 50.00      Sequence
DRB1_0404  150  AGSRGDSAAGSSGGR  GSRGDSAAG        0.0511      28750.5                 50.00      Sequence
DRB1_0404  149  GAGSRGDSAAGSSGG  GSRGDSAAG        0.0510      28789.8                 50.00      Sequence
DRB1_0404  148  GGAGSRGDSAAGSSG  GAGSRGDSA        0.0453      30642.1                 50.00      Sequence
DRB1_0404  141  APARPAEGGAGSRGD  ARPAEGGAG        0.0449      30769.3                 50.00      Sequence
DRB1_0404  142  PARPAEGGAGSRGDS  ARPAEGGAG        0.0443      30959.3                 50.00      Sequence
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   DRB1_0404  147  EGGAGSRGDSAAGSS  AGSRGDSAA        0.0442      30989.5                 50.00     Sequence
   DRB1_0404  143  ARPAEGGAGSRGDSA  PAEGGAGSR        0.0429      31431.5                 50.00     Sequence
   DRB1_0404  144  RPAEGGAGSRGDSAA  PAEGGAGSR        0.0419      31774.8                 50.00     Sequence
   DRB1_0404  145  PAEGGAGSRGDSAAG  PAEGGAGSR        0.0412      32021.3                 50.00     Sequence
   DRB1_0404  146  AEGGAGSRGDSAAGS  GAGSRGDSA        0.0401      32412.0                 50.00     Sequence
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Allele: DRB1_0404. Number of high binders 13. Number of weak binders 60. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405  279  TIGAFVYNLITDLIG  AFVYNLITD        0.7353         17.5         SB     2.00     Sequence
   DRB1_0405  280  IGAFVYNLITDLIGG  AFVYNLITD        0.7327         18.0         SB     2.00     Sequence
   DRB1_0405  281  GAFVYNLITDLIGGI  FVYNLITDL        0.7112         22.7         SB     2.00     Sequence
   DRB1_0405  278  ATIGAFVYNLITDLI  AFVYNLITD        0.7086         23.4         SB     4.00     Sequence
   DRB1_0405  268  LVNIVLMTALATIGA  VLMTALATI        0.7041         24.6         SB     4.00     Sequence
   DRB1_0405  269  VNIVLMTALATIGAF  VLMTALATI        0.6989         26.0         SB     4.00     Sequence
   DRB1_0405  270  NIVLMTALATIGAFV  VLMTALATI        0.6972         26.5         SB     4.00     Sequence
   DRB1_0405  277  LATIGAFVYNLITDL  AFVYNLITD        0.6808         31.6         SB     4.00     Sequence
   DRB1_0405  267  GLVNIVLMTALATIG  VLMTALATI        0.6790         32.2         SB     4.00     Sequence
   DRB1_0405  282  AFVYNLITDLIGGIE  FVYNLITDL        0.6671         36.7         SB     8.00     Sequence
   DRB1_0405  266  IGLVNIVLMTALATI  VLMTALATI        0.6664         36.9         SB     8.00     Sequence
   DRB1_0405  271  IVLMTALATIGAFVY  VLMTALATI        0.6637         38.1         SB     8.00     Sequence
   DRB1_0405  272  VLMTALATIGAFVYN  VLMTALATI        0.6351         51.8         WB     8.00     Sequence
   DRB1_0405  209  VALFFVWMITVAFLY  FFVWMITVA        0.6237         58.6         WB    16.00     Sequence
   DRB1_0405  276  ALATIGAFVYNLITD  AFVYNLITD        0.6154         64.2         WB    16.00     Sequence
   DRB1_0405  198  WSTLKVSLLLSVALF  LKVSLLLSV        0.6143         64.9         WB    16.00     Sequence
   DRB1_0405  199  STLKVSLLLSVALFF  LKVSLLLSV        0.6100         68.1         WB    16.00     Sequence
   DRB1_0405  210  ALFFVWMITVAFLYL  FFVWMITVA        0.6097         68.3         WB    16.00     Sequence
   DRB1_0405  197  PWSTLKVSLLLSVAL  LKVSLLLSV        0.6094         68.4         WB    16.00     Sequence
   DRB1_0405  208  SVALFFVWMITVAFL  FFVWMITVA        0.6090         68.7         WB    16.00     Sequence
   DRB1_0405  261  GGAFLIGLVNIVLMT  FLIGLVNIV        0.6086         69.1         WB    16.00     Sequence
   DRB1_0405  265  LIGLVNIVLMTALAT  LVNIVLMTA        0.6083         69.3         WB    16.00     Sequence
   DRB1_0405  260  FGGAFLIGLVNIVLM  FLIGLVNIV        0.6072         70.1         WB    16.00     Sequence
   DRB1_0405  207  LSVALFFVWMITVAF  FFVWMITVA        0.5994         76.3         WB    16.00     Sequence
   DRB1_0405  262  GAFLIGLVNIVLMTA  FLIGLVNIV        0.5970         78.3         WB    16.00     Sequence
   DRB1_0405  200  TLKVSLLLSVALFFV  LKVSLLLSV        0.5963         78.9         WB    16.00     Sequence
   DRB1_0405  218  TVAFLYLVLGGMGVW  FLYLVLGGM        0.5931         81.7         WB    16.00     Sequence
   DRB1_0405  196  DPWSTLKVSLLLSVA  LKVSLLLSV        0.5923         82.4         WB    16.00     Sequence
   DRB1_0405  211  LFFVWMITVAFLYLV  FFVWMITVA        0.5912         83.3         WB    16.00     Sequence
   DRB1_0405  227  GGMGVWAKLNSNVGD  GVWAKLNSN        0.5909         83.6         WB    16.00     Sequence
   DRB1_0405  283  FVYNLITDLIGGIEV  FVYNLITDL        0.5775         96.6         WB    16.00     Sequence
   DRB1_0405  259  IFGGAFLIGLVNIVL  AFLIGLVNI        0.5766         97.6         WB    16.00     Sequence
   DRB1_0405  217  ITVAFLYLVLGGMGV  FLYLVLGGM        0.5751         99.2         WB    16.00     Sequence
   DRB1_0405  195  IDPWSTLKVSLLLSV  LKVSLLLSV        0.5747         99.7         WB    16.00     Sequence
   DRB1_0405  226  LGGMGVWAKLNSNVG  GVWAKLNSN        0.5740        100.4         WB    16.00     Sequence
   DRB1_0405  264  FLIGLVNIVLMTALA  IGLVNIVLM        0.5736        100.8         WB    16.00     Sequence
   DRB1_0405  219  VAFLYLVLGGMGVWA  FLYLVLGGM        0.5726        101.9         WB    16.00     Sequence
   DRB1_0405  263  AFLIGLVNIVLMTAL  FLIGLVNIV        0.5723        102.3         WB    16.00     Sequence
   DRB1_0405  220  AFLYLVLGGMGVWAK  FLYLVLGGM        0.5571        120.5         WB    32.00     Sequence
   DRB1_0405  212  FFVWMITVAFLYLVL  FFVWMITVA        0.5548        123.6         WB    32.00     Sequence
   DRB1_0405  201  LKVSLLLSVALFFVW  LKVSLLLSV        0.5546        123.8         WB    32.00     Sequence
   DRB1_0405  228  GMGVWAKLNSNVGDL  GVWAKLNSN        0.5516        128.0         WB    32.00     Sequence
   DRB1_0405  258  TIFGGAFLIGLVNIV  AFLIGLVNI        0.5466        135.0         WB    32.00     Sequence
   DRB1_0405  229  MGVWAKLNSNVGDLL  GVWAKLNSN        0.5457        136.3         WB    32.00     Sequence
   DRB1_0405  225  VLGGMGVWAKLNSNV  GVWAKLNSN        0.5433        140.0         WB    32.00     Sequence
   DRB1_0405  194  RIDPWSTLKVSLLLS  DPWSTLKVS        0.5423        141.5         WB    32.00     Sequence
   DRB1_0405  230  GVWAKLNSNVGDLLN  GVWAKLNSN        0.5360        151.4         WB    32.00     Sequence
   DRB1_0405  275  TALATIGAFVYNLIT  GAFVYNLIT        0.5346        153.8         WB    32.00     Sequence
   DRB1_0405  193  RRIDPWSTLKVSLLL  DPWSTLKVS        0.5331        156.3         WB    32.00     Sequence
   DRB1_0405  273  LMTALATIGAFVYNL  TALATIGAF        0.5323        157.6         WB    32.00     Sequence
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DRB1_0405  216  MITVAFLYLVLGGMG  FLYLVLGGM        0.5306        160.7         WB    32.00      Sequence
DRB1_0405  221  FLYLVLGGMGVWAKL  FLYLVLGGM        0.5303        161.1         WB    32.00      Sequence
DRB1_0405  224  LVLGGMGVWAKLNSN  GVWAKLNSN        0.5225        175.4         WB    32.00      Sequence
DRB1_0405  215  WMITVAFLYLVLGGM  FLYLVLGGM        0.5205        179.2         WB    32.00      Sequence
DRB1_0405  192  IRRIDPWSTLKVSLL  WSTLKVSLL        0.5122        196.0         WB    32.00      Sequence
DRB1_0405  248  GSSAELVSSGTIFGG  AELVSSGTI        0.5112        198.1         WB    32.00      Sequence
DRB1_0405  249  SSAELVSSGTIFGGA  AELVSSGTI        0.5079        205.4         WB    32.00      Sequence
DRB1_0405  247  SGSSAELVSSGTIFG  AELVSSGTI        0.4981        228.3         WB    32.00      Sequence
DRB1_0405  206  LLSVALFFVWMITVA  FFVWMITVA        0.4963        232.6         WB    32.00      Sequence
DRB1_0405  257  GTIFGGAFLIGLVNI  AFLIGLVNI        0.4919        244.1         WB    32.00      Sequence
DRB1_0405  250  SAELVSSGTIFGGAF  AELVSSGTI        0.4892        251.3         WB    32.00      Sequence
DRB1_0405  274  MTALATIGAFVYNLI  TALATIGAF        0.4876        255.8         WB    32.00      Sequence
DRB1_0405   79  ARLNRFISGASAPVT  FISGASAPV        0.4820        271.6         WB    32.00      Sequence
DRB1_0405   80  RLNRFISGASAPVTG  NRFISGASA        0.4764        288.6         WB    32.00      Sequence
DRB1_0405  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.4747        293.9         WB    50.00      Sequence
DRB1_0405   78  DARLNRFISGASAPV  NRFISGASA        0.4694        311.2         WB    50.00      Sequence
DRB1_0405   81  LNRFISGASAPVTGP  FISGASAPV        0.4692        312.1         WB    50.00      Sequence
DRB1_0405   82  NRFISGASAPVTGPA  FISGASAPV        0.4561        359.5         WB    50.00      Sequence
DRB1_0405  222  LYLVLGGMGVWAKLN  YLVLGGMGV        0.4548        364.8         WB    50.00      Sequence
DRB1_0405  159  GSSGGRSITAESRDA  GGRSITAES        0.4534        370.0         WB    50.00      Sequence
DRB1_0405  158  AGSSGGRSITAESRD  GGRSITAES        0.4452        404.5         WB    50.00      Sequence
DRB1_0405  246  ASGSSAELVSSGTIF  AELVSSGTI        0.4428        415.1         WB    50.00      Sequence
DRB1_0405  213  FVWMITVAFLYLVLG  FVWMITVAF        0.4413        422.1         WB    50.00      Sequence
DRB1_0405  191  QIRRIDPWSTLKVSL  DPWSTLKVS        0.4398        428.9         WB    50.00      Sequence
DRB1_0405  251  AELVSSGTIFGGAFL  AELVSSGTI        0.4356        449.0         WB    50.00      Sequence
DRB1_0405  183  RGPVRASMQIRRIDP  GPVRASMQI        0.4314        469.5         WB    50.00      Sequence
DRB1_0405  160  SSGGRSITAESRDAR  GGRSITAES        0.4311        471.5         WB    50.00      Sequence
DRB1_0405  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.4310        471.7         WB    50.00      Sequence
DRB1_0405  169  ESRDARVQLSARRSR  RVQLSARRS        0.4292        480.8         WB    50.00      Sequence
DRB1_0405  182  SRGPVRASMQIRRID  GPVRASMQI        0.4236        511.3               50.00      Sequence
DRB1_0405  231  VWAKLNSNVGDLLNN  WAKLNSNVG        0.4215        523.0               50.00      Sequence
DRB1_0405  184  GPVRASMQIRRIDPW  GPVRASMQI        0.4190        537.0               50.00      Sequence
DRB1_0405  171  RDARVQLSARRSRGP  RVQLSARRS        0.4188        538.5               50.00      Sequence
DRB1_0405   83  RFISGASAPVTGPAA  FISGASAPV        0.4099        593.0               50.00      Sequence
DRB1_0405  172  DARVQLSARRSRGPV  RVQLSARRS        0.4089        599.3               50.00      Sequence
DRB1_0405  284  VYNLITDLIGGIEVT  YNLITDLIG        0.4080        605.3               50.00      Sequence
DRB1_0405  161  SGGRSITAESRDARV  GGRSITAES        0.4069        612.1               50.00      Sequence
DRB1_0405  190  MQIRRIDPWSTLKVS  QIRRIDPWS        0.4065        615.0               50.00      Sequence
DRB1_0405  232  WAKLNSNVGDLLNNA  WAKLNSNVG        0.4032        637.1               50.00      Sequence
DRB1_0405  181  RSRGPVRASMQIRRI  GPVRASMQI        0.4003        657.6               50.00      Sequence
DRB1_0405  245  NASGSSAELVSSGTI  AELVSSGTI        0.3986        670.1               50.00      Sequence
DRB1_0405  170  SRDARVQLSARRSRG  RVQLSARRS        0.3972        679.7               50.00      Sequence
DRB1_0405  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.3962        687.2               50.00      Sequence
DRB1_0405   77  ADARLNRFISGASAP  NRFISGASA        0.3898        736.7               50.00      Sequence
DRB1_0405  205  LLLSVALFFVWMITV  LFFVWMITV        0.3892        741.3               50.00      Sequence
DRB1_0405  157  AAGSSGGRSITAESR  GGRSITAES        0.3869        760.5               50.00      Sequence
DRB1_0405  189  SMQIRRIDPWSTLKV  QIRRIDPWS        0.3830        793.0               50.00      Sequence
DRB1_0405  173  ARVQLSARRSRGPVR  RVQLSARRS        0.3806        813.6               50.00      Sequence
DRB1_0405  256  SGTIFGGAFLIGLVN  GAFLIGLVN        0.3806        814.2               50.00      Sequence
DRB1_0405  174  RVQLSARRSRGPVRA  RVQLSARRS        0.3791        827.2               50.00      Sequence
DRB1_0405  214  VWMITVAFLYLVLGG  WMITVAFLY        0.3789        828.7               50.00      Sequence
DRB1_0405  289  TDLIGGIEVTLADRD  GGIEVTLAD        0.3789        829.3               50.00      Sequence
DRB1_0405  168  AESRDARVQLSARRS  RVQLSARRS        0.3759        856.4               50.00      Sequence
DRB1_0405  119  EAYASELPDLSGPTP  YASELPDLS        0.3753        861.6               50.00      Sequence
DRB1_0405  118  AEAYASELPDLSGPT  YASELPDLS        0.3705        908.1               50.00      Sequence
DRB1_0405  117  PAEAYASELPDLSGP  YASELPDLS        0.3647        966.7               50.00      Sequence
DRB1_0405   76  AADARLNRFISGASA  NRFISGASA        0.3598       1019.4               50.00      Sequence
DRB1_0405  185  PVRASMQIRRIDPWS  PVRASMQIR        0.3575       1045.5               50.00      Sequence
DRB1_0405  204  SLLLSVALFFVWMIT  SLLLSVALF        0.3556       1067.1               50.00      Sequence
DRB1_0405  116  SPAEAYASELPDLSG  YASELPDLS        0.3535       1091.2               50.00      Sequence
DRB1_0405  187  RASMQIRRIDPWSTL  MQIRRIDPW        0.3528       1099.9               50.00      Sequence
DRB1_0405  188  ASMQIRRIDPWSTLK  QIRRIDPWS        0.3523       1105.6               50.00      Sequence
DRB1_0405  233  AKLNSNVGDLLNNAS  LNSNVGDLL        0.3464       1178.9               50.00      Sequence
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DRB1_0405  180  RRSRGPVRASMQIRR  GPVRASMQI        0.3462       1181.1               50.00      Sequence
DRB1_0405   84  FISGASAPVTGPAAA  FISGASAPV        0.3460       1182.7               50.00      Sequence
DRB1_0405   42  PPPWQRAATRQSQAG  WQRAATRQS        0.3387       1281.0               50.00      Sequence
DRB1_0405  156  SAAGSSGGRSITAES  GGRSITAES        0.3369       1306.2               50.00      Sequence
DRB1_0405   43  PPWQRAATRQSQAGH  WQRAATRQS        0.3344       1341.7               50.00      Sequence
DRB1_0405  288  ITDLIGGIEVTLADR  GGIEVTLAD        0.3339       1348.5               50.00      Sequence
DRB1_0405  186  VRASMQIRRIDPWST  SMQIRRIDP        0.3308       1395.3               50.00      Sequence
DRB1_0405   41  DPPPWQRAATRQSQA  WQRAATRQS        0.3242       1499.0               50.00      Sequence
DRB1_0405  115  GSPAEAYASELPDLS  EAYASELPD        0.3227       1523.4               50.00      Sequence
DRB1_0405   44  PWQRAATRQSQAGHR  WQRAATRQS        0.3219       1535.1               50.00      Sequence
DRB1_0405  234  KLNSNVGDLLNNASG  LNSNVGDLL        0.3172       1616.2               50.00      Sequence
DRB1_0405  162  GGRSITAESRDARVQ  GGRSITAES        0.3159       1638.9               50.00      Sequence
DRB1_0405  285  YNLITDLIGGIEVTL  YNLITDLIG        0.3145       1664.3               50.00      Sequence
DRB1_0405  255  SSGTIFGGAFLIGLV  GTIFGGAFL        0.3134       1684.0               50.00      Sequence
DRB1_0405  120  AYASELPDLSGPTPR  YASELPDLS        0.3087       1771.1               50.00      Sequence
DRB1_0405  178  SARRSRGPVRASMQI  GPVRASMQI        0.3057       1830.0               50.00      Sequence
DRB1_0405  287  LITDLIGGIEVTLAD  GGIEVTLAD        0.2991       1965.8               50.00      Sequence
DRB1_0405   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.2965       2022.4               50.00      Sequence
DRB1_0405  179  ARRSRGPVRASMQIR  GPVRASMQI        0.2954       2046.0               50.00      Sequence
DRB1_0405  235  LNSNVGDLLNNASGS  SNVGDLLNN        0.2925       2110.1               50.00      Sequence
DRB1_0405   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.2914       2136.9               50.00      Sequence
DRB1_0405  252  ELVSSGTIFGGAFLI  ELVSSGTIF        0.2839       2318.1               50.00      Sequence
DRB1_0405  121  YASELPDLSGPTPRA  YASELPDLS        0.2807       2399.2               50.00      Sequence
DRB1_0405  254  VSSGTIFGGAFLIGL  GTIFGGAFL        0.2789       2444.6               50.00      Sequence
DRB1_0405  175  VQLSARRSRGPVRAS  VQLSARRSR        0.2787       2450.5               50.00      Sequence
DRB1_0405  236  NSNVGDLLNNASGSS  SNVGDLLNN        0.2747       2559.8               50.00      Sequence
DRB1_0405   53  SQAGHRQPPPVSHPE  GHRQPPPVS        0.2683       2742.2               50.00      Sequence
DRB1_0405   54  QAGHRQPPPVSHPEG  GHRQPPPVS        0.2651       2840.2               50.00      Sequence
DRB1_0405   75  AAADARLNRFISGAS  LNRFISGAS        0.2645       2859.7               50.00      Sequence
DRB1_0405  110  LGCGDGSPAEAYASE  GCGDGSPAE        0.2643       2864.5               50.00      Sequence
DRB1_0405  237  SNVGDLLNNASGSSA  SNVGDLLNN        0.2637       2882.1               50.00      Sequence
DRB1_0405  109  SLGCGDGSPAEAYAS  GCGDGSPAE        0.2637       2884.5               50.00      Sequence
DRB1_0405   39  AGDPPPWQRAATRQS  WQRAATRQS        0.2627       2913.5               50.00      Sequence
DRB1_0405  167  TAESRDARVQLSARR  ESRDARVQL        0.2581       3064.0               50.00      Sequence
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DRB1_0405   52  QSQAGHRQPPPVSHP  AGHRQPPPV        0.2539       3206.9               50.00      Sequence
DRB1_0405  111  GCGDGSPAEAYASEL  GCGDGSPAE        0.2537       3213.0               50.00      Sequence
DRB1_0405  239  VGDLLNNASGSSAEL  LLNNASGSS        0.2529       3241.2               50.00      Sequence
DRB1_0405  149  GAGSRGDSAAGSSGG  GSRGDSAAG        0.2501       3339.1               50.00      Sequence
DRB1_0405  238  NVGDLLNNASGSSAE  VGDLLNNAS        0.2499       3347.9               50.00      Sequence
DRB1_0405   95  PAAAVRTPQPDPDAS  AAVRTPQPD        0.2497       3352.8               50.00      Sequence
DRB1_0405  148  GGAGSRGDSAAGSSG  GSRGDSAAG        0.2486       3394.8               50.00      Sequence
DRB1_0405   55  AGHRQPPPVSHPEGR  GHRQPPPVS        0.2442       3562.1               50.00      Sequence
DRB1_0405  286  NLITDLIGGIEVTLA  LIGGIEVTL        0.2440       3567.5               50.00      Sequence
DRB1_0405  114  DGSPAEAYASELPDL  EAYASELPD        0.2432       3600.9               50.00      Sequence
DRB1_0405  108  ASLGCGDGSPAEAYA  GCGDGSPAE        0.2427       3619.6               50.00      Sequence
DRB1_0405  150  AGSRGDSAAGSSGGR  GSRGDSAAG        0.2427       3620.2               50.00      Sequence
DRB1_0405  240  GDLLNNASGSSAELV  LLNNASGSS        0.2423       3633.2               50.00      Sequence
DRB1_0405  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.2376       3822.5               50.00      Sequence
DRB1_0405   93  TGPAAAVRTPQPDPD  AAVRTPQPD        0.2322       4054.4               50.00      Sequence
DRB1_0405   65  HPEGRPTNPPAAADA  GRPTNPPAA        0.2290       4196.2               50.00      Sequence
DRB1_0405  166  ITAESRDARVQLSAR  ESRDARVQL        0.2289       4202.9               50.00      Sequence
DRB1_0405   85  ISGASAPVTGPAAAV  ISGASAPVT        0.2286       4215.2               50.00      Sequence
DRB1_0405  241  DLLNNASGSSAELVS  LLNNASGSS        0.2284       4222.0               50.00      Sequence
DRB1_0405  113  GDGSPAEAYASELPD  EAYASELPD        0.2270       4289.1               50.00      Sequence
DRB1_0405   96  AAAVRTPQPDPDASL  AAVRTPQPD        0.2260       4335.8               50.00      Sequence
DRB1_0405  147  EGGAGSRGDSAAGSS  GSRGDSAAG        0.2241       4425.2               50.00      Sequence
DRB1_0405   51  RQSQAGHRQPPPVSH  GHRQPPPVS        0.2233       4462.5               50.00      Sequence
DRB1_0405   64  SHPEGRPTNPPAAAD  EGRPTNPPA        0.2230       4478.0               50.00      Sequence
DRB1_0405  151  GSRGDSAAGSSGGRS  GSRGDSAAG        0.2184       4707.3               50.00      Sequence
DRB1_0405   66  PEGRPTNPPAAADAR  GRPTNPPAA        0.2144       4915.4               50.00      Sequence
DRB1_0405  244  NNASGSSAELVSSGT  SAELVSSGT        0.2132       4979.7               50.00      Sequence
DRB1_0405  176  QLSARRSRGPVRASM  SARRSRGPV        0.2130       4990.2               50.00      Sequence
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DRB1_0405   50  TRQSQAGHRQPPPVS  GHRQPPPVS        0.2124        5024.5               50.00     Sequence
DRB1_0405  123  SELPDLSGPTPRAPQ  LPDLSGPTP        0.2114        5075.8               50.00     Sequence
DRB1_0405  122  ASELPDLSGPTPRAP  LPDLSGPTP        0.2094        5188.8               50.00     Sequence
DRB1_0405  107  DASLGCGDGSPAEAY  GCGDGSPAE        0.2093        5192.7               50.00     Sequence
DRB1_0405  242  LLNNASGSSAELVSS  LLNNASGSS        0.2088        5223.2               50.00     Sequence
DRB1_0405   67  EGRPTNPPAAADARL  GRPTNPPAA        0.2072        5311.1               50.00     Sequence
DRB1_0405  124  ELPDLSGPTPRAPQR  LPDLSGPTP        0.2060        5381.2               50.00     Sequence
DRB1_0405   92  VTGPAAAVRTPQPDP  AVRTPQPDP        0.2059        5386.7               50.00     Sequence
DRB1_0405  177  LSARRSRGPVRASMQ  SARRSRGPV        0.2054        5416.8               50.00     Sequence
DRB1_0405  112  CGDGSPAEAYASELP  CGDGSPAEA        0.2038        5514.3               50.00     Sequence
DRB1_0405  164  RSITAESRDARVQLS  RSITAESRD        0.2028        5570.8               50.00     Sequence
DRB1_0405  165  SITAESRDARVQLSA  ESRDARVQL        0.1993        5787.4               50.00     Sequence
DRB1_0405  163  GRSITAESRDARVQL  RSITAESRD        0.1990        5805.3               50.00     Sequence
DRB1_0405   97  AAVRTPQPDPDASLG  AVRTPQPDP        0.1963        5977.8               50.00     Sequence
DRB1_0405   63  VSHPEGRPTNPPAAA  EGRPTNPPA        0.1954        6036.9               50.00     Sequence
DRB1_0405   32  GPGRIPDAGDPPPWQ  PGRIPDAGD        0.1935        6158.8               50.00     Sequence
DRB1_0405   30  ATGPGRIPDAGDPPP  PGRIPDAGD        0.1882        6528.3               50.00     Sequence
DRB1_0405   31  TGPGRIPDAGDPPPW  PGRIPDAGD        0.1875        6578.0               50.00     Sequence
DRB1_0405  146  AEGGAGSRGDSAAGS  GSRGDSAAG        0.1864        6651.0               50.00     Sequence
DRB1_0405   62  PVSHPEGRPTNPPAA  EGRPTNPPA        0.1854        6724.3               50.00     Sequence
DRB1_0405   74  PAAADARLNRFISGA  DARLNRFIS        0.1845        6795.0               50.00     Sequence
DRB1_0405  125  LPDLSGPTPRAPQRN  LPDLSGPTP        0.1750        7527.3               50.00     Sequence
DRB1_0405  243  LNNASGSSAELVSSG  LNNASGSSA        0.1733        7667.5               50.00     Sequence
DRB1_0405   33  PGRIPDAGDPPPWQR  PGRIPDAGD        0.1713        7838.9               50.00     Sequence
DRB1_0405  106  PDASLGCGDGSPAEA  GCGDGSPAE        0.1709        7869.3               50.00     Sequence
DRB1_0405   13  DGPNADGLVDRGGAH  GPNADGLVD        0.1699        7954.9               50.00     Sequence
DRB1_0405   46  QRAATRQSQAGHRQP  RAATRQSQA        0.1686        8066.7               50.00     Sequence
DRB1_0405   28  RAATGPGRIPDAGDP  PGRIPDAGD        0.1684        8082.2               50.00     Sequence
DRB1_0405   29  AATGPGRIPDAGDPP  PGRIPDAGD        0.1679        8127.8               50.00     Sequence
DRB1_0405   14  GPNADGLVDRGGAHR  GPNADGLVD        0.1661        8288.8               50.00     Sequence
DRB1_0405   47  RAATRQSQAGHRQPP  RAATRQSQA        0.1637        8504.7               50.00     Sequence
DRB1_0405   12  GDGPNADGLVDRGGA  GPNADGLVD        0.1632        8549.8               50.00     Sequence
DRB1_0405   27  HRAATGPGRIPDAGD  PGRIPDAGD        0.1614        8721.7               50.00     Sequence
DRB1_0405   91  PVTGPAAAVRTPQPD  AAAVRTPQP        0.1601        8840.7               50.00     Sequence
DRB1_0405   56  GHRQPPPVSHPEGRP  GHRQPPPVS        0.1584        9009.3               50.00     Sequence
DRB1_0405  133  PRAPQRNPAPARPAE  PQRNPAPAR        0.1575        9098.1               50.00     Sequence
DRB1_0405  132  TPRAPQRNPAPARPA  PQRNPAPAR        0.1563        9217.2               50.00     Sequence
DRB1_0405   34  GRIPDAGDPPPWQRA  RIPDAGDPP        0.1528        9566.3               50.00     Sequence
DRB1_0405   90  APVTGPAAAVRTPQP  AAAVRTPQP        0.1528        9576.3               50.00     Sequence
DRB1_0405   98  AVRTPQPDPDASLGC  AVRTPQPDP        0.1495        9921.3               50.00     Sequence
DRB1_0405  155  DSAAGSSGGRSITAE  SGGRSITAE        0.1477       10115.6               50.00     Sequence
DRB1_0405   61  PPVSHPEGRPTNPPA  EGRPTNPPA        0.1464       10257.1               50.00     Sequence
DRB1_0405   11  KGDGPNADGLVDRGG  GPNADGLVD        0.1463       10270.7               50.00     Sequence
DRB1_0405   86  SGASAPVTGPAAAVR  SAPVTGPAA        0.1452       10392.1               50.00     Sequence
DRB1_0405   68  GRPTNPPAAADARLN  GRPTNPPAA        0.1450       10418.4               50.00     Sequence
DRB1_0405   73  PPAAADARLNRFISG  DARLNRFIS        0.1447       10442.8               50.00     Sequence
DRB1_0405    5  EPGALSKGDGPNADG  LSKGDGPNA        0.1446       10464.5               50.00     Sequence
DRB1_0405   49  ATRQSQAGHRQPPPV  AGHRQPPPV        0.1437       10557.4               50.00     Sequence
DRB1_0405   35  RIPDAGDPPPWQRAA  IPDAGDPPP        0.1427       10675.3               50.00     Sequence
DRB1_0405    6  PGALSKGDGPNADGL  LSKGDGPNA        0.1411       10858.9               50.00     Sequence
DRB1_0405    4  NEPGALSKGDGPNAD  LSKGDGPNA        0.1405       10938.3               50.00     Sequence
DRB1_0405  134  RAPQRNPAPARPAEG  PQRNPAPAR        0.1392       11085.0               50.00     Sequence
DRB1_0405  131  PTPRAPQRNPAPARP  TPRAPQRNP        0.1373       11314.4               50.00     Sequence
DRB1_0405    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.1360       11482.0               50.00     Sequence
DRB1_0405   10  SKGDGPNADGLVDRG  GPNADGLVD        0.1356       11532.4               50.00     Sequence
DRB1_0405   16  NADGLVDRGGAHRAA  NADGLVDRG        0.1350       11604.0               50.00     Sequence
DRB1_0405    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.1350       11609.3               50.00     Sequence
DRB1_0405   87  GASAPVTGPAAAVRT  APVTGPAAA        0.1345       11661.4               50.00     Sequence
DRB1_0405   15  PNADGLVDRGGAHRA  NADGLVDRG        0.1335       11795.2               50.00     Sequence
DRB1_0405    3  PNEPGALSKGDGPNA  GALSKGDGP        0.1329       11864.4               50.00     Sequence
DRB1_0405    7  GALSKGDGPNADGLV  LSKGDGPNA        0.1322       11966.9               50.00     Sequence
DRB1_0405  130  GPTPRAPQRNPAPAR  TPRAPQRNP        0.1294       12331.1               50.00     Sequence
DRB1_0405    2  APNEPGALSKGDGPN  GALSKGDGP        0.1275       12584.7               50.00     Sequence
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   DRB1_0405  135  APQRNPAPARPAEGG  PQRNPAPAR        0.1268      12677.9                    50.00     Sequence
   DRB1_0405    1  TAPNEPGALSKGDGP  APNEPGALS        0.1260      12785.2                    50.00     Sequence
   DRB1_0405   88  ASAPVTGPAAAVRTP  APVTGPAAA        0.1251      12913.2                    50.00     Sequence
   DRB1_0405  145  PAEGGAGSRGDSAAG  GSRGDSAAG        0.1240      13074.2                    50.00     Sequence
   DRB1_0405   89  SAPVTGPAAAVRTPQ  PVTGPAAAV        0.1237      13119.0                    50.00     Sequence
   DRB1_0405  105  DPDASLGCGDGSPAE  GCGDGSPAE        0.1234      13154.7                    50.00     Sequence
   DRB1_0405   36  IPDAGDPPPWQRAAT  IPDAGDPPP        0.1199      13664.7                    50.00     Sequence
   DRB1_0405  152  SRGDSAAGSSGGRSI  SRGDSAAGS        0.1174      14036.5                    50.00     Sequence
   DRB1_0405    0  VTAPNEPGALSKGDG  EPGALSKGD        0.1167      14140.8                    50.00     Sequence
   DRB1_0405  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.1157      14301.3                    50.00     Sequence
   DRB1_0405   48  AATRQSQAGHRQPPP  ATRQSQAGH        0.1148      14434.3                    50.00     Sequence
   DRB1_0405  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.1135      14639.3                    50.00     Sequence
   DRB1_0405   17  ADGLVDRGGAHRAAT  GLVDRGGAH        0.1133      14671.3                    50.00     Sequence
   DRB1_0405   18  DGLVDRGGAHRAATG  GLVDRGGAH        0.1112      15007.0                    50.00     Sequence
   DRB1_0405   24  GGAHRAATGPGRIPD  GAHRAATGP        0.1107      15088.7                    50.00     Sequence
   DRB1_0405   23  RGGAHRAATGPGRIP  GAHRAATGP        0.1107      15095.9                    50.00     Sequence
   DRB1_0405   22  DRGGAHRAATGPGRI  HRAATGPGR        0.1095      15294.0                    50.00     Sequence
   DRB1_0405   60  PPPVSHPEGRPTNPP  VSHPEGRPT        0.1074      15634.5                    50.00     Sequence
   DRB1_0405   38  DAGDPPPWQRAATRQ  PPWQRAATR        0.1074      15648.9                    50.00     Sequence
   DRB1_0405   37  PDAGDPPPWQRAATR  PPWQRAATR        0.1067      15766.0                    50.00     Sequence
   DRB1_0405  136  PQRNPAPARPAEGGA  PQRNPAPAR        0.1055      15963.9                    50.00     Sequence
   DRB1_0405  129  SGPTPRAPQRNPAPA  TPRAPQRNP        0.1055      15975.2                    50.00     Sequence
   DRB1_0405   25  GAHRAATGPGRIPDA  GAHRAATGP        0.1053      16009.1                    50.00     Sequence
   DRB1_0405   26  AHRAATGPGRIPDAG  RAATGPGRI        0.1046      16130.4                    50.00     Sequence
   DRB1_0405  128  LSGPTPRAPQRNPAP  TPRAPQRNP        0.1037      16278.4                    50.00     Sequence
   DRB1_0405   72  NPPAAADARLNRFIS  DARLNRFIS        0.1016      16662.4                    50.00     Sequence
   DRB1_0405  154  GDSAAGSSGGRSITA  AAGSSGGRS        0.0973      17444.4                    50.00     Sequence
   DRB1_0405  153  RGDSAAGSSGGRSIT  AAGSSGGRS        0.0965      17596.7                    50.00     Sequence
   DRB1_0405   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.0961      17670.1                    50.00     Sequence
   DRB1_0405   19  GLVDRGGAHRAATGP  GLVDRGGAH        0.0948      17926.6                    50.00     Sequence
   DRB1_0405  100  RTPQPDPDASLGCGD  RTPQPDPDA        0.0938      18113.8                    50.00     Sequence
   DRB1_0405   57  HRQPPPVSHPEGRPT  HRQPPPVSH        0.0935      18186.8                    50.00     Sequence
   DRB1_0405   21  VDRGGAHRAATGPGR  GGAHRAATG        0.0929      18302.5                    50.00     Sequence
   DRB1_0405  102  PQPDPDASLGCGDGS  PQPDPDASL        0.0876      19384.2                    50.00     Sequence
   DRB1_0405   69  RPTNPPAAADARLNR  RPTNPPAAA        0.0866      19600.6                    50.00     Sequence
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   DRB1_0405  101  TPQPDPDASLGCGDG  PQPDPDASL        0.0833      20292.7                    50.00     Sequence
   DRB1_0405   59  QPPPVSHPEGRPTNP  VSHPEGRPT        0.0828      20416.2                    50.00     Sequence
   DRB1_0405  104  PDPDASLGCGDGSPA  LGCGDGSPA        0.0823      20512.3                    50.00     Sequence
   DRB1_0405   58  RQPPPVSHPEGRPTN  PVSHPEGRP        0.0823      20526.1                    50.00     Sequence
   DRB1_0405  138  RNPAPARPAEGGAGS  NPAPARPAE        0.0781      21467.1                    50.00     Sequence
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   DRB1_0405   20  LVDRGGAHRAATGPG  LVDRGGAHR        0.0776      21597.8                    50.00     Sequence
   DRB1_0405  137  QRNPAPARPAEGGAG  QRNPAPARP        0.0731      22680.3                    50.00     Sequence
   DRB1_0405  142  PARPAEGGAGSRGDS  EGGAGSRGD        0.0712      23142.4                    50.00     Sequence
   DRB1_0405  103  QPDPDASLGCGDGSP  SLGCGDGSP        0.0701      23411.4                    50.00     Sequence
   DRB1_0405  139  NPAPARPAEGGAGSR  RPAEGGAGS        0.0660      24487.6                    50.00     Sequence
   DRB1_0405  141  APARPAEGGAGSRGD  EGGAGSRGD        0.0627      25364.3                    50.00     Sequence
   DRB1_0405   70  PTNPPAAADARLNRF  PPAAADARL        0.0596      26240.2                    50.00     Sequence
   DRB1_0405   71  TNPPAAADARLNRFI  PAAADARLN        0.0583      26619.1                    50.00     Sequence
   DRB1_0405  140  PAPARPAEGGAGSRG  RPAEGGAGS        0.0578      26749.4                    50.00     Sequence
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Allele: DRB1_0405. Number of high binders 12. Number of weak binders 67. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701   78  DARLNRFISGASAPV  FISGASAPV        0.8737          3.9         SB     1.00     Sequence
   DRB1_0701   79  ARLNRFISGASAPVT  FISGASAPV        0.8707          4.1         SB     1.00     Sequence
   DRB1_0701   80  RLNRFISGASAPVTG  FISGASAPV        0.8439          5.4         SB     2.00     Sequence
   DRB1_0701   81  LNRFISGASAPVTGP  FISGASAPV        0.8102          7.8         SB     4.00     Sequence
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DRB1_0701  192  IRRIDPWSTLKVSLL  WSTLKVSLL        0.8064           8.1        SB      4.00    Sequence
DRB1_0701  193  RRIDPWSTLKVSLLL  WSTLKVSLL        0.8027           8.5        SB      4.00    Sequence
DRB1_0701   82  NRFISGASAPVTGPA  FISGASAPV        0.7902           9.7        SB      4.00    Sequence
DRB1_0701  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.7747          11.4        SB      8.00    Sequence
DRB1_0701   83  RFISGASAPVTGPAA  FISGASAPV        0.7669          12.5        SB      8.00    Sequence
DRB1_0701  195  IDPWSTLKVSLLLSV  WSTLKVSLL        0.7668          12.5        SB      8.00    Sequence
DRB1_0701  196  DPWSTLKVSLLLSVA  WSTLKVSLL        0.7447          15.8        SB      8.00    Sequence
DRB1_0701  197  PWSTLKVSLLLSVAL  WSTLKVSLL        0.7435          16.0        SB      8.00    Sequence
DRB1_0701   84  FISGASAPVTGPAAA  FISGASAPV        0.7321          18.2        SB      8.00    Sequence
DRB1_0701  198  WSTLKVSLLLSVALF  WSTLKVSLL        0.7141          22.0        SB      8.00    Sequence
DRB1_0701  245  NASGSSAELVSSGTI  AELVSSGTI        0.6949          27.1        SB     16.00    Sequence
DRB1_0701  277  LATIGAFVYNLITDL  FVYNLITDL        0.6617          38.9        SB     16.00    Sequence
DRB1_0701  246  ASGSSAELVSSGTIF  AELVSSGTI        0.6592          40.0        SB     16.00    Sequence
DRB1_0701  267  GLVNIVLMTALATIG  VLMTALATI        0.6554          41.6        SB     16.00    Sequence
DRB1_0701  247  SGSSAELVSSGTIFG  AELVSSGTI        0.6497          44.3        SB     16.00    Sequence
DRB1_0701  278  ATIGAFVYNLITDLI  FVYNLITDL        0.6453          46.4        SB     16.00    Sequence
DRB1_0701  268  LVNIVLMTALATIGA  LMTALATIG        0.6242          58.3        WB     16.00    Sequence
DRB1_0701  266  IGLVNIVLMTALATI  VLMTALATI        0.6100          68.0        WB     16.00    Sequence
DRB1_0701  279  TIGAFVYNLITDLIG  FVYNLITDL        0.6015          74.6        WB     16.00    Sequence
DRB1_0701  199  STLKVSLLLSVALFF  VSLLLSVAL        0.5910          83.5        WB     32.00    Sequence
DRB1_0701  269  VNIVLMTALATIGAF  LMTALATIG        0.5891          85.2        WB     32.00    Sequence
DRB1_0701  248  GSSAELVSSGTIFGG  AELVSSGTI        0.5766          97.6        WB     32.00    Sequence
DRB1_0701  270  NIVLMTALATIGAFV  LMTALATIG        0.5628         113.3        WB     32.00    Sequence
DRB1_0701  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.5461         135.8        WB     32.00    Sequence
DRB1_0701  271  IVLMTALATIGAFVY  LMTALATIG        0.5442         138.7        WB     32.00    Sequence
DRB1_0701  249  SSAELVSSGTIFGGA  AELVSSGTI        0.5335         155.7        WB     32.00    Sequence
DRB1_0701  211  LFFVWMITVAFLYLV  ITVAFLYLV        0.5280         165.2        WB     32.00    Sequence
DRB1_0701  280  IGAFVYNLITDLIGG  FVYNLITDL        0.5126         195.0        WB     32.00    Sequence
DRB1_0701  201  LKVSLLLSVALFFVW  VSLLLSVAL        0.5110         198.6        WB     32.00    Sequence
DRB1_0701  229  MGVWAKLNSNVGDLL  LNSNVGDLL        0.5014         220.2        WB     32.00    Sequence
DRB1_0701  209  VALFFVWMITVAFLY  WMITVAFLY        0.5013         220.4        WB     32.00    Sequence
DRB1_0701  272  VLMTALATIGAFVYN  LMTALATIG        0.5013         220.5        WB     32.00    Sequence
DRB1_0701  212  FFVWMITVAFLYLVL  ITVAFLYLV        0.4944         237.5        WB     32.00    Sequence
DRB1_0701  250  SAELVSSGTIFGGAF  AELVSSGTI        0.4862         259.8        WB     32.00    Sequence
DRB1_0701  273  LMTALATIGAFVYNL  LMTALATIG        0.4826         270.0        WB     32.00    Sequence
DRB1_0701  210  ALFFVWMITVAFLYL  WMITVAFLY        0.4807         275.4        WB     32.00    Sequence
DRB1_0701  240  GDLLNNASGSSAELV  ASGSSAELV        0.4768         287.3        WB     32.00    Sequence
DRB1_0701  281  GAFVYNLITDLIGGI  FVYNLITDL        0.4751         292.7        WB     32.00    Sequence
DRB1_0701   85  ISGASAPVTGPAAAV  ISGASAPVT        0.4691         312.4        WB     32.00    Sequence
DRB1_0701  230  GVWAKLNSNVGDLLN  LNSNVGDLL        0.4602         344.1        WB     32.00    Sequence
DRB1_0701   22  DRGGAHRAATGPGRI  RAATGPGRI        0.4567         357.4        WB     32.00    Sequence
DRB1_0701  251  AELVSSGTIFGGAFL  AELVSSGTI        0.4525         373.9        WB     50.00    Sequence
DRB1_0701  213  FVWMITVAFLYLVLG  WMITVAFLY        0.4468         397.8        WB     50.00    Sequence
DRB1_0701  265  LIGLVNIVLMTALAT  IVLMTALAT        0.4451         404.9        WB     50.00    Sequence
DRB1_0701  241  DLLNNASGSSAELVS  ASGSSAELV        0.4387         434.2        WB     50.00    Sequence
DRB1_0701  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.4299         477.4        WB     50.00    Sequence
DRB1_0701  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.4287         483.5        WB     50.00    Sequence
DRB1_0701  282  AFVYNLITDLIGGIE  FVYNLITDL        0.4235         511.8               50.00    Sequence
DRB1_0701  275  TALATIGAFVYNLIT  TIGAFVYNL        0.4213         524.1               50.00    Sequence
DRB1_0701  283  FVYNLITDLIGGIEV  FVYNLITDL        0.4167         550.7               50.00    Sequence
DRB1_0701  231  VWAKLNSNVGDLLNN  LNSNVGDLL        0.4163         553.2               50.00    Sequence
DRB1_0701  263  AFLIGLVNIVLMTAL  VNIVLMTAL        0.4162         553.9               50.00    Sequence
DRB1_0701   23  RGGAHRAATGPGRIP  RAATGPGRI        0.4116         581.7               50.00    Sequence
DRB1_0701  186  VRASMQIRRIDPWST  IRRIDPWST        0.4103         589.9               50.00    Sequence
DRB1_0701  180  RRSRGPVRASMQIRR  VRASMQIRR        0.4026         641.4               50.00    Sequence
DRB1_0701  242  LLNNASGSSAELVSS  ASGSSAELV        0.3981         673.4               50.00    Sequence
DRB1_0701  217  ITVAFLYLVLGGMGV  YLVLGGMGV        0.3967         684.1               50.00    Sequence
DRB1_0701  274  MTALATIGAFVYNLI  TIGAFVYNL        0.3932         710.0               50.00    Sequence
DRB1_0701  214  VWMITVAFLYLVLGG  WMITVAFLY        0.3853         773.7               50.00    Sequence
DRB1_0701  208  SVALFFVWMITVAFL  VWMITVAFL        0.3794         824.6               50.00    Sequence
DRB1_0701  187  RASMQIRRIDPWSTL  IRRIDPWST        0.3783         834.2               50.00    Sequence
DRB1_0701  264  FLIGLVNIVLMTALA  VNIVLMTAL        0.3770         846.6               50.00    Sequence
DRB1_0701  179  ARRSRGPVRASMQIR  PVRASMQIR        0.3767         848.6               50.00    Sequence
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DRB1_0701  232  WAKLNSNVGDLLNNA  LNSNVGDLL        0.3741        873.0                50.00      Sequence
DRB1_0701  276  ALATIGAFVYNLITD  TIGAFVYNL        0.3734        880.2                50.00      Sequence
DRB1_0701  259  IFGGAFLIGLVNIVL  FLIGLVNIV        0.3727        886.7                50.00      Sequence
DRB1_0701  181  RSRGPVRASMQIRRI  VRASMQIRR        0.3719        894.5                50.00      Sequence
DRB1_0701   39  AGDPPPWQRAATRQS  WQRAATRQS        0.3682        930.9                50.00      Sequence
DRB1_0701   24  GGAHRAATGPGRIPD  RAATGPGRI        0.3660        953.0                50.00      Sequence
DRB1_0701  258  TIFGGAFLIGLVNIV  FLIGLVNIV        0.3652        961.1                50.00      Sequence
DRB1_0701  111  GCGDGSPAEAYASEL  PAEAYASEL        0.3649        964.3                50.00      Sequence
DRB1_0701  260  FGGAFLIGLVNIVLM  LIGLVNIVL        0.3611       1005.2                50.00      Sequence
DRB1_0701  189  SMQIRRIDPWSTLKV  IRRIDPWST        0.3570       1050.2                50.00      Sequence
DRB1_0701  226  LGGMGVWAKLNSNVG  WAKLNSNVG        0.3566       1055.5                50.00      Sequence
DRB1_0701  285  YNLITDLIGGIEVTL  LIGGIEVTL        0.3463       1180.1                50.00      Sequence
DRB1_0701  218  TVAFLYLVLGGMGVW  YLVLGGMGV        0.3443       1205.6                50.00      Sequence
DRB1_0701  243  LNNASGSSAELVSSG  ASGSSAELV        0.3422       1232.9                50.00      Sequence
DRB1_0701  178  SARRSRGPVRASMQI  GPVRASMQI        0.3393       1273.0                50.00      Sequence
DRB1_0701  215  WMITVAFLYLVLGGM  WMITVAFLY        0.3384       1284.9                50.00      Sequence
DRB1_0701  188  ASMQIRRIDPWSTLK  IRRIDPWST        0.3349       1334.9                50.00      Sequence
DRB1_0701  252  ELVSSGTIFGGAFLI  LVSSGTIFG        0.3347       1336.9                50.00      Sequence
DRB1_0701  222  LYLVLGGMGVWAKLN  GMGVWAKLN        0.3333       1357.7                50.00      Sequence
DRB1_0701  254  VSSGTIFGGAFLIGL  FGGAFLIGL        0.3333       1357.9                50.00      Sequence
DRB1_0701  191  QIRRIDPWSTLKVSL  IRRIDPWST        0.3324       1371.2                50.00      Sequence
DRB1_0701  233  AKLNSNVGDLLNNAS  LNSNVGDLL        0.3303       1401.8                50.00      Sequence
DRB1_0701   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.3245       1493.1                50.00      Sequence
DRB1_0701   25  GAHRAATGPGRIPDA  RAATGPGRI        0.3230       1517.6                50.00      Sequence
DRB1_0701   86  SGASAPVTGPAAAVR  VTGPAAAVR        0.3199       1569.3                50.00      Sequence
DRB1_0701  190  MQIRRIDPWSTLKVS  IRRIDPWST        0.3150       1655.1                50.00      Sequence
DRB1_0701  112  CGDGSPAEAYASELP  PAEAYASEL        0.3140       1673.2                50.00      Sequence
DRB1_0701  219  VAFLYLVLGGMGVWA  YLVLGGMGV        0.3136       1681.0                50.00      Sequence
DRB1_0701  182  SRGPVRASMQIRRID  VRASMQIRR        0.3130       1691.1                50.00      Sequence
DRB1_0701  261  GGAFLIGLVNIVLMT  LIGLVNIVL        0.3122       1705.2                50.00      Sequence
DRB1_0701  234  KLNSNVGDLLNNASG  LNSNVGDLL        0.3089       1767.6                50.00      Sequence
DRB1_0701  227  GGMGVWAKLNSNVGD  WAKLNSNVG        0.3056       1831.7                50.00      Sequence
DRB1_0701  173  ARVQLSARRSRGPVR  ARRSRGPVR        0.3053       1837.5                50.00      Sequence
DRB1_0701  255  SSGTIFGGAFLIGLV  FGGAFLIGL        0.3051       1842.6                50.00      Sequence
DRB1_0701   87  GASAPVTGPAAAVRT  VTGPAAAVR        0.3046       1851.1                50.00      Sequence
DRB1_0701   26  AHRAATGPGRIPDAG  RAATGPGRI        0.3046       1852.5                50.00      Sequence
DRB1_0701  223  YLVLGGMGVWAKLNS  GMGVWAKLN        0.3046       1852.8                50.00      Sequence
DRB1_0701  244  NNASGSSAELVSSGT  ASGSSAELV        0.3042       1859.5                50.00      Sequence
DRB1_0701  225  VLGGMGVWAKLNSNV  VWAKLNSNV        0.3001       1943.6                50.00      Sequence
DRB1_0701  174  RVQLSARRSRGPVRA  ARRSRGPVR        0.3001       1944.2                50.00      Sequence
DRB1_0701  204  SLLLSVALFFVWMIT  VALFFVWMI        0.2989       1970.9                50.00      Sequence
DRB1_0701  286  NLITDLIGGIEVTLA  LIGGIEVTL        0.2985       1979.3                50.00      Sequence
DRB1_0701  228  GMGVWAKLNSNVGDL  KLNSNVGDL        0.2955       2042.7                50.00      Sequence
DRB1_0701  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.2930       2099.0                50.00      Sequence
DRB1_0701  262  GAFLIGLVNIVLMTA  FLIGLVNIV        0.2926       2108.4                50.00      Sequence
DRB1_0701  284  VYNLITDLIGGIEVT  VYNLITDLI        0.2910       2145.2                50.00      Sequence
DRB1_0701   41  DPPPWQRAATRQSQA  WQRAATRQS        0.2847       2296.2                50.00      Sequence
DRB1_0701  235  LNSNVGDLLNNASGS  LNSNVGDLL        0.2801       2414.4                50.00      Sequence
DRB1_0701   27  HRAATGPGRIPDAGD  RAATGPGRI        0.2767       2505.8                50.00      Sequence
DRB1_0701  256  SGTIFGGAFLIGLVN  FGGAFLIGL        0.2752       2546.1                50.00      Sequence
DRB1_0701  220  AFLYLVLGGMGVWAK  YLVLGGMGV        0.2733       2598.0                50.00      Sequence
DRB1_0701  205  LLLSVALFFVWMITV  VALFFVWMI        0.2701       2689.8                50.00      Sequence
DRB1_0701  171  RDARVQLSARRSRGP  LSARRSRGP        0.2671       2779.2                50.00      Sequence
DRB1_0701  224  LVLGGMGVWAKLNSN  GMGVWAKLN        0.2662       2805.8                50.00      Sequence
DRB1_0701  113  GDGSPAEAYASELPD  PAEAYASEL        0.2659       2815.2                50.00      Sequence
DRB1_0701  287  LITDLIGGIEVTLAD  LIGGIEVTL        0.2658       2819.3                50.00      Sequence
DRB1_0701  216  MITVAFLYLVLGGMG  ITVAFLYLV        0.2644       2860.7                50.00      Sequence
DRB1_0701  207  LSVALFFVWMITVAF  FVWMITVAF        0.2641       2869.8                50.00      Sequence
DRB1_0701  183  RGPVRASMQIRRIDP  VRASMQIRR        0.2628       2911.9                50.00      Sequence
DRB1_0701   71  TNPPAAADARLNRFI  ADARLNRFI        0.2613       2957.8                50.00      Sequence
DRB1_0701  161  SGGRSITAESRDARV  TAESRDARV        0.2610       2968.3                50.00      Sequence
DRB1_0701  132  TPRAPQRNPAPARPA  RNPAPARPA        0.2601       2996.7                50.00      Sequence
DRB1_0701  175  VQLSARRSRGPVRAS  ARRSRGPVR        0.2591       3030.3                50.00      Sequence
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DRB1_0701   88  ASAPVTGPAAAVRTP  VTGPAAAVR        0.2581        3064.1              50.00      Sequence
DRB1_0701   28  RAATGPGRIPDAGDP  RAATGPGRI        0.2535        3218.5              50.00      Sequence
DRB1_0701  221  FLYLVLGGMGVWAKL  YLVLGGMGV        0.2483        3407.6              50.00      Sequence
DRB1_0701  184  GPVRASMQIRRIDPW  VRASMQIRR        0.2479        3419.7              50.00      Sequence
DRB1_0701  257  GTIFGGAFLIGLVNI  FGGAFLIGL        0.2473        3443.1              50.00      Sequence
DRB1_0701  172  DARVQLSARRSRGPV  LSARRSRGP        0.2472        3447.2              50.00      Sequence
DRB1_0701   15  PNADGLVDRGGAHRA  LVDRGGAHR        0.2439        3570.4              50.00      Sequence
DRB1_0701   44  PWQRAATRQSQAGHR  WQRAATRQS        0.2422        3639.6              50.00      Sequence
DRB1_0701  152  SRGDSAAGSSGGRSI  AGSSGGRSI        0.2418        3652.1              50.00      Sequence
DRB1_0701  153  RGDSAAGSSGGRSIT  AGSSGGRSI        0.2417        3656.0              50.00      Sequence
DRB1_0701   57  HRQPPPVSHPEGRPT  VSHPEGRPT        0.2395        3746.2              50.00      Sequence
DRB1_0701  114  DGSPAEAYASELPDL  PAEAYASEL        0.2357        3904.0              50.00      Sequence
DRB1_0701   42  PPPWQRAATRQSQAG  WQRAATRQS        0.2335        3999.1              50.00      Sequence
DRB1_0701  154  GDSAAGSSGGRSITA  AGSSGGRSI        0.2305        4129.6              50.00      Sequence
DRB1_0701   72  NPPAAADARLNRFIS  ADARLNRFI        0.2289        4203.2              50.00      Sequence
DRB1_0701  133  PRAPQRNPAPARPAE  RNPAPARPA        0.2273        4274.6              50.00      Sequence
DRB1_0701  288  ITDLIGGIEVTLADR  LIGGIEVTL        0.2246        4403.6              50.00      Sequence
DRB1_0701   89  SAPVTGPAAAVRTPQ  VTGPAAAVR        0.2240        4432.0              50.00      Sequence
DRB1_0701  176  QLSARRSRGPVRASM  ARRSRGPVR        0.2236        4448.4              50.00      Sequence
DRB1_0701  115  GSPAEAYASELPDLS  PAEAYASEL        0.2215        4552.6              50.00      Sequence
DRB1_0701  162  GGRSITAESRDARVQ  TAESRDARV        0.2206        4597.4              50.00      Sequence
DRB1_0701  289  TDLIGGIEVTLADRD  LIGGIEVTL        0.2195        4652.8              50.00      Sequence
DRB1_0701   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.2191        4672.5              50.00      Sequence
DRB1_0701   16  NADGLVDRGGAHRAA  LVDRGGAHR        0.2168        4786.9              50.00      Sequence
DRB1_0701   58  RQPPPVSHPEGRPTN  VSHPEGRPT        0.2162        4820.6              50.00      Sequence
DRB1_0701   43  PPWQRAATRQSQAGH  WQRAATRQS        0.2154        4863.3              50.00      Sequence
DRB1_0701  237  SNVGDLLNNASGSSA  LNNASGSSA        0.2115        5069.7              50.00      Sequence
DRB1_0701   20  LVDRGGAHRAATGPG  AHRAATGPG        0.2100        5152.9              50.00      Sequence
DRB1_0701   14  GPNADGLVDRGGAHR  LVDRGGAHR        0.2080        5269.5              50.00      Sequence
DRB1_0701  157  AAGSSGGRSITAESR  AGSSGGRSI        0.2078        5277.2              50.00      Sequence
DRB1_0701  169  ESRDARVQLSARRSR  VQLSARRSR        0.2047        5460.8              50.00      Sequence
DRB1_0701  177  LSARRSRGPVRASMQ  ARRSRGPVR        0.2028        5573.4              50.00      Sequence
DRB1_0701   90  APVTGPAAAVRTPQP  VTGPAAAVR        0.2013        5660.3              50.00      Sequence
DRB1_0701  155  DSAAGSSGGRSITAE  AGSSGGRSI        0.1984        5841.7              50.00      Sequence
DRB1_0701  116  SPAEAYASELPDLSG  PAEAYASEL        0.1982        5853.8              50.00      Sequence
DRB1_0701  185  PVRASMQIRRIDPWS  VRASMQIRR        0.1966        5956.9              50.00      Sequence
DRB1_0701  158  AGSSGGRSITAESRD  AGSSGGRSI        0.1963        5974.9              50.00      Sequence
DRB1_0701  163  GRSITAESRDARVQL  TAESRDARV        0.1954        6033.5              50.00      Sequence
DRB1_0701  156  SAAGSSGGRSITAES  AGSSGGRSI        0.1942        6118.3              50.00      Sequence
DRB1_0701  206  LLSVALFFVWMITVA  VALFFVWMI        0.1910        6328.1              50.00      Sequence
DRB1_0701   73  PPAAADARLNRFISG  ADARLNRFI        0.1908        6341.7              50.00      Sequence
DRB1_0701   17  ADGLVDRGGAHRAAT  LVDRGGAHR        0.1908        6346.4              50.00      Sequence
DRB1_0701  239  VGDLLNNASGSSAEL  LNNASGSSA        0.1902        6382.8              50.00      Sequence
DRB1_0701  134  RAPQRNPAPARPAEG  RNPAPARPA        0.1888        6485.2              50.00      Sequence
DRB1_0701   59  QPPPVSHPEGRPTNP  VSHPEGRPT        0.1862        6667.1              50.00      Sequence
DRB1_0701  238  NVGDLLNNASGSSAE  LNNASGSSA        0.1852        6743.9              50.00      Sequence
DRB1_0701   91  PVTGPAAAVRTPQPD  VTGPAAAVR        0.1827        6926.7              50.00      Sequence
DRB1_0701  170  SRDARVQLSARRSRG  VQLSARRSR        0.1781        7275.7              50.00      Sequence
DRB1_0701  159  GSSGGRSITAESRDA  SITAESRDA        0.1764        7412.7              50.00      Sequence
DRB1_0701   75  AAADARLNRFISGAS  ADARLNRFI        0.1742        7595.8              50.00      Sequence
DRB1_0701  117  PAEAYASELPDLSGP  PAEAYASEL        0.1737        7633.4              50.00      Sequence
DRB1_0701   18  DGLVDRGGAHRAATG  LVDRGGAHR        0.1700        7945.2              50.00      Sequence
DRB1_0701   92  VTGPAAAVRTPQPDP  VTGPAAAVR        0.1668        8222.1              50.00      Sequence
DRB1_0701   76  AADARLNRFISGASA  ADARLNRFI        0.1660        8296.9              50.00      Sequence
DRB1_0701   19  GLVDRGGAHRAATGP  LVDRGGAHR        0.1642        8464.2              50.00      Sequence
DRB1_0701   77  ADARLNRFISGASAP  ADARLNRFI        0.1637        8505.3              50.00      Sequence
DRB1_0701   60  PPPVSHPEGRPTNPP  VSHPEGRPT        0.1637        8506.6              50.00      Sequence
DRB1_0701   74  PAAADARLNRFISGA  ADARLNRFI        0.1632        8555.8              50.00      Sequence
DRB1_0701  164  RSITAESRDARVQLS  TAESRDARV        0.1631        8566.3              50.00      Sequence
DRB1_0701   70  PTNPPAAADARLNRF  AADARLNRF        0.1599        8861.1              50.00      Sequence
DRB1_0701   21  VDRGGAHRAATGPGR  AHRAATGPG        0.1582        9029.1              50.00      Sequence
DRB1_0701  168  AESRDARVQLSARRS  RVQLSARRS        0.1575        9098.7              50.00      Sequence
DRB1_0701  135  APQRNPAPARPAEGG  RNPAPARPA        0.1553        9315.0              50.00      Sequence
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DRB1_0701   61  PPVSHPEGRPTNPPA  VSHPEGRPT        0.1546        9383.0                   50.00      Sequence
DRB1_0701   62  PVSHPEGRPTNPPAA  VSHPEGRPT        0.1496        9911.4                   50.00      Sequence
DRB1_0701  165  SITAESRDARVQLSA  TAESRDARV        0.1467       10223.6                   50.00      Sequence
DRB1_0701  160  SSGGRSITAESRDAR  SITAESRDA        0.1457       10337.3                   50.00      Sequence
DRB1_0701   46  QRAATRQSQAGHRQP  TRQSQAGHR        0.1412       10851.6                   50.00      Sequence
DRB1_0701  136  PQRNPAPARPAEGGA  RNPAPARPA        0.1397       11029.3                   50.00      Sequence
DRB1_0701   68  GRPTNPPAAADARLN  PAAADARLN        0.1362       11451.2                   50.00      Sequence
DRB1_0701   63  VSHPEGRPTNPPAAA  VSHPEGRPT        0.1352       11579.1                   50.00      Sequence
DRB1_0701  137  QRNPAPARPAEGGAG  RNPAPARPA        0.1259       12800.8                   50.00      Sequence
DRB1_0701   50  TRQSQAGHRQPPPVS  TRQSQAGHR        0.1257       12826.3                   50.00      Sequence
DRB1_0701  166  ITAESRDARVQLSAR  TAESRDARV        0.1256       12846.2                   50.00      Sequence
DRB1_0701   47  RAATRQSQAGHRQPP  TRQSQAGHR        0.1226       13265.9                   50.00      Sequence
DRB1_0701   49  ATRQSQAGHRQPPPV  TRQSQAGHR        0.1208       13538.5                   50.00      Sequence
DRB1_0701  167  TAESRDARVQLSARR  TAESRDARV        0.1200       13644.3                   50.00      Sequence
DRB1_0701    6  PGALSKGDGPNADGL  GDGPNADGL        0.1200       13644.5                   50.00      Sequence
DRB1_0701   93  TGPAAAVRTPQPDPD  AVRTPQPDP        0.1145       14486.0                   50.00      Sequence
DRB1_0701   69  RPTNPPAAADARLNR  PAAADARLN        0.1135       14644.3                   50.00      Sequence
DRB1_0701    7  GALSKGDGPNADGLV  GDGPNADGL        0.1123       14826.7                   50.00      Sequence
DRB1_0701  107  DASLGCGDGSPAEAY  GDGSPAEAY        0.1121       14864.0                   50.00      Sequence
DRB1_0701   48  AATRQSQAGHRQPPP  TRQSQAGHR        0.1109       15054.5                   50.00      Sequence
DRB1_0701  138  RNPAPARPAEGGAGS  RNPAPARPA        0.1107       15101.5                   50.00      Sequence
DRB1_0701    8  ALSKGDGPNADGLVD  GDGPNADGL        0.1095       15282.8                   50.00      Sequence
DRB1_0701  236  NSNVGDLLNNASGSS  LLNNASGSS        0.1061       15856.5                   50.00      Sequence
DRB1_0701   94  GPAAAVRTPQPDPDA  AVRTPQPDP        0.1001       16918.9                   50.00      Sequence
DRB1_0701  108  ASLGCGDGSPAEAYA  GDGSPAEAY        0.0992       17084.9                   50.00      Sequence
DRB1_0701  109  SLGCGDGSPAEAYAS  GDGSPAEAY        0.0989       17147.1                   50.00      Sequence
DRB1_0701   96  AAAVRTPQPDPDASL  PQPDPDASL        0.0987       17188.7                   50.00      Sequence
DRB1_0701  120  AYASELPDLSGPTPR  PDLSGPTPR        0.0943       18017.0                   50.00      Sequence
DRB1_0701    9  LSKGDGPNADGLVDR  GDGPNADGL        0.0936       18164.6                   50.00      Sequence
DRB1_0701  122  ASELPDLSGPTPRAP  LSGPTPRAP        0.0924       18401.6                   50.00      Sequence
DRB1_0701   67  EGRPTNPPAAADARL  PPAAADARL        0.0918       18511.0                   50.00      Sequence
DRB1_0701  151  GSRGDSAAGSSGGRS  GDSAAGSSG        0.0916       18551.3                   50.00      Sequence
DRB1_0701   95  PAAAVRTPQPDPDAS  VRTPQPDPD        0.0891       19069.7                   50.00      Sequence
DRB1_0701  149  GAGSRGDSAAGSSGG  GDSAAGSSG        0.0889       19107.9                   50.00      Sequence
DRB1_0701   97  AAVRTPQPDPDASLG  AVRTPQPDP        0.0875       19393.0                   50.00      Sequence
DRB1_0701  148  GGAGSRGDSAAGSSG  GDSAAGSSG        0.0867       19564.0                   50.00      Sequence
DRB1_0701  110  LGCGDGSPAEAYASE  GDGSPAEAY        0.0857       19792.4                   50.00      Sequence
DRB1_0701  121  YASELPDLSGPTPRA  PDLSGPTPR        0.0853       19858.9                   50.00      Sequence
DRB1_0701   98  AVRTPQPDPDASLGC  AVRTPQPDP        0.0838       20191.3                   50.00      Sequence
DRB1_0701  125  LPDLSGPTPRAPQRN  GPTPRAPQR        0.0824       20491.5                   50.00      Sequence
DRB1_0701   10  SKGDGPNADGLVDRG  GDGPNADGL        0.0822       20555.4                   50.00      Sequence
DRB1_0701   52  QSQAGHRQPPPVSHP  RQPPPVSHP        0.0814       20726.0                   50.00      Sequence
DRB1_0701  150  AGSRGDSAAGSSGGR  GDSAAGSSG        0.0801       21011.2                   50.00      Sequence
DRB1_0701  123  SELPDLSGPTPRAPQ  LSGPTPRAP        0.0796       21130.7                   50.00      Sequence
DRB1_0701   51  RQSQAGHRQPPPVSH  AGHRQPPPV        0.0793       21194.5                   50.00      Sequence
DRB1_0701  124  ELPDLSGPTPRAPQR  LSGPTPRAP        0.0765       21842.4                   50.00      Sequence
DRB1_0701  126  PDLSGPTPRAPQRNP  LSGPTPRAP        0.0746       22296.4                   50.00      Sequence
DRB1_0701   11  KGDGPNADGLVDRGG  GDGPNADGL        0.0745       22334.0                   50.00      Sequence
DRB1_0701  130  GPTPRAPQRNPAPAR  PQRNPAPAR        0.0723       22862.9                   50.00      Sequence
DRB1_0701  145  PAEGGAGSRGDSAAG  GSRGDSAAG        0.0704       23334.5                   50.00      Sequence
DRB1_0701   53  SQAGHRQPPPVSHPE  RQPPPVSHP        0.0692       23651.7                   50.00      Sequence
DRB1_0701  118  AEAYASELPDLSGPT  YASELPDLS        0.0688       23755.6                   50.00      Sequence
DRB1_0701  131  PTPRAPQRNPAPARP  PQRNPAPAR        0.0683       23880.0                   50.00      Sequence
DRB1_0701   12  GDGPNADGLVDRGGA  GDGPNADGL        0.0681       23919.9                   50.00      Sequence
DRB1_0701    3  PNEPGALSKGDGPNA  ALSKGDGPN        0.0681       23934.1                   50.00      Sequence
DRB1_0701   99  VRTPQPDPDASLGCG  VRTPQPDPD        0.0672       24159.9                   50.00      Sequence
DRB1_0701  127  DLSGPTPRAPQRNPA  LSGPTPRAP        0.0672       24165.7                   50.00      Sequence
DRB1_0701  119  EAYASELPDLSGPTP  YASELPDLS        0.0640       25011.9                   50.00      Sequence
DRB1_0701  146  AEGGAGSRGDSAAGS  GSRGDSAAG        0.0617       25647.7                   50.00      Sequence
DRB1_0701   54  QAGHRQPPPVSHPEG  RQPPPVSHP        0.0615       25709.7                   50.00      Sequence
DRB1_0701   56  GHRQPPPVSHPEGRP  PVSHPEGRP        0.0609       25882.7                   50.00      Sequence
DRB1_0701   33  PGRIPDAGDPPPWQR  AGDPPPWQR        0.0604       25997.8                   50.00      Sequence
DRB1_0701  147  EGGAGSRGDSAAGSS  GAGSRGDSA        0.0590       26397.2                   50.00      Sequence
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   DRB1_0701  128  LSGPTPRAPQRNPAP  LSGPTPRAP        0.0586      26533.4                 50.00     Sequence
   DRB1_0701   55  AGHRQPPPVSHPEGR  RQPPPVSHP        0.0584      26577.1                 50.00     Sequence
   DRB1_0701    2  APNEPGALSKGDGPN  ALSKGDGPN        0.0584      26582.9                 50.00     Sequence
   DRB1_0701    4  NEPGALSKGDGPNAD  ALSKGDGPN        0.0572      26939.3                 50.00     Sequence
   DRB1_0701   65  HPEGRPTNPPAAADA  TNPPAAADA        0.0571      26954.2                 50.00     Sequence
   DRB1_0701  143  ARPAEGGAGSRGDSA  GAGSRGDSA        0.0569      27013.7                 50.00     Sequence
   DRB1_0701   34  GRIPDAGDPPPWQRA  AGDPPPWQR        0.0564      27153.8                 50.00     Sequence
   DRB1_0701  144  RPAEGGAGSRGDSAA  GAGSRGDSA        0.0561      27262.1                 50.00     Sequence
   DRB1_0701   66  PEGRPTNPPAAADAR  TNPPAAADA        0.0554      27448.0                 50.00     Sequence
   DRB1_0701   64  SHPEGRPTNPPAAAD  GRPTNPPAA        0.0530      28164.3                 50.00     Sequence
   DRB1_0701   35  RIPDAGDPPPWQRAA  AGDPPPWQR        0.0517      28580.3                 50.00     Sequence
   DRB1_0701  106  PDASLGCGDGSPAEA  GCGDGSPAE        0.0516      28611.5                 50.00     Sequence
   DRB1_0701   13  DGPNADGLVDRGGAH  GLVDRGGAH        0.0515      28639.1                 50.00     Sequence
   DRB1_0701   31  TGPGRIPDAGDPPPW  GRIPDAGDP        0.0510      28797.5                 50.00     Sequence
   DRB1_0701    1  TAPNEPGALSKGDGP  GALSKGDGP        0.0497      29202.3                 50.00     Sequence
   DRB1_0701    5  EPGALSKGDGPNADG  LSKGDGPNA        0.0484      29606.0                 50.00     Sequence
   DRB1_0701  129  SGPTPRAPQRNPAPA  GPTPRAPQR        0.0476      29890.2                 50.00     Sequence
   DRB1_0701    0  VTAPNEPGALSKGDG  VTAPNEPGA        0.0473      29983.2                 50.00     Sequence
   DRB1_0701  141  APARPAEGGAGSRGD  EGGAGSRGD        0.0468      30117.8                 50.00     Sequence
   DRB1_0701  105  DPDASLGCGDGSPAE  GCGDGSPAE        0.0466      30211.8                 50.00     Sequence
   DRB1_0701   32  GPGRIPDAGDPPPWQ  GRIPDAGDP        0.0460      30392.5                 50.00     Sequence
   DRB1_0701   36  IPDAGDPPPWQRAAT  AGDPPPWQR        0.0458      30472.5                 50.00     Sequence
   DRB1_0701   30  ATGPGRIPDAGDPPP  GRIPDAGDP        0.0452      30660.0                 50.00     Sequence
   DRB1_0701  100  RTPQPDPDASLGCGD  PQPDPDASL        0.0450      30718.4                 50.00     Sequence
   DRB1_0701   38  DAGDPPPWQRAATRQ  AGDPPPWQR        0.0448      30784.3                 50.00     Sequence
   DRB1_0701  142  PARPAEGGAGSRGDS  EGGAGSRGD        0.0445      30908.5                 50.00     Sequence
   DRB1_0701   37  PDAGDPPPWQRAATR  AGDPPPWQR        0.0437      31152.5                 50.00     Sequence
   DRB1_0701   29  AATGPGRIPDAGDPP  GRIPDAGDP        0.0425      31556.2                 50.00     Sequence
   DRB1_0701  101  TPQPDPDASLGCGDG  PQPDPDASL        0.0420      31740.8                 50.00     Sequence
   DRB1_0701  102  PQPDPDASLGCGDGS  PQPDPDASL        0.0395      32615.0                 50.00     Sequence
   DRB1_0701  139  NPAPARPAEGGAGSR  PAEGGAGSR        0.0385      32948.4                 50.00     Sequence
   DRB1_0701  140  PAPARPAEGGAGSRG  PAEGGAGSR        0.0381      33092.4                 50.00     Sequence
   DRB1_0701  104  PDPDASLGCGDGSPA  PDPDASLGC        0.0349      34286.0                 50.00     Sequence
   DRB1_0701  103  QPDPDASLGCGDGSP  PDPDASLGC        0.0340      34595.3                 50.00     Sequence
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Allele: DRB1_0701. Number of high binders 20. Number of weak binders 31. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802  187  RASMQIRRIDPWSTL  RASMQIRRI        0.6101         67.9          WB     2.00     Sequence
   DRB1_0802  186  VRASMQIRRIDPWST  RASMQIRRI        0.5915         83.1          WB     4.00     Sequence
   DRB1_0802  188  ASMQIRRIDPWSTLK  QIRRIDPWS        0.5765         97.8          WB     4.00     Sequence
   DRB1_0802  189  SMQIRRIDPWSTLKV  QIRRIDPWS        0.5516        128.0          WB     4.00     Sequence
   DRB1_0802  190  MQIRRIDPWSTLKVS  QIRRIDPWS        0.5495        130.9          WB     4.00     Sequence
   DRB1_0802   78  DARLNRFISGASAPV  RLNRFISGA        0.5423        141.5          WB     8.00     Sequence
   DRB1_0802  173  ARVQLSARRSRGPVR  RVQLSARRS        0.5326        157.1          WB     8.00     Sequence
   DRB1_0802   80  RLNRFISGASAPVTG  RLNRFISGA        0.5312        159.6          WB     8.00     Sequence
   DRB1_0802   77  ADARLNRFISGASAP  RLNRFISGA        0.5284        164.5          WB     8.00     Sequence
   DRB1_0802  174  RVQLSARRSRGPVRA  RVQLSARRS        0.5266        167.6          WB     8.00     Sequence
   DRB1_0802  191  QIRRIDPWSTLKVSL  QIRRIDPWS        0.5186        182.8          WB     8.00     Sequence
   DRB1_0802   79  ARLNRFISGASAPVT  RLNRFISGA        0.5143        191.6          WB     8.00     Sequence
   DRB1_0802  172  DARVQLSARRSRGPV  RVQLSARRS        0.5102        200.1          WB     8.00     Sequence
   DRB1_0802  185  PVRASMQIRRIDPWS  RASMQIRRI        0.5006        222.3          WB     8.00     Sequence
   DRB1_0802  171  RDARVQLSARRSRGP  RVQLSARRS        0.4929        241.4          WB     8.00     Sequence
   DRB1_0802   81  LNRFISGASAPVTGP  RFISGASAP        0.4797        278.4          WB    16.00     Sequence
   DRB1_0802  175  VQLSARRSRGPVRAS  QLSARRSRG        0.4767        287.7          WB    16.00     Sequence
   DRB1_0802   76  AADARLNRFISGASA  RLNRFISGA        0.4673        318.7          WB    16.00     Sequence
   DRB1_0802  170  SRDARVQLSARRSRG  RVQLSARRS        0.4590        348.4          WB    16.00     Sequence
   DRB1_0802  176  QLSARRSRGPVRASM  QLSARRSRG        0.4561        359.5          WB    16.00     Sequence
   DRB1_0802   44  PWQRAATRQSQAGHR  WQRAATRQS        0.4503        382.9          WB    16.00     Sequence
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DRB1_0802  192  IRRIDPWSTLKVSLL  RIDPWSTLK        0.4477        393.6         WB     16.00     Sequence
DRB1_0802   43  PPWQRAATRQSQAGH  WQRAATRQS        0.4464        399.4         WB     16.00     Sequence
DRB1_0802  197  PWSTLKVSLLLSVAL  PWSTLKVSL        0.4462        400.3         WB     16.00     Sequence
DRB1_0802  196  DPWSTLKVSLLLSVA  PWSTLKVSL        0.4400        428.1         WB     16.00     Sequence
DRB1_0802   75  AAADARLNRFISGAS  RLNRFISGA        0.4336        458.7         WB     16.00     Sequence
DRB1_0802  194  RIDPWSTLKVSLLLS  PWSTLKVSL        0.4320        466.6         WB     16.00     Sequence
DRB1_0802   42  PPPWQRAATRQSQAG  WQRAATRQS        0.4284        485.0         WB     16.00     Sequence
DRB1_0802   82  NRFISGASAPVTGPA  RFISGASAP        0.4274        490.6         WB     16.00     Sequence
DRB1_0802  184  GPVRASMQIRRIDPW  RASMQIRRI        0.4254        501.3                16.00     Sequence
DRB1_0802   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.4225        517.1                16.00     Sequence
DRB1_0802  183  RGPVRASMQIRRIDP  RASMQIRRI        0.4204        529.3                16.00     Sequence
DRB1_0802  193  RRIDPWSTLKVSLLL  PWSTLKVSL        0.4197        532.9                16.00     Sequence
DRB1_0802  195  IDPWSTLKVSLLLSV  PWSTLKVSL        0.4189        537.9                16.00     Sequence
DRB1_0802  180  RRSRGPVRASMQIRR  RRSRGPVRA        0.4154        558.2                16.00     Sequence
DRB1_0802   83  RFISGASAPVTGPAA  RFISGASAP        0.4120        579.5                16.00     Sequence
DRB1_0802  227  GGMGVWAKLNSNVGD  GMGVWAKLN        0.4095        595.1                32.00     Sequence
DRB1_0802   41  DPPPWQRAATRQSQA  WQRAATRQS        0.4039        632.4                32.00     Sequence
DRB1_0802  226  LGGMGVWAKLNSNVG  GMGVWAKLN        0.4036        634.4                32.00     Sequence
DRB1_0802  182  SRGPVRASMQIRRID  RASMQIRRI        0.4007        654.8                32.00     Sequence
DRB1_0802  177  LSARRSRGPVRASMQ  LSARRSRGP        0.3990        666.6                32.00     Sequence
DRB1_0802  225  VLGGMGVWAKLNSNV  GMGVWAKLN        0.3986        669.7                32.00     Sequence
DRB1_0802   74  PAAADARLNRFISGA  RLNRFISGA        0.3958        690.3                32.00     Sequence
DRB1_0802  228  GMGVWAKLNSNVGDL  GMGVWAKLN        0.3957        690.9                32.00     Sequence
DRB1_0802  181  RSRGPVRASMQIRRI  RSRGPVRAS        0.3944        700.8                32.00     Sequence
DRB1_0802  198  WSTLKVSLLLSVALF  WSTLKVSLL        0.3944        700.9                32.00     Sequence
DRB1_0802  179  ARRSRGPVRASMQIR  RRSRGPVRA        0.3939        704.6                32.00     Sequence
DRB1_0802  224  LVLGGMGVWAKLNSN  GMGVWAKLN        0.3854        773.0                32.00     Sequence
DRB1_0802  169  ESRDARVQLSARRSR  RVQLSARRS        0.3822        800.0                32.00     Sequence
DRB1_0802  178  SARRSRGPVRASMQI  RRSRGPVRA        0.3738        876.4                32.00     Sequence
DRB1_0802   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.3677        935.9                32.00     Sequence
DRB1_0802  168  AESRDARVQLSARRS  RVQLSARRS        0.3657        956.0                32.00     Sequence
DRB1_0802  223  YLVLGGMGVWAKLNS  VLGGMGVWA        0.3642        972.1                32.00     Sequence
DRB1_0802  230  GVWAKLNSNVGDLLN  WAKLNSNVG        0.3481       1157.2                32.00     Sequence
DRB1_0802   39  AGDPPPWQRAATRQS  WQRAATRQS        0.3475       1164.6                32.00     Sequence
DRB1_0802  267  GLVNIVLMTALATIG  NIVLMTALA        0.3443       1205.7                32.00     Sequence
DRB1_0802  229  MGVWAKLNSNVGDLL  WAKLNSNVG        0.3436       1214.0                32.00     Sequence
DRB1_0802  222  LYLVLGGMGVWAKLN  VLGGMGVWA        0.3380       1290.9                32.00     Sequence
DRB1_0802  270  NIVLMTALATIGAFV  NIVLMTALA        0.3295       1414.1                32.00     Sequence
DRB1_0802   19  GLVDRGGAHRAATGP  LVDRGGAHR        0.3249       1487.3                32.00     Sequence
DRB1_0802  269  VNIVLMTALATIGAF  NIVLMTALA        0.3215       1542.9                32.00     Sequence
DRB1_0802  268  LVNIVLMTALATIGA  NIVLMTALA        0.3188       1588.6                50.00     Sequence
DRB1_0802  199  STLKVSLLLSVALFF  KVSLLLSVA        0.3162       1634.3                50.00     Sequence
DRB1_0802  213  FVWMITVAFLYLVLG  WMITVAFLY        0.3150       1654.6                50.00     Sequence
DRB1_0802  265  LIGLVNIVLMTALAT  NIVLMTALA        0.3133       1686.4                50.00     Sequence
DRB1_0802  266  IGLVNIVLMTALATI  NIVLMTALA        0.3119       1712.0                50.00     Sequence
DRB1_0802  132  TPRAPQRNPAPARPA  RAPQRNPAP        0.3118       1714.1                50.00     Sequence
DRB1_0802   51  RQSQAGHRQPPPVSH  RQSQAGHRQ        0.3104       1739.1                50.00     Sequence
DRB1_0802  221  FLYLVLGGMGVWAKL  VLGGMGVWA        0.3094       1758.7                50.00     Sequence
DRB1_0802  214  VWMITVAFLYLVLGG  WMITVAFLY        0.3079       1787.6                50.00     Sequence
DRB1_0802  215  WMITVAFLYLVLGGM  WMITVAFLY        0.3054       1835.3                50.00     Sequence
DRB1_0802  231  VWAKLNSNVGDLLNN  WAKLNSNVG        0.3045       1853.8                50.00     Sequence
DRB1_0802  133  PRAPQRNPAPARPAE  RAPQRNPAP        0.3021       1902.7                50.00     Sequence
DRB1_0802   20  LVDRGGAHRAATGPG  LVDRGGAHR        0.3011       1923.3                50.00     Sequence
DRB1_0802  212  FFVWMITVAFLYLVL  WMITVAFLY        0.3004       1938.6                50.00     Sequence
DRB1_0802  264  FLIGLVNIVLMTALA  NIVLMTALA        0.3001       1945.0                50.00     Sequence
DRB1_0802   73  PPAAADARLNRFISG  ADARLNRFI        0.2959       2034.2                50.00     Sequence
DRB1_0802   50  TRQSQAGHRQPPPVS  RQSQAGHRQ        0.2955       2044.6                50.00     Sequence
DRB1_0802  201  LKVSLLLSVALFFVW  KVSLLLSVA        0.2954       2045.7                50.00     Sequence
DRB1_0802   21  VDRGGAHRAATGPGR  VDRGGAHRA        0.2954       2046.3                50.00     Sequence
DRB1_0802  200  TLKVSLLLSVALFFV  KVSLLLSVA        0.2951       2053.3                50.00     Sequence
DRB1_0802  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.2944       2067.8                50.00     Sequence
DRB1_0802  202  KVSLLLSVALFFVWM  KVSLLLSVA        0.2943       2070.5                50.00     Sequence
DRB1_0802   84  FISGASAPVTGPAAA  FISGASAPV        0.2939       2078.8                50.00     Sequence
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DRB1_0802  271  IVLMTALATIGAFVY  LMTALATIG       0.2923      2115.2            50.00     Sequence
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DRB1_0802  131  PTPRAPQRNPAPARP  RAPQRNPAP       0.2892      2187.1            50.00     Sequence
DRB1_0802  252  ELVSSGTIFGGAFLI  LVSSGTIFG       0.2876      2224.9            50.00     Sequence
DRB1_0802   94  GPAAAVRTPQPDPDA  GPAAAVRTP       0.2875      2227.4            50.00     Sequence
DRB1_0802  211  LFFVWMITVAFLYLV  WMITVAFLY       0.2868      2246.3            50.00     Sequence
DRB1_0802  220  AFLYLVLGGMGVWAK  VLGGMGVWA       0.2865      2252.1            50.00     Sequence
DRB1_0802   17  ADGLVDRGGAHRAAT  LVDRGGAHR       0.2834      2329.0            50.00     Sequence
DRB1_0802  272  VLMTALATIGAFVYN  LMTALATIG       0.2800      2416.2            50.00     Sequence
DRB1_0802   52  QSQAGHRQPPPVSHP  QSQAGHRQP       0.2798      2421.1            50.00     Sequence
DRB1_0802  232  WAKLNSNVGDLLNNA  WAKLNSNVG       0.2767      2505.8            50.00     Sequence
DRB1_0802   46  QRAATRQSQAGHRQP  RAATRQSQA       0.2742      2573.5            50.00     Sequence
DRB1_0802  256  SGTIFGGAFLIGLVN  GTIFGGAFL       0.2737      2587.2            50.00     Sequence
DRB1_0802  257  GTIFGGAFLIGLVNI  GTIFGGAFL       0.2719      2637.8            50.00     Sequence
DRB1_0802  251  AELVSSGTIFGGAFL  LVSSGTIFG       0.2718      2641.8            50.00     Sequence
DRB1_0802  167  TAESRDARVQLSARR  ARVQLSARR       0.2690      2723.3            50.00     Sequence
DRB1_0802   72  NPPAAADARLNRFIS  DARLNRFIS       0.2683      2743.9            50.00     Sequence
DRB1_0802  262  GAFLIGLVNIVLMTA  GAFLIGLVN       0.2669      2785.4            50.00     Sequence
DRB1_0802  134  RAPQRNPAPARPAEG  RAPQRNPAP       0.2649      2845.5            50.00     Sequence
DRB1_0802   23  RGGAHRAATGPGRIP  RGGAHRAAT       0.2642      2866.5            50.00     Sequence
DRB1_0802  281  GAFVYNLITDLIGGI  YNLITDLIG       0.2622      2931.4            50.00     Sequence
DRB1_0802   22  DRGGAHRAATGPGRI  RGGAHRAAT       0.2621      2934.0            50.00     Sequence
DRB1_0802  273  LMTALATIGAFVYNL  LMTALATIG       0.2605      2985.0            50.00     Sequence
DRB1_0802   47  RAATRQSQAGHRQPP  RAATRQSQA       0.2600      3000.1            50.00     Sequence
DRB1_0802  279  TIGAFVYNLITDLIG  YNLITDLIG       0.2599      3003.6            50.00     Sequence
DRB1_0802   93  TGPAAAVRTPQPDPD  GPAAAVRTP       0.2595      3015.7            50.00     Sequence
DRB1_0802  130  GPTPRAPQRNPAPAR  RAPQRNPAP       0.2585      3050.0            50.00     Sequence
DRB1_0802  219  VAFLYLVLGGMGVWA  VLGGMGVWA       0.2578      3072.2            50.00     Sequence
DRB1_0802  261  GGAFLIGLVNIVLMT  GAFLIGLVN       0.2558      3140.0            50.00     Sequence
DRB1_0802   92  VTGPAAAVRTPQPDP  GPAAAVRTP       0.2550      3167.1            50.00     Sequence
DRB1_0802  162  GGRSITAESRDARVQ  GGRSITAES       0.2543      3192.8            50.00     Sequence
DRB1_0802   91  PVTGPAAAVRTPQPD  GPAAAVRTP       0.2519      3277.4            50.00     Sequence
DRB1_0802  158  AGSSGGRSITAESRD  GSSGGRSIT       0.2514      3294.0            50.00     Sequence
DRB1_0802  210  ALFFVWMITVAFLYL  WMITVAFLY       0.2512      3300.5            50.00     Sequence
DRB1_0802  283  FVYNLITDLIGGIEV  YNLITDLIG       0.2499      3345.9            50.00     Sequence
DRB1_0802  276  ALATIGAFVYNLITD  ALATIGAFV       0.2462      3483.5            50.00     Sequence
DRB1_0802  165  SITAESRDARVQLSA  SITAESRDA       0.2460      3491.9            50.00     Sequence
DRB1_0802   90  APVTGPAAAVRTPQP  PVTGPAAAV       0.2457      3501.4            50.00     Sequence
DRB1_0802  255  SSGTIFGGAFLIGLV  GTIFGGAFL       0.2448      3537.9            50.00     Sequence
DRB1_0802  280  IGAFVYNLITDLIGG  FVYNLITDL       0.2434      3590.5            50.00     Sequence
DRB1_0802  129  SGPTPRAPQRNPAPA  RAPQRNPAP       0.2427      3619.7            50.00     Sequence
DRB1_0802  260  FGGAFLIGLVNIVLM  GAFLIGLVN       0.2426      3621.4            50.00     Sequence
DRB1_0802  275  TALATIGAFVYNLIT  ALATIGAFV       0.2412      3677.5            50.00     Sequence
DRB1_0802   49  ATRQSQAGHRQPPPV  RQSQAGHRQ       0.2408      3695.5            50.00     Sequence
DRB1_0802  263  AFLIGLVNIVLMTAL  FLIGLVNIV       0.2406      3700.8            50.00     Sequence
DRB1_0802   16  NADGLVDRGGAHRAA  LVDRGGAHR       0.2392      3756.9            50.00     Sequence
DRB1_0802  282  AFVYNLITDLIGGIE  YNLITDLIG       0.2383      3795.2            50.00     Sequence
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DRB1_0802  157  AAGSSGGRSITAESR  GSSGGRSIT       0.2357      3903.7            50.00     Sequence
DRB1_0802  164  RSITAESRDARVQLS  SITAESRDA       0.2351      3928.3            50.00     Sequence
DRB1_0802  209  VALFFVWMITVAFLY  WMITVAFLY       0.2338      3986.3            50.00     Sequence
DRB1_0802  163  GRSITAESRDARVQL  SITAESRDA       0.2330      4019.6            50.00     Sequence
DRB1_0802  159  GSSGGRSITAESRDA  GSSGGRSIT       0.2324      4047.2            50.00     Sequence
DRB1_0802   48  AATRQSQAGHRQPPP  RQSQAGHRQ       0.2319      4068.3            50.00     Sequence
DRB1_0802  259  IFGGAFLIGLVNIVL  GAFLIGLVN       0.2315      4086.8            50.00     Sequence
DRB1_0802  128  LSGPTPRAPQRNPAP  RAPQRNPAP       0.2310      4104.8            50.00     Sequence
DRB1_0802  161  SGGRSITAESRDARV  GGRSITAES       0.2288      4204.2            50.00     Sequence
DRB1_0802  254  VSSGTIFGGAFLIGL  GTIFGGAFL       0.2267      4302.9            50.00     Sequence
DRB1_0802   95  PAAAVRTPQPDPDAS  AAAVRTPQP       0.2261      4332.7            50.00     Sequence
DRB1_0802   15  PNADGLVDRGGAHRA  LVDRGGAHR       0.2208      4586.6            50.00     Sequence
DRB1_0802   89  SAPVTGPAAAVRTPQ  VTGPAAAVR       0.2204      4605.0            50.00     Sequence
DRB1_0802  216  MITVAFLYLVLGGMG  MITVAFLYL       0.2191      4672.0            50.00     Sequence
DRB1_0802  277  LATIGAFVYNLITDL  GAFVYNLIT       0.2177      4744.1            50.00     Sequence
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DRB1_0802  278  ATIGAFVYNLITDLI  GAFVYNLIT        0.2160       4828.3               50.00     Sequence
DRB1_0802  258  TIFGGAFLIGLVNIV  GAFLIGLVN        0.2155       4856.2               50.00     Sequence
DRB1_0802  207  LSVALFFVWMITVAF  FVWMITVAF        0.2141       4932.5               50.00     Sequence
DRB1_0802  284  VYNLITDLIGGIEVT  VYNLITDLI        0.2140       4937.7               50.00     Sequence
DRB1_0802  217  ITVAFLYLVLGGMGV  ITVAFLYLV        0.2137       4953.8               50.00     Sequence
DRB1_0802  160  SSGGRSITAESRDAR  GGRSITAES        0.2136       4956.8               50.00     Sequence
DRB1_0802   24  GGAHRAATGPGRIPD  GAHRAATGP        0.2132       4976.7               50.00     Sequence
DRB1_0802  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.2119       5048.9               50.00     Sequence
DRB1_0802   53  SQAGHRQPPPVSHPE  QAGHRQPPP        0.2094       5185.9               50.00     Sequence
DRB1_0802   54  QAGHRQPPPVSHPEG  QAGHRQPPP        0.2059       5386.7               50.00     Sequence
DRB1_0802  274  MTALATIGAFVYNLI  ALATIGAFV        0.2031       5551.1               50.00     Sequence
DRB1_0802   25  GAHRAATGPGRIPDA  GAHRAATGP        0.2009       5686.8               50.00     Sequence
DRB1_0802  156  SAAGSSGGRSITAES  GSSGGRSIT        0.2002       5734.0               50.00     Sequence
DRB1_0802  218  TVAFLYLVLGGMGVW  YLVLGGMGV        0.1968       5943.1               50.00     Sequence
DRB1_0802   88  ASAPVTGPAAAVRTP  VTGPAAAVR        0.1961       5992.2               50.00     Sequence
DRB1_0802  285  YNLITDLIGGIEVTL  YNLITDLIG        0.1953       6041.1               50.00     Sequence
DRB1_0802  206  LLSVALFFVWMITVA  LLSVALFFV        0.1922       6250.3               50.00     Sequence
DRB1_0802  118  AEAYASELPDLSGPT  YASELPDLS        0.1906       6361.5               50.00     Sequence
DRB1_0802  117  PAEAYASELPDLSGP  YASELPDLS        0.1897       6421.3               50.00     Sequence
DRB1_0802  208  SVALFFVWMITVAFL  FVWMITVAF        0.1869       6616.1               50.00     Sequence
DRB1_0802  136  PQRNPAPARPAEGGA  RNPAPARPA        0.1853       6734.7               50.00     Sequence
DRB1_0802  234  KLNSNVGDLLNNASG  KLNSNVGDL        0.1851       6751.2               50.00     Sequence
DRB1_0802  115  GSPAEAYASELPDLS  YASELPDLS        0.1842       6814.9               50.00     Sequence
DRB1_0802  205  LLLSVALFFVWMITV  LLSVALFFV        0.1832       6890.1               50.00     Sequence
DRB1_0802  137  QRNPAPARPAEGGAG  RNPAPARPA        0.1828       6922.0               50.00     Sequence
DRB1_0802  135  APQRNPAPARPAEGG  RNPAPARPA        0.1815       7017.2               50.00     Sequence
DRB1_0802  116  SPAEAYASELPDLSG  YASELPDLS        0.1778       7302.7               50.00     Sequence
DRB1_0802  237  SNVGDLLNNASGSSA  GDLLNNASG        0.1760       7446.5               50.00     Sequence
DRB1_0802  238  NVGDLLNNASGSSAE  GDLLNNASG        0.1760       7450.2               50.00     Sequence
DRB1_0802  125  LPDLSGPTPRAPQRN  LSGPTPRAP        0.1759       7451.8               50.00     Sequence
DRB1_0802  240  GDLLNNASGSSAELV  LLNNASGSS        0.1750       7523.6               50.00     Sequence
DRB1_0802  124  ELPDLSGPTPRAPQR  GPTPRAPQR        0.1749       7539.5               50.00     Sequence
DRB1_0802   38  DAGDPPPWQRAATRQ  PWQRAATRQ        0.1748       7546.7               50.00     Sequence
DRB1_0802  204  SLLLSVALFFVWMIT  LLSVALFFV        0.1745       7564.5               50.00     Sequence
DRB1_0802  127  DLSGPTPRAPQRNPA  LSGPTPRAP        0.1744       7575.8               50.00     Sequence
DRB1_0802   96  AAAVRTPQPDPDASL  AAAVRTPQP        0.1743       7585.2               50.00     Sequence
DRB1_0802  239  VGDLLNNASGSSAEL  LLNNASGSS        0.1742       7591.1               50.00     Sequence
DRB1_0802  250  SAELVSSGTIFGGAF  LVSSGTIFG        0.1737       7636.4               50.00     Sequence
DRB1_0802  138  RNPAPARPAEGGAGS  RNPAPARPA        0.1726       7726.5               50.00     Sequence
DRB1_0802   62  PVSHPEGRPTNPPAA  VSHPEGRPT        0.1716       7811.1               50.00     Sequence
DRB1_0802  154  GDSAAGSSGGRSITA  GSSGGRSIT        0.1675       8167.3               50.00     Sequence
DRB1_0802   85  ISGASAPVTGPAAAV  ISGASAPVT        0.1674       8174.8               50.00     Sequence
DRB1_0802  155  DSAAGSSGGRSITAE  GSSGGRSIT        0.1653       8356.8               50.00     Sequence
DRB1_0802  248  GSSAELVSSGTIFGG  LVSSGTIFG        0.1639       8490.5               50.00     Sequence
DRB1_0802  153  RGDSAAGSSGGRSIT  GSSGGRSIT        0.1637       8509.2               50.00     Sequence
DRB1_0802  249  SSAELVSSGTIFGGA  LVSSGTIFG        0.1632       8551.3               50.00     Sequence
DRB1_0802  247  SGSSAELVSSGTIFG  LVSSGTIFG        0.1630       8572.7               50.00     Sequence
DRB1_0802  120  AYASELPDLSGPTPR  YASELPDLS        0.1624       8625.1               50.00     Sequence
DRB1_0802  236  NSNVGDLLNNASGSS  GDLLNNASG        0.1620       8666.9               50.00     Sequence
DRB1_0802   63  VSHPEGRPTNPPAAA  VSHPEGRPT        0.1607       8783.1               50.00     Sequence
DRB1_0802  121  YASELPDLSGPTPRA  YASELPDLS        0.1604       8816.7               50.00     Sequence
DRB1_0802  126  PDLSGPTPRAPQRNP  LSGPTPRAP        0.1597       8883.5               50.00     Sequence
DRB1_0802  119  EAYASELPDLSGPTP  YASELPDLS        0.1586       8991.1               50.00     Sequence
DRB1_0802  242  LLNNASGSSAELVSS  LLNNASGSS        0.1564       9206.0               50.00     Sequence
DRB1_0802   87  GASAPVTGPAAAVRT  SAPVTGPAA        0.1547       9378.5               50.00     Sequence
DRB1_0802   28  RAATGPGRIPDAGDP  RAATGPGRI        0.1542       9425.5               50.00     Sequence
DRB1_0802  148  GGAGSRGDSAAGSSG  GSRGDSAAG        0.1541       9436.6               50.00     Sequence
DRB1_0802  149  GAGSRGDSAAGSSGG  GSRGDSAAG        0.1535       9503.3               50.00     Sequence
DRB1_0802   29  AATGPGRIPDAGDPP  AATGPGRIP        0.1534       9508.4               50.00     Sequence
DRB1_0802   86  SGASAPVTGPAAAVR  SAPVTGPAA        0.1522       9631.9               50.00     Sequence
DRB1_0802  123  SELPDLSGPTPRAPQ  LPDLSGPTP        0.1513       9725.2               50.00     Sequence
DRB1_0802  150  AGSRGDSAAGSSGGR  GSRGDSAAG        0.1510       9759.4               50.00     Sequence
DRB1_0802   14  GPNADGLVDRGGAHR  LVDRGGAHR        0.1501       9852.5               50.00     Sequence
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DRB1_0802  288  ITDLIGGIEVTLADR  LIGGIEVTL         0.1492       9949.9                 50.00      Sequence
DRB1_0802   26  AHRAATGPGRIPDAG  AHRAATGPG         0.1479      10095.1                 50.00      Sequence
DRB1_0802  289  TDLIGGIEVTLADRD  LIGGIEVTL         0.1461      10286.7                 50.00      Sequence
DRB1_0802  151  GSRGDSAAGSSGGRS  GSRGDSAAG         0.1437      10562.5                 50.00      Sequence
DRB1_0802   56  GHRQPPPVSHPEGRP  GHRQPPPVS         0.1437      10564.9                 50.00      Sequence
DRB1_0802   27  HRAATGPGRIPDAGD  HRAATGPGR         0.1432      10615.1                 50.00      Sequence
DRB1_0802   65  HPEGRPTNPPAAADA  PEGRPTNPP         0.1392      11084.2                 50.00      Sequence
DRB1_0802  122  ASELPDLSGPTPRAP  LPDLSGPTP         0.1374      11311.0                 50.00      Sequence
DRB1_0802  147  EGGAGSRGDSAAGSS  GSRGDSAAG         0.1373      11318.5                 50.00      Sequence
DRB1_0802  235  LNSNVGDLLNNASGS  LNSNVGDLL         0.1364      11424.6                 50.00      Sequence
DRB1_0802   66  PEGRPTNPPAAADAR  EGRPTNPPA         0.1362      11451.4                 50.00      Sequence
DRB1_0802   61  PPVSHPEGRPTNPPA  VSHPEGRPT         0.1349      11619.7                 50.00      Sequence
DRB1_0802   55  AGHRQPPPVSHPEGR  GHRQPPPVS         0.1343      11693.3                 50.00      Sequence
DRB1_0802  286  NLITDLIGGIEVTLA  LIGGIEVTL         0.1332      11828.5                 50.00      Sequence
DRB1_0802  146  AEGGAGSRGDSAAGS  GSRGDSAAG         0.1330      11851.5                 50.00      Sequence
DRB1_0802   64  SHPEGRPTNPPAAAD  PEGRPTNPP         0.1326      11904.4                 50.00      Sequence
DRB1_0802   58  RQPPPVSHPEGRPTN  PVSHPEGRP         0.1325      11918.1                 50.00      Sequence
DRB1_0802  287  LITDLIGGIEVTLAD  LIGGIEVTL         0.1319      12004.3                 50.00      Sequence
DRB1_0802   60  PPPVSHPEGRPTNPP  PVSHPEGRP         0.1318      12011.2                 50.00      Sequence
DRB1_0802  233  AKLNSNVGDLLNNAS  KLNSNVGDL         0.1306      12165.4                 50.00      Sequence
DRB1_0802  145  PAEGGAGSRGDSAAG  GSRGDSAAG         0.1299      12264.1                 50.00      Sequence
DRB1_0802   57  HRQPPPVSHPEGRPT  PVSHPEGRP         0.1290      12376.5                 50.00      Sequence
DRB1_0802  241  DLLNNASGSSAELVS  LNNASGSSA         0.1285      12451.4                 50.00      Sequence
DRB1_0802   59  QPPPVSHPEGRPTNP  PVSHPEGRP         0.1244      13014.4                 50.00      Sequence
DRB1_0802    6  PGALSKGDGPNADGL  LSKGDGPNA         0.1230      13210.1                 50.00      Sequence
DRB1_0802  109  SLGCGDGSPAEAYAS  SLGCGDGSP         0.1198      13677.2                 50.00      Sequence
DRB1_0802   71  TNPPAAADARLNRFI  ADARLNRFI         0.1197      13700.4                 50.00      Sequence
DRB1_0802   37  PDAGDPPPWQRAATR  PPWQRAATR         0.1195      13718.2                 50.00      Sequence
DRB1_0802  243  LNNASGSSAELVSSG  LNNASGSSA         0.1187      13835.5                 50.00      Sequence
DRB1_0802   31  TGPGRIPDAGDPPPW  GPGRIPDAG         0.1173      14059.6                 50.00      Sequence
DRB1_0802   34  GRIPDAGDPPPWQRA  RIPDAGDPP         0.1172      14062.4                 50.00      Sequence
DRB1_0802  114  DGSPAEAYASELPDL  GSPAEAYAS         0.1164      14197.0                 50.00      Sequence
DRB1_0802    5  EPGALSKGDGPNADG  LSKGDGPNA         0.1159      14260.9                 50.00      Sequence
DRB1_0802   30  ATGPGRIPDAGDPPP  GPGRIPDAG         0.1141      14542.3                 50.00      Sequence
DRB1_0802    7  GALSKGDGPNADGLV  ALSKGDGPN         0.1137      14617.7                 50.00      Sequence
DRB1_0802  152  SRGDSAAGSSGGRSI  GDSAAGSSG         0.1126      14791.3                 50.00      Sequence
DRB1_0802   35  RIPDAGDPPPWQRAA  RIPDAGDPP         0.1116      14945.8                 50.00      Sequence
DRB1_0802    3  PNEPGALSKGDGPNA  LSKGDGPNA         0.1108      15078.8                 50.00      Sequence
DRB1_0802    4  NEPGALSKGDGPNAD  LSKGDGPNA         0.1087      15422.7                 50.00      Sequence
DRB1_0802  246  ASGSSAELVSSGTIF  GSSAELVSS         0.1083      15484.4                 50.00      Sequence
DRB1_0802   32  GPGRIPDAGDPPPWQ  GPGRIPDAG         0.1044      16159.8                 50.00      Sequence
DRB1_0802   36  IPDAGDPPPWQRAAT  IPDAGDPPP         0.1044      16165.7                 50.00      Sequence
DRB1_0802   13  DGPNADGLVDRGGAH  GLVDRGGAH         0.1028      16443.2                 50.00      Sequence
DRB1_0802  113  GDGSPAEAYASELPD  GSPAEAYAS         0.1018      16619.7                 50.00      Sequence
DRB1_0802    8  ALSKGDGPNADGLVD  LSKGDGPNA         0.1015      16678.8                 50.00      Sequence
DRB1_0802   97  AAVRTPQPDPDASLG  AVRTPQPDP         0.1001      16935.4                 50.00      Sequence
DRB1_0802   67  EGRPTNPPAAADARL  EGRPTNPPA         0.0971      17487.9                 50.00      Sequence
DRB1_0802   33  PGRIPDAGDPPPWQR  RIPDAGDPP         0.0957      17751.5                 50.00      Sequence
DRB1_0802  245  NASGSSAELVSSGTI  GSSAELVSS         0.0939      18103.4                 50.00      Sequence
DRB1_0802  110  LGCGDGSPAEAYASE  LGCGDGSPA         0.0930      18284.5                 50.00      Sequence
DRB1_0802  112  CGDGSPAEAYASELP  AEAYASELP         0.0923      18427.9                 50.00      Sequence
DRB1_0802  244  NNASGSSAELVSSGT  GSSAELVSS         0.0919      18503.4                 50.00      Sequence
DRB1_0802    2  APNEPGALSKGDGPN  APNEPGALS         0.0917      18533.7                 50.00      Sequence
DRB1_0802   68  GRPTNPPAAADARLN  GRPTNPPAA         0.0903      18828.8                 50.00      Sequence
DRB1_0802   98  AVRTPQPDPDASLGC  AVRTPQPDP         0.0895      18983.0                 50.00      Sequence
DRB1_0802  144  RPAEGGAGSRGDSAA  GGAGSRGDS         0.0851      19910.5                 50.00      Sequence
DRB1_0802  108  ASLGCGDGSPAEAYA  SLGCGDGSP         0.0838      20201.3                 50.00      Sequence
DRB1_0802  143  ARPAEGGAGSRGDSA  GGAGSRGDS         0.0808      20861.7                 50.00      Sequence
DRB1_0802    0  VTAPNEPGALSKGDG  VTAPNEPGA         0.0805      20926.6                 50.00      Sequence
DRB1_0802  139  NPAPARPAEGGAGSR  NPAPARPAE         0.0803      20962.6                 50.00      Sequence
DRB1_0802  111  GCGDGSPAEAYASEL  GSPAEAYAS         0.0790      21278.2                 50.00      Sequence
DRB1_0802  106  PDASLGCGDGSPAEA  SLGCGDGSP         0.0780      21498.3                 50.00      Sequence
DRB1_0802  142  PARPAEGGAGSRGDS  GGAGSRGDS         0.0777      21571.0                 50.00      Sequence
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   DRB1_0802  107  DASLGCGDGSPAEAY  SLGCGDGSP        0.0771      21719.2                 50.00     Sequence
   DRB1_0802  140  PAPARPAEGGAGSRG  PAPARPAEG        0.0766      21829.2                 50.00     Sequence
   DRB1_0802   12  GDGPNADGLVDRGGA  DGLVDRGGA        0.0746      22298.8                 50.00     Sequence
   DRB1_0802    1  TAPNEPGALSKGDGP  PGALSKGDG        0.0743      22382.2                 50.00     Sequence
   DRB1_0802  105  DPDASLGCGDGSPAE  LGCGDGSPA        0.0679      23983.4                 50.00     Sequence
   DRB1_0802    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.0650      24737.4                 50.00     Sequence
   DRB1_0802  141  APARPAEGGAGSRGD  RPAEGGAGS        0.0638      25084.0                 50.00     Sequence
   DRB1_0802  104  PDPDASLGCGDGSPA  LGCGDGSPA        0.0618      25629.7                 50.00     Sequence
   DRB1_0802   69  RPTNPPAAADARLNR  RPTNPPAAA        0.0613      25765.9                 50.00     Sequence
   DRB1_0802   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.0575      26829.0                 50.00     Sequence
   DRB1_0802   70  PTNPPAAADARLNRF  PAAADARLN        0.0575      26833.4                 50.00     Sequence
   DRB1_0802  103  QPDPDASLGCGDGSP  SLGCGDGSP        0.0548      27647.7                 50.00     Sequence
   DRB1_0802   11  KGDGPNADGLVDRGG  GPNADGLVD        0.0531      28157.6                 50.00     Sequence
   DRB1_0802  100  RTPQPDPDASLGCGD  RTPQPDPDA        0.0460      30405.9                 50.00     Sequence
   DRB1_0802   10  SKGDGPNADGLVDRG  GPNADGLVD        0.0407      32206.8                 50.00     Sequence
   DRB1_0802  102  PQPDPDASLGCGDGS  QPDPDASLG        0.0345      34418.3                 50.00     Sequence
   DRB1_0802  101  TPQPDPDASLGCGDG  QPDPDASLG        0.0323      35242.5                 50.00     Sequence
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Allele: DRB1_0802. Number of high binders 0. Number of weak binders 29. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901   81  LNRFISGASAPVTGP  FISGASAPV        0.7501         14.9           SB     0.10     Sequence
   DRB1_0901   82  NRFISGASAPVTGPA  FISGASAPV        0.7443         15.9           SB     0.15     Sequence
   DRB1_0901   80  RLNRFISGASAPVTG  FISGASAPV        0.7410         16.5           SB     0.15     Sequence
   DRB1_0901   79  ARLNRFISGASAPVT  FISGASAPV        0.7168         21.4           SB     0.30     Sequence
   DRB1_0901   83  RFISGASAPVTGPAA  FISGASAPV        0.7009         25.4           SB     0.40     Sequence
   DRB1_0901   78  DARLNRFISGASAPV  FISGASAPV        0.6742         34.0           SB     0.80     Sequence
   DRB1_0901  280  IGAFVYNLITDLIGG  IGAFVYNLI        0.6377         50.4           WB     2.00     Sequence
   DRB1_0901  279  TIGAFVYNLITDLIG  IGAFVYNLI        0.6211         60.3           WB     4.00     Sequence
   DRB1_0901  281  GAFVYNLITDLIGGI  VYNLITDLI        0.5999         75.8           WB     4.00     Sequence
   DRB1_0901  278  ATIGAFVYNLITDLI  IGAFVYNLI        0.5955         79.6           WB     4.00     Sequence
   DRB1_0901   84  FISGASAPVTGPAAA  FISGASAPV        0.5898         84.6           WB     8.00     Sequence
   DRB1_0901  282  AFVYNLITDLIGGIE  VYNLITDLI        0.5627        113.5           WB     8.00     Sequence
   DRB1_0901  289  TDLIGGIEVTLADRD  LIGGIEVTL        0.5588        118.3           WB     8.00     Sequence
   DRB1_0901  197  PWSTLKVSLLLSVAL  WSTLKVSLL        0.5310        159.9           WB    16.00     Sequence
   DRB1_0901  270  NIVLMTALATIGAFV  VLMTALATI        0.5304        161.0           WB    16.00     Sequence
   DRB1_0901   90  APVTGPAAAVRTPQP  VTGPAAAVR        0.5302        161.3           WB    16.00     Sequence
   DRB1_0901  288  ITDLIGGIEVTLADR  DLIGGIEVT        0.5298        162.0           WB    16.00     Sequence
   DRB1_0901  242  LLNNASGSSAELVSS  LLNNASGSS        0.5256        169.5           WB    16.00     Sequence
   DRB1_0901   89  SAPVTGPAAAVRTPQ  VTGPAAAVR        0.5247        171.2           WB    16.00     Sequence
   DRB1_0901  241  DLLNNASGSSAELVS  LNNASGSSA        0.5227        175.0           WB    16.00     Sequence
   DRB1_0901  193  RRIDPWSTLKVSLLL  WSTLKVSLL        0.5208        178.5           WB    16.00     Sequence
   DRB1_0901  229  MGVWAKLNSNVGDLL  WAKLNSNVG        0.5203        179.6           WB    16.00     Sequence
   DRB1_0901  192  IRRIDPWSTLKVSLL  WSTLKVSLL        0.5200        180.1           WB    16.00     Sequence
   DRB1_0901  227  GGMGVWAKLNSNVGD  WAKLNSNVG        0.5193        181.5           WB    16.00     Sequence
   DRB1_0901  287  LITDLIGGIEVTLAD  DLIGGIEVT        0.5162        187.6           WB    16.00     Sequence
   DRB1_0901  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.5140        192.1           WB    16.00     Sequence
   DRB1_0901  195  IDPWSTLKVSLLLSV  WSTLKVSLL        0.5137        192.8           WB    16.00     Sequence
   DRB1_0901  226  LGGMGVWAKLNSNVG  WAKLNSNVG        0.5128        194.7           WB    16.00     Sequence
   DRB1_0901  277  LATIGAFVYNLITDL  IGAFVYNLI        0.5105        199.6           WB    16.00     Sequence
   DRB1_0901  198  WSTLKVSLLLSVALF  WSTLKVSLL        0.5104        199.9           WB    16.00     Sequence
   DRB1_0901   88  ASAPVTGPAAAVRTP  PVTGPAAAV        0.5076        205.9           WB    16.00     Sequence
   DRB1_0901   91  PVTGPAAAVRTPQPD  TGPAAAVRT        0.5074        206.4           WB    16.00     Sequence
   DRB1_0901  269  VNIVLMTALATIGAF  VLMTALATI        0.5055        210.7           WB    16.00     Sequence
   DRB1_0901  283  FVYNLITDLIGGIEV  VYNLITDLI        0.5052        211.4           WB    16.00     Sequence
   DRB1_0901  243  LNNASGSSAELVSSG  LNNASGSSA        0.5041        213.9           WB    16.00     Sequence
   DRB1_0901  228  GMGVWAKLNSNVGDL  WAKLNSNVG        0.5010        221.2           WB    16.00     Sequence
   DRB1_0901  196  DPWSTLKVSLLLSVA  WSTLKVSLL        0.4993        225.2           WB    16.00     Sequence
   DRB1_0901  271  IVLMTALATIGAFVY  VLMTALATI        0.4977        229.2           WB    16.00     Sequence
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DRB1_0901  211  LFFVWMITVAFLYLV  FFVWMITVA        0.4886         253.1          WB    32.00      Sequence
DRB1_0901  240  GDLLNNASGSSAELV  NASGSSAEL        0.4874         256.4          WB    32.00      Sequence
DRB1_0901  230  GVWAKLNSNVGDLLN  WAKLNSNVG        0.4861         259.8          WB    32.00      Sequence
DRB1_0901   77  ADARLNRFISGASAP  RFISGASAP        0.4824         270.6          WB    32.00      Sequence
DRB1_0901   43  PPWQRAATRQSQAGH  WQRAATRQS        0.4817         272.6          WB    32.00      Sequence
DRB1_0901   87  GASAPVTGPAAAVRT  PVTGPAAAV        0.4811         274.3          WB    32.00      Sequence
DRB1_0901  272  VLMTALATIGAFVYN  VLMTALATI        0.4801         277.3          WB    32.00      Sequence
DRB1_0901  115  GSPAEAYASELPDLS  PAEAYASEL        0.4792         280.2          WB    32.00      Sequence
DRB1_0901  268  LVNIVLMTALATIGA  VLMTALATI        0.4790         280.7          WB    32.00      Sequence
DRB1_0901  284  VYNLITDLIGGIEVT  VYNLITDLI        0.4788         281.2          WB    32.00      Sequence
DRB1_0901  210  ALFFVWMITVAFLYL  WMITVAFLY        0.4774         285.5          WB    32.00      Sequence
DRB1_0901   42  PPPWQRAATRQSQAG  WQRAATRQS        0.4770         286.8          WB    32.00      Sequence
DRB1_0901  264  FLIGLVNIVLMTALA  FLIGLVNIV        0.4762         289.3          WB    32.00      Sequence
DRB1_0901  286  NLITDLIGGIEVTLA  DLIGGIEVT        0.4754         291.8          WB    32.00      Sequence
DRB1_0901  116  SPAEAYASELPDLSG  PAEAYASEL        0.4746         294.3          WB    32.00      Sequence
DRB1_0901  182  SRGPVRASMQIRRID  PVRASMQIR        0.4734         298.3          WB    32.00      Sequence
DRB1_0901  231  VWAKLNSNVGDLLNN  WAKLNSNVG        0.4716         304.1          WB    32.00      Sequence
DRB1_0901   41  DPPPWQRAATRQSQA  WQRAATRQS        0.4710         306.0          WB    32.00      Sequence
DRB1_0901   85  ISGASAPVTGPAAAV  ISGASAPVT        0.4695         311.0          WB    32.00      Sequence
DRB1_0901  285  YNLITDLIGGIEVTL  LIGGIEVTL        0.4690         312.6          WB    32.00      Sequence
DRB1_0901  114  DGSPAEAYASELPDL  PAEAYASEL        0.4681         315.8          WB    32.00      Sequence
DRB1_0901  263  AFLIGLVNIVLMTAL  FLIGLVNIV        0.4656         324.6          WB    32.00      Sequence
DRB1_0901  183  RGPVRASMQIRRIDP  PVRASMQIR        0.4635         331.9          WB    32.00      Sequence
DRB1_0901  212  FFVWMITVAFLYLVL  FVWMITVAF        0.4621         337.0          WB    32.00      Sequence
DRB1_0901  184  GPVRASMQIRRIDPW  PVRASMQIR        0.4612         340.2          WB    32.00      Sequence
DRB1_0901  181  RSRGPVRASMQIRRI  PVRASMQIR        0.4598         345.6          WB    32.00      Sequence
DRB1_0901  180  RRSRGPVRASMQIRR  PVRASMQIR        0.4588         349.1          WB    32.00      Sequence
DRB1_0901   67  EGRPTNPPAAADARL  PTNPPAAAD        0.4578         353.0          WB    32.00      Sequence
DRB1_0901  266  IGLVNIVLMTALATI  IGLVNIVLM        0.4563         358.8          WB    32.00      Sequence
DRB1_0901   66  PEGRPTNPPAAADAR  PTNPPAAAD        0.4522         375.0          WB    32.00      Sequence
DRB1_0901   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.4518         376.5          WB    32.00      Sequence
DRB1_0901  209  VALFFVWMITVAFLY  FFVWMITVA        0.4479         392.9          WB    32.00      Sequence
DRB1_0901  276  ALATIGAFVYNLITD  IGAFVYNLI        0.4444         407.9          WB    32.00      Sequence
DRB1_0901  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.4426         416.0          WB    32.00      Sequence
DRB1_0901  267  GLVNIVLMTALATIG  GLVNIVLMT        0.4425         416.7          WB    32.00      Sequence
DRB1_0901  232  WAKLNSNVGDLLNNA  WAKLNSNVG        0.4421         418.5          WB    32.00      Sequence
DRB1_0901  274  MTALATIGAFVYNLI  MTALATIGA        0.4414         421.5          WB    32.00      Sequence
DRB1_0901  262  GAFLIGLVNIVLMTA  FLIGLVNIV        0.4414         421.7          WB    32.00      Sequence
DRB1_0901   68  GRPTNPPAAADARLN  PTNPPAAAD        0.4406         425.2          WB    32.00      Sequence
DRB1_0901   39  AGDPPPWQRAATRQS  WQRAATRQS        0.4401         427.5          WB    32.00      Sequence
DRB1_0901  213  FVWMITVAFLYLVLG  WMITVAFLY        0.4391         432.0          WB    32.00      Sequence
DRB1_0901  112  CGDGSPAEAYASELP  CGDGSPAEA        0.4380         437.1          WB    32.00      Sequence
DRB1_0901   65  HPEGRPTNPPAAADA  PTNPPAAAD        0.4375         439.8          WB    32.00      Sequence
DRB1_0901  244  NNASGSSAELVSSGT  NASGSSAEL        0.4351         451.5          WB    32.00      Sequence
DRB1_0901  201  LKVSLLLSVALFFVW  SLLLSVALF        0.4342         455.5          WB    32.00      Sequence
DRB1_0901   86  SGASAPVTGPAAAVR  PVTGPAAAV        0.4340         456.9          WB    32.00      Sequence
DRB1_0901  275  TALATIGAFVYNLIT  IGAFVYNLI        0.4339         457.0          WB    32.00      Sequence
DRB1_0901  113  GDGSPAEAYASELPD  PAEAYASEL        0.4310         471.9          WB    32.00      Sequence
DRB1_0901  136  PQRNPAPARPAEGGA  RNPAPARPA        0.4308         472.8          WB    32.00      Sequence
DRB1_0901  265  LIGLVNIVLMTALAT  IGLVNIVLM        0.4293         480.4          WB    32.00      Sequence
DRB1_0901  225  VLGGMGVWAKLNSNV  GGMGVWAKL        0.4286         484.2          WB    32.00      Sequence
DRB1_0901  224  LVLGGMGVWAKLNSN  GGMGVWAKL        0.4283         485.6          WB    32.00      Sequence
DRB1_0901  261  GGAFLIGLVNIVLMT  FLIGLVNIV        0.4283         485.6          WB    32.00      Sequence
DRB1_0901   92  VTGPAAAVRTPQPDP  TGPAAAVRT        0.4277         488.9          WB    32.00      Sequence
DRB1_0901   44  PWQRAATRQSQAGHR  WQRAATRQS        0.4272         491.8          WB    32.00      Sequence
DRB1_0901  273  LMTALATIGAFVYNL  LMTALATIG        0.4268         493.4          WB    32.00      Sequence
DRB1_0901   64  SHPEGRPTNPPAAAD  PTNPPAAAD        0.4259         498.6          WB    50.00      Sequence
DRB1_0901   23  RGGAHRAATGPGRIP  RGGAHRAAT        0.4256         500.4                50.00      Sequence
DRB1_0901  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.4247         505.0                50.00      Sequence
DRB1_0901  135  APQRNPAPARPAEGG  RNPAPARPA        0.4209         526.0                50.00      Sequence
DRB1_0901  117  PAEAYASELPDLSGP  PAEAYASEL        0.4198         532.2                50.00      Sequence
DRB1_0901   69  RPTNPPAAADARLNR  RPTNPPAAA        0.4194         534.8                50.00      Sequence
DRB1_0901  245  NASGSSAELVSSGTI  NASGSSAEL        0.4187         538.7                50.00      Sequence
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DRB1_0901  199  STLKVSLLLSVALFF  LKVSLLLSV        0.4161        554.6                 50.00      Sequence
DRB1_0901  239  VGDLLNNASGSSAEL  LNNASGSSA        0.4157        556.5                 50.00      Sequence
DRB1_0901   55  AGHRQPPPVSHPEGR  AGHRQPPPV        0.4147        563.0                 50.00      Sequence
DRB1_0901   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.4134        570.6                 50.00      Sequence
DRB1_0901   20  LVDRGGAHRAATGPG  AHRAATGPG        0.4100        591.9                 50.00      Sequence
DRB1_0901   54  QAGHRQPPPVSHPEG  AGHRQPPPV        0.4082        603.9                 50.00      Sequence
DRB1_0901   22  DRGGAHRAATGPGRI  GGAHRAATG        0.4044        629.3                 50.00      Sequence
DRB1_0901  111  GCGDGSPAEAYASEL  CGDGSPAEA        0.4038        632.9                 50.00      Sequence
DRB1_0901   53  SQAGHRQPPPVSHPE  GHRQPPPVS        0.4020        645.3                 50.00      Sequence
DRB1_0901  179  ARRSRGPVRASMQIR  PVRASMQIR        0.4012        651.2                 50.00      Sequence
DRB1_0901  260  FGGAFLIGLVNIVLM  FLIGLVNIV        0.3988        668.5                 50.00      Sequence
DRB1_0901   24  GGAHRAATGPGRIPD  AHRAATGPG        0.3985        670.5                 50.00      Sequence
DRB1_0901  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.3983        672.2                 50.00      Sequence
DRB1_0901  191  QIRRIDPWSTLKVSL  IDPWSTLKV        0.3973        679.3                 50.00      Sequence
DRB1_0901  185  PVRASMQIRRIDPWS  PVRASMQIR        0.3948        697.7                 50.00      Sequence
DRB1_0901  134  RAPQRNPAPARPAEG  RNPAPARPA        0.3909        727.8                 50.00      Sequence
DRB1_0901  246  ASGSSAELVSSGTIF  ASGSSAELV        0.3880        751.1                 50.00      Sequence
DRB1_0901  258  TIFGGAFLIGLVNIV  TIFGGAFLI        0.3878        753.1                 50.00      Sequence
DRB1_0901   21  VDRGGAHRAATGPGR  RGGAHRAAT        0.3836        788.2                 50.00      Sequence
DRB1_0901   52  QSQAGHRQPPPVSHP  AGHRQPPPV        0.3817        804.5                 50.00      Sequence
DRB1_0901  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.3816        805.5                 50.00      Sequence
DRB1_0901   76  AADARLNRFISGASA  LNRFISGAS        0.3812        808.5                 50.00      Sequence
DRB1_0901  208  SVALFFVWMITVAFL  FFVWMITVA        0.3791        827.3                 50.00      Sequence
DRB1_0901  190  MQIRRIDPWSTLKVS  IDPWSTLKV        0.3774        842.9                 50.00      Sequence
DRB1_0901   50  TRQSQAGHRQPPPVS  GHRQPPPVS        0.3759        856.4                 50.00      Sequence
DRB1_0901  137  QRNPAPARPAEGGAG  RNPAPARPA        0.3749        866.0                 50.00      Sequence
DRB1_0901   56  GHRQPPPVSHPEGRP  GHRQPPPVS        0.3705        908.1                 50.00      Sequence
DRB1_0901  257  GTIFGGAFLIGLVNI  TIFGGAFLI        0.3694        918.8                 50.00      Sequence
DRB1_0901  161  SGGRSITAESRDARV  RSITAESRD        0.3689        923.8                 50.00      Sequence
DRB1_0901  233  AKLNSNVGDLLNNAS  LNSNVGDLL        0.3688        924.7                 50.00      Sequence
DRB1_0901  133  PRAPQRNPAPARPAE  RNPAPARPA        0.3687        925.4                 50.00      Sequence
DRB1_0901  214  VWMITVAFLYLVLGG  VWMITVAFL        0.3680        932.9                 50.00      Sequence
DRB1_0901  259  IFGGAFLIGLVNIVL  FLIGLVNIV        0.3675        937.3                 50.00      Sequence
DRB1_0901  178  SARRSRGPVRASMQI  GPVRASMQI        0.3673        939.4                 50.00      Sequence
DRB1_0901  189  SMQIRRIDPWSTLKV  IDPWSTLKV        0.3663        950.2                 50.00      Sequence
DRB1_0901  174  RVQLSARRSRGPVRA  RVQLSARRS        0.3644        970.2                 50.00      Sequence
DRB1_0901   25  GAHRAATGPGRIPDA  AHRAATGPG        0.3630        984.4                 50.00      Sequence
DRB1_0901  222  LYLVLGGMGVWAKLN  YLVLGGMGV        0.3629        985.7                 50.00      Sequence
DRB1_0901  175  VQLSARRSRGPVRAS  VQLSARRSR        0.3617        998.0                 50.00      Sequence
DRB1_0901  162  GGRSITAESRDARVQ  RSITAESRD        0.3616        999.4                 50.00      Sequence
DRB1_0901   51  RQSQAGHRQPPPVSH  GHRQPPPVS        0.3581       1038.7                 50.00      Sequence
DRB1_0901   70  PTNPPAAADARLNRF  PTNPPAAAD        0.3519       1110.2                 50.00      Sequence
DRB1_0901  110  LGCGDGSPAEAYASE  CGDGSPAEA        0.3498       1135.3                 50.00      Sequence
DRB1_0901  173  ARVQLSARRSRGPVR  ARVQLSARR        0.3487       1149.6                 50.00      Sequence
DRB1_0901   19  GLVDRGGAHRAATGP  LVDRGGAHR        0.3484       1153.5                 50.00      Sequence
DRB1_0901  221  FLYLVLGGMGVWAKL  FLYLVLGGM        0.3449       1197.1                 50.00      Sequence
DRB1_0901  160  SSGGRSITAESRDAR  RSITAESRD        0.3438       1212.0                 50.00      Sequence
DRB1_0901  132  TPRAPQRNPAPARPA  RNPAPARPA        0.3415       1243.1                 50.00      Sequence
DRB1_0901  256  SGTIFGGAFLIGLVN  TIFGGAFLI        0.3410       1249.8                 50.00      Sequence
DRB1_0901  164  RSITAESRDARVQLS  RSITAESRD        0.3384       1285.5                 50.00      Sequence
DRB1_0901  158  AGSSGGRSITAESRD  AGSSGGRSI        0.3361       1317.4                 50.00      Sequence
DRB1_0901  159  GSSGGRSITAESRDA  GGRSITAES        0.3322       1373.8                 50.00      Sequence
DRB1_0901  234  KLNSNVGDLLNNASG  LNSNVGDLL        0.3277       1443.1                 50.00      Sequence
DRB1_0901  118  AEAYASELPDLSGPT  AEAYASELP        0.3276       1443.8                 50.00      Sequence
DRB1_0901   93  TGPAAAVRTPQPDPD  TGPAAAVRT        0.3270       1453.4                 50.00      Sequence
DRB1_0901   26  AHRAATGPGRIPDAG  RAATGPGRI        0.3257       1473.6                 50.00      Sequence
DRB1_0901  238  NVGDLLNNASGSSAE  LNNASGSSA        0.3249       1486.3                 50.00      Sequence
DRB1_0901  153  RGDSAAGSSGGRSIT  RGDSAAGSS        0.3244       1494.6                 50.00      Sequence
DRB1_0901  109  SLGCGDGSPAEAYAS  DGSPAEAYA        0.3237       1506.2                 50.00      Sequence
DRB1_0901   28  RAATGPGRIPDAGDP  RAATGPGRI        0.3223       1529.2                 50.00      Sequence
DRB1_0901  138  RNPAPARPAEGGAGS  RNPAPARPA        0.3223       1529.8                 50.00      Sequence
DRB1_0901  207  LSVALFFVWMITVAF  FFVWMITVA        0.3216       1540.4                 50.00      Sequence
DRB1_0901   63  VSHPEGRPTNPPAAA  RPTNPPAAA        0.3216       1541.4                 50.00      Sequence
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DRB1_0901  172  DARVQLSARRSRGPV  ARVQLSARR        0.3207       1555.9               50.00      Sequence
DRB1_0901  220  AFLYLVLGGMGVWAK  YLVLGGMGV        0.3198       1571.3               50.00      Sequence
DRB1_0901  150  AGSRGDSAAGSSGGR  RGDSAAGSS        0.3168       1623.4               50.00      Sequence
DRB1_0901  247  SGSSAELVSSGTIFG  SGSSAELVS        0.3166       1625.7               50.00      Sequence
DRB1_0901  152  SRGDSAAGSSGGRSI  RGDSAAGSS        0.3164       1629.6               50.00      Sequence
DRB1_0901  177  LSARRSRGPVRASMQ  RRSRGPVRA        0.3158       1640.8               50.00      Sequence
DRB1_0901   18  DGLVDRGGAHRAATG  LVDRGGAHR        0.3146       1662.7               50.00      Sequence
DRB1_0901  255  SSGTIFGGAFLIGLV  TIFGGAFLI        0.3138       1676.3               50.00      Sequence
DRB1_0901  163  GRSITAESRDARVQL  RSITAESRD        0.3135       1682.5               50.00      Sequence
DRB1_0901  186  VRASMQIRRIDPWST  VRASMQIRR        0.3129       1692.9               50.00      Sequence
DRB1_0901  219  VAFLYLVLGGMGVWA  YLVLGGMGV        0.3109       1730.0               50.00      Sequence
DRB1_0901   57  HRQPPPVSHPEGRPT  PVSHPEGRP        0.3105       1737.2               50.00      Sequence
DRB1_0901   58  RQPPPVSHPEGRPTN  PVSHPEGRP        0.3102       1743.5               50.00      Sequence
DRB1_0901  215  WMITVAFLYLVLGGM  WMITVAFLY        0.3068       1808.7               50.00      Sequence
DRB1_0901  169  ESRDARVQLSARRSR  ESRDARVQL        0.3045       1853.8               50.00      Sequence
DRB1_0901    0  VTAPNEPGALSKGDG  APNEPGALS        0.3038       1868.5               50.00      Sequence
DRB1_0901  151  GSRGDSAAGSSGGRS  RGDSAAGSS        0.3034       1876.2               50.00      Sequence
DRB1_0901  176  QLSARRSRGPVRASM  SARRSRGPV        0.3034       1876.5               50.00      Sequence
DRB1_0901  149  GAGSRGDSAAGSSGG  RGDSAAGSS        0.3004       1938.2               50.00      Sequence
DRB1_0901  167  TAESRDARVQLSARR  TAESRDARV        0.2990       1967.1               50.00      Sequence
DRB1_0901  188  ASMQIRRIDPWSTLK  IRRIDPWST        0.2987       1974.2               50.00      Sequence
DRB1_0901   27  HRAATGPGRIPDAGD  RAATGPGRI        0.2985       1977.6               50.00      Sequence
DRB1_0901  157  AAGSSGGRSITAESR  AGSSGGRSI        0.2982       1985.1               50.00      Sequence
DRB1_0901   62  PVSHPEGRPTNPPAA  PVSHPEGRP        0.2962       2028.3               50.00      Sequence
DRB1_0901  251  AELVSSGTIFGGAFL  AELVSSGTI        0.2948       2059.7               50.00      Sequence
DRB1_0901  204  SLLLSVALFFVWMIT  SLLLSVALF        0.2936       2086.4               50.00      Sequence
DRB1_0901  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.2918       2127.6               50.00      Sequence
DRB1_0901  171  RDARVQLSARRSRGP  RVQLSARRS        0.2915       2134.7               50.00      Sequence
DRB1_0901  170  SRDARVQLSARRSRG  ARVQLSARR        0.2889       2195.1               50.00      Sequence
DRB1_0901  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.2887       2200.6               50.00      Sequence
DRB1_0901  108  ASLGCGDGSPAEAYA  CGDGSPAEA        0.2863       2258.3               50.00      Sequence
DRB1_0901    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.2851       2287.1               50.00      Sequence
DRB1_0901  187  RASMQIRRIDPWSTL  QIRRIDPWS        0.2819       2368.4               50.00      Sequence
DRB1_0901  168  AESRDARVQLSARRS  ESRDARVQL        0.2819       2368.7               50.00      Sequence
DRB1_0901  147  EGGAGSRGDSAAGSS  RGDSAAGSS        0.2809       2394.1               50.00      Sequence
DRB1_0901   75  AAADARLNRFISGAS  LNRFISGAS        0.2808       2395.3               50.00      Sequence
DRB1_0901   49  ATRQSQAGHRQPPPV  AGHRQPPPV        0.2806       2401.1               50.00      Sequence
DRB1_0901  254  VSSGTIFGGAFLIGL  GTIFGGAFL        0.2797       2426.1               50.00      Sequence
DRB1_0901  218  TVAFLYLVLGGMGVW  YLVLGGMGV        0.2792       2438.3               50.00      Sequence
DRB1_0901  156  SAAGSSGGRSITAES  AGSSGGRSI        0.2787       2451.2               50.00      Sequence
DRB1_0901  250  SAELVSSGTIFGGAF  LVSSGTIFG        0.2772       2490.5               50.00      Sequence
DRB1_0901  148  GGAGSRGDSAAGSSG  RGDSAAGSS        0.2769       2499.7               50.00      Sequence
DRB1_0901  248  GSSAELVSSGTIFGG  GSSAELVSS        0.2752       2545.6               50.00      Sequence
DRB1_0901    7  GALSKGDGPNADGLV  LSKGDGPNA        0.2745       2565.1               50.00      Sequence
DRB1_0901  119  EAYASELPDLSGPTP  YASELPDLS        0.2742       2573.0               50.00      Sequence
DRB1_0901  125  LPDLSGPTPRAPQRN  DLSGPTPRA        0.2728       2613.6               50.00      Sequence
DRB1_0901  252  ELVSSGTIFGGAFLI  ELVSSGTIF        0.2699       2696.9               50.00      Sequence
DRB1_0901  131  PTPRAPQRNPAPARP  PQRNPAPAR        0.2691       2718.7               50.00      Sequence
DRB1_0901  129  SGPTPRAPQRNPAPA  SGPTPRAPQ        0.2650       2842.3               50.00      Sequence
DRB1_0901  145  PAEGGAGSRGDSAAG  AGSRGDSAA        0.2633       2895.2               50.00      Sequence
DRB1_0901  144  RPAEGGAGSRGDSAA  AGSRGDSAA        0.2631       2902.0               50.00      Sequence
DRB1_0901   61  PPVSHPEGRPTNPPA  PVSHPEGRP        0.2628       2911.6               50.00      Sequence
DRB1_0901  139  NPAPARPAEGGAGSR  NPAPARPAE        0.2626       2918.6               50.00      Sequence
DRB1_0901   29  AATGPGRIPDAGDPP  AATGPGRIP        0.2612       2961.3               50.00      Sequence
DRB1_0901   17  ADGLVDRGGAHRAAT  LVDRGGAHR        0.2610       2969.9               50.00      Sequence
DRB1_0901  124  ELPDLSGPTPRAPQR  DLSGPTPRA        0.2582       3059.1               50.00      Sequence
DRB1_0901  237  SNVGDLLNNASGSSA  LNNASGSSA        0.2575       3082.9               50.00      Sequence
DRB1_0901   59  QPPPVSHPEGRPTNP  PVSHPEGRP        0.2563       3122.6               50.00      Sequence
DRB1_0901  206  LLSVALFFVWMITVA  FFVWMITVA        0.2563       3124.3               50.00      Sequence
DRB1_0901  249  SSAELVSSGTIFGGA  ELVSSGTIF        0.2560       3135.2               50.00      Sequence
DRB1_0901  165  SITAESRDARVQLSA  TAESRDARV        0.2558       3141.0               50.00      Sequence
DRB1_0901  235  LNSNVGDLLNNASGS  LNSNVGDLL        0.2547       3176.8               50.00      Sequence
DRB1_0901  166  ITAESRDARVQLSAR  TAESRDARV        0.2547       3178.8               50.00      Sequence
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DRB1_0901   97  AAVRTPQPDPDASLG  VRTPQPDPD         0.2545       3185.4                 50.00      Sequence
DRB1_0901  216  MITVAFLYLVLGGMG  LYLVLGGMG         0.2530       3237.3                 50.00      Sequence
DRB1_0901   60  PPPVSHPEGRPTNPP  PVSHPEGRP         0.2523       3261.8                 50.00      Sequence
DRB1_0901    9  LSKGDGPNADGLVDR  LSKGDGPNA         0.2519       3276.4                 50.00      Sequence
DRB1_0901  128  LSGPTPRAPQRNPAP  SGPTPRAPQ         0.2518       3277.5                 50.00      Sequence
DRB1_0901    1  TAPNEPGALSKGDGP  APNEPGALS         0.2518       3280.6                 50.00      Sequence
DRB1_0901  253  LVSSGTIFGGAFLIG  GTIFGGAFL         0.2516       3285.6                 50.00      Sequence
DRB1_0901  130  GPTPRAPQRNPAPAR  PQRNPAPAR         0.2501       3340.6                 50.00      Sequence
DRB1_0901    2  APNEPGALSKGDGPN  APNEPGALS         0.2482       3409.4                 50.00      Sequence
DRB1_0901  107  DASLGCGDGSPAEAY  CGDGSPAEA         0.2473       3442.8                 50.00      Sequence
DRB1_0901   98  AVRTPQPDPDASLGC  VRTPQPDPD         0.2469       3457.9                 50.00      Sequence
DRB1_0901  142  PARPAEGGAGSRGDS  EGGAGSRGD         0.2466       3468.6                 50.00      Sequence
DRB1_0901   71  TNPPAAADARLNRFI  TNPPAAADA         0.2460       3490.1                 50.00      Sequence
DRB1_0901   99  VRTPQPDPDASLGCG  VRTPQPDPD         0.2440       3566.9                 50.00      Sequence
DRB1_0901  217  ITVAFLYLVLGGMGV  FLYLVLGGM         0.2406       3700.9                 50.00      Sequence
DRB1_0901   38  DAGDPPPWQRAATRQ  PWQRAATRQ         0.2403       3713.5                 50.00      Sequence
DRB1_0901   96  AAAVRTPQPDPDASL  VRTPQPDPD         0.2364       3872.0                 50.00      Sequence
DRB1_0901  155  DSAAGSSGGRSITAE  AGSSGGRSI         0.2364       3872.7                 50.00      Sequence
DRB1_0901  123  SELPDLSGPTPRAPQ  DLSGPTPRA         0.2354       3916.7                 50.00      Sequence
DRB1_0901  143  ARPAEGGAGSRGDSA  RPAEGGAGS         0.2343       3963.1                 50.00      Sequence
DRB1_0901  106  PDASLGCGDGSPAEA  CGDGSPAEA         0.2292       4187.7                 50.00      Sequence
DRB1_0901  146  AEGGAGSRGDSAAGS  EGGAGSRGD         0.2290       4195.9                 50.00      Sequence
DRB1_0901  141  APARPAEGGAGSRGD  PARPAEGGA         0.2262       4326.7                 50.00      Sequence
DRB1_0901  121  YASELPDLSGPTPRA  YASELPDLS         0.2256       4353.4                 50.00      Sequence
DRB1_0901  120  AYASELPDLSGPTPR  YASELPDLS         0.2251       4378.1                 50.00      Sequence
DRB1_0901   13  DGPNADGLVDRGGAH  DGPNADGLV         0.2214       4557.7                 50.00      Sequence
DRB1_0901   10  SKGDGPNADGLVDRG  DGPNADGLV         0.2214       4558.3                 50.00      Sequence
DRB1_0901   94  GPAAAVRTPQPDPDA  GPAAAVRTP         0.2187       4693.6                 50.00      Sequence
DRB1_0901   30  ATGPGRIPDAGDPPP  PGRIPDAGD         0.2165       4803.6                 50.00      Sequence
DRB1_0901   16  NADGLVDRGGAHRAA  LVDRGGAHR         0.2151       4879.2                 50.00      Sequence
DRB1_0901   11  KGDGPNADGLVDRGG  DGPNADGLV         0.2121       5039.3                 50.00      Sequence
DRB1_0901  100  RTPQPDPDASLGCGD  RTPQPDPDA         0.2114       5074.3                 50.00      Sequence
DRB1_0901  236  NSNVGDLLNNASGSS  LLNNASGSS         0.2108       5111.1                 50.00      Sequence
DRB1_0901  140  PAPARPAEGGAGSRG  PARPAEGGA         0.2097       5171.3                 50.00      Sequence
DRB1_0901   46  QRAATRQSQAGHRQP  TRQSQAGHR         0.2078       5277.5                 50.00      Sequence
DRB1_0901  154  GDSAAGSSGGRSITA  AGSSGGRSI         0.2073       5307.0                 50.00      Sequence
DRB1_0901   95  PAAAVRTPQPDPDAS  VRTPQPDPD         0.2060       5382.7                 50.00      Sequence
DRB1_0901   12  GDGPNADGLVDRGGA  DGPNADGLV         0.2055       5414.0                 50.00      Sequence
DRB1_0901    3  PNEPGALSKGDGPNA  LSKGDGPNA         0.2049       5445.6                 50.00      Sequence
DRB1_0901   47  RAATRQSQAGHRQPP  TRQSQAGHR         0.2047       5461.2                 50.00      Sequence
DRB1_0901   31  TGPGRIPDAGDPPPW  TGPGRIPDA         0.2044       5477.8                 50.00      Sequence
DRB1_0901   72  NPPAAADARLNRFIS  PPAAADARL         0.2044       5478.1                 50.00      Sequence
DRB1_0901  205  LLLSVALFFVWMITV  LLLSVALFF         0.2016       5644.9                 50.00      Sequence
DRB1_0901    4  NEPGALSKGDGPNAD  LSKGDGPNA         0.2005       5714.3                 50.00      Sequence
DRB1_0901    6  PGALSKGDGPNADGL  LSKGDGPNA         0.1991       5802.1                 50.00      Sequence
DRB1_0901  122  ASELPDLSGPTPRAP  DLSGPTPRA         0.1955       6028.0                 50.00      Sequence
DRB1_0901   15  PNADGLVDRGGAHRA  DGLVDRGGA         0.1940       6130.0                 50.00      Sequence
DRB1_0901    5  EPGALSKGDGPNADG  LSKGDGPNA         0.1937       6151.4                 50.00      Sequence
DRB1_0901  101  TPQPDPDASLGCGDG  PQPDPDASL         0.1876       6567.4                 50.00      Sequence
DRB1_0901  102  PQPDPDASLGCGDGS  QPDPDASLG         0.1875       6573.9                 50.00      Sequence
DRB1_0901   37  PDAGDPPPWQRAATR  AGDPPPWQR         0.1850       6755.5                 50.00      Sequence
DRB1_0901   48  AATRQSQAGHRQPPP  TRQSQAGHR         0.1835       6868.6                 50.00      Sequence
DRB1_0901   74  PAAADARLNRFISGA  DARLNRFIS         0.1825       6937.3                 50.00      Sequence
DRB1_0901   33  PGRIPDAGDPPPWQR  PGRIPDAGD         0.1794       7178.1                 50.00      Sequence
DRB1_0901   14  GPNADGLVDRGGAHR  DGLVDRGGA         0.1784       7252.8                 50.00      Sequence
DRB1_0901  105  DPDASLGCGDGSPAE  LGCGDGSPA         0.1776       7318.9                 50.00      Sequence
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DRB1_0901  104  PDPDASLGCGDGSPA  LGCGDGSPA         0.1726       7728.6                 50.00      Sequence
DRB1_0901  103  QPDPDASLGCGDGSP  QPDPDASLG         0.1704       7909.6                 50.00      Sequence
DRB1_0901   32  GPGRIPDAGDPPPWQ  PGRIPDAGD         0.1685       8076.2                 50.00      Sequence
DRB1_0901   36  IPDAGDPPPWQRAAT  IPDAGDPPP         0.1407      10912.4                 50.00      Sequence
DRB1_0901   34  GRIPDAGDPPPWQRA  IPDAGDPPP         0.1334      11812.3                 50.00      Sequence
DRB1_0901   35  RIPDAGDPPPWQRAA  IPDAGDPPP         0.1177      13991.3                 50.00      Sequence
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Allele: DRB1_0901. Number of high binders 6. Number of weak binders 89. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  268  LVNIVLMTALATIGA  IVLMTALAT        0.6453         46.4         SB     4.00     Sequence
   DRB1_1101  267  GLVNIVLMTALATIG  IVLMTALAT        0.6323         53.5         WB     8.00     Sequence
   DRB1_1101  270  NIVLMTALATIGAFV  IVLMTALAT        0.6305         54.5         WB     8.00     Sequence
   DRB1_1101  269  VNIVLMTALATIGAF  IVLMTALAT        0.6190         61.7         WB     8.00     Sequence
   DRB1_1101  266  IGLVNIVLMTALATI  IVLMTALAT        0.5978         77.6         WB     8.00     Sequence
   DRB1_1101  271  IVLMTALATIGAFVY  IVLMTALAT        0.5863         87.9         WB     8.00     Sequence
   DRB1_1101  172  DARVQLSARRSRGPV  RVQLSARRS        0.5794         94.7         WB     8.00     Sequence
   DRB1_1101  173  ARVQLSARRSRGPVR  RVQLSARRS        0.5743        100.1         WB     8.00     Sequence
   DRB1_1101  171  RDARVQLSARRSRGP  RVQLSARRS        0.5700        104.9         WB     8.00     Sequence
   DRB1_1101   79  ARLNRFISGASAPVT  LNRFISGAS        0.5676        107.6         WB     8.00     Sequence
   DRB1_1101  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.5660        109.5         WB    16.00     Sequence
   DRB1_1101   80  RLNRFISGASAPVTG  LNRFISGAS        0.5647        111.1         WB    16.00     Sequence
   DRB1_1101  265  LIGLVNIVLMTALAT  LVNIVLMTA        0.5514        128.2         WB    16.00     Sequence
   DRB1_1101   81  LNRFISGASAPVTGP  FISGASAPV        0.5493        131.2         WB    16.00     Sequence
   DRB1_1101  199  STLKVSLLLSVALFF  VSLLLSVAL        0.5451        137.3         WB    16.00     Sequence
   DRB1_1101   78  DARLNRFISGASAPV  LNRFISGAS        0.5409        143.7         WB    16.00     Sequence
   DRB1_1101  174  RVQLSARRSRGPVRA  RVQLSARRS        0.5294        162.7         WB    16.00     Sequence
   DRB1_1101  201  LKVSLLLSVALFFVW  VSLLLSVAL        0.5288        163.8         WB    16.00     Sequence
   DRB1_1101  170  SRDARVQLSARRSRG  RVQLSARRS        0.5214        177.5         WB    16.00     Sequence
   DRB1_1101  198  WSTLKVSLLLSVALF  VSLLLSVAL        0.5108        199.0         WB    16.00     Sequence
   DRB1_1101   77  ADARLNRFISGASAP  LNRFISGAS        0.4923        243.1         WB    16.00     Sequence
   DRB1_1101  222  LYLVLGGMGVWAKLN  LYLVLGGMG        0.4902        248.7         WB    16.00     Sequence
   DRB1_1101  197  PWSTLKVSLLLSVAL  TLKVSLLLS        0.4833        268.0         WB    16.00     Sequence
   DRB1_1101  226  LGGMGVWAKLNSNVG  MGVWAKLNS        0.4738        296.9         WB    16.00     Sequence
   DRB1_1101  221  FLYLVLGGMGVWAKL  LYLVLGGMG        0.4723        301.8         WB    32.00     Sequence
   DRB1_1101   82  NRFISGASAPVTGPA  FISGASAPV        0.4653        325.6         WB    32.00     Sequence
   DRB1_1101  169  ESRDARVQLSARRSR  RVQLSARRS        0.4641        329.6         WB    32.00     Sequence
   DRB1_1101  264  FLIGLVNIVLMTALA  LVNIVLMTA        0.4617        338.6         WB    32.00     Sequence
   DRB1_1101  220  AFLYLVLGGMGVWAK  LYLVLGGMG        0.4616        338.9         WB    32.00     Sequence
   DRB1_1101  225  VLGGMGVWAKLNSNV  MGVWAKLNS        0.4575        354.1         WB    32.00     Sequence
   DRB1_1101  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.4460        401.3         WB    32.00     Sequence
   DRB1_1101   76  AADARLNRFISGASA  ARLNRFISG        0.4448        406.3         WB    32.00     Sequence
   DRB1_1101  227  GGMGVWAKLNSNVGD  MGVWAKLNS        0.4416        420.6         WB    32.00     Sequence
   DRB1_1101  219  VAFLYLVLGGMGVWA  LYLVLGGMG        0.4360        446.8         WB    32.00     Sequence
   DRB1_1101  272  VLMTALATIGAFVYN  MTALATIGA        0.4307        473.3         WB    32.00     Sequence
   DRB1_1101  224  LVLGGMGVWAKLNSN  MGVWAKLNS        0.4241        508.4               32.00     Sequence
   DRB1_1101  223  YLVLGGMGVWAKLNS  YLVLGGMGV        0.4191        536.3               32.00     Sequence
   DRB1_1101  228  GMGVWAKLNSNVGDL  MGVWAKLNS        0.4163        553.3               32.00     Sequence
   DRB1_1101   75  AAADARLNRFISGAS  ADARLNRFI        0.4040        631.9               32.00     Sequence
   DRB1_1101  273  LMTALATIGAFVYNL  MTALATIGA        0.3979        674.8               32.00     Sequence
   DRB1_1101  184  GPVRASMQIRRIDPW  VRASMQIRR        0.3906        730.4               32.00     Sequence
   DRB1_1101  175  VQLSARRSRGPVRAS  VQLSARRSR        0.3906        730.7               32.00     Sequence
   DRB1_1101  185  PVRASMQIRRIDPWS  VRASMQIRR        0.3903        732.9               32.00     Sequence
   DRB1_1101  218  TVAFLYLVLGGMGVW  LYLVLGGMG        0.3892        741.7               32.00     Sequence
   DRB1_1101  196  DPWSTLKVSLLLSVA  TLKVSLLLS        0.3887        746.0               32.00     Sequence
   DRB1_1101  186  VRASMQIRRIDPWST  VRASMQIRR        0.3879        752.2               32.00     Sequence
   DRB1_1101  229  MGVWAKLNSNVGDLL  WAKLNSNVG        0.3832        791.3               32.00     Sequence
   DRB1_1101  210  ALFFVWMITVAFLYL  FVWMITVAF        0.3825        796.9               32.00     Sequence
   DRB1_1101  183  RGPVRASMQIRRIDP  VRASMQIRR        0.3799        820.2               32.00     Sequence
   DRB1_1101  263  AFLIGLVNIVLMTAL  LVNIVLMTA        0.3782        835.0               32.00     Sequence
   DRB1_1101  211  LFFVWMITVAFLYLV  FVWMITVAF        0.3666        946.5               32.00     Sequence
   DRB1_1101   83  RFISGASAPVTGPAA  FISGASAPV        0.3663        950.4               32.00     Sequence
   DRB1_1101  209  VALFFVWMITVAFLY  LFFVWMITV        0.3645        969.2               32.00     Sequence
   DRB1_1101  168  AESRDARVQLSARRS  RVQLSARRS        0.3637        977.5               32.00     Sequence
   DRB1_1101   74  PAAADARLNRFISGA  DARLNRFIS        0.3565       1055.9               32.00     Sequence
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DRB1_1101  208  SVALFFVWMITVAFL  LFFVWMITV        0.3449       1198.0                 50.00      Sequence
DRB1_1101  217  ITVAFLYLVLGGMGV  LYLVLGGMG        0.3432       1220.2                 50.00      Sequence
DRB1_1101  195  IDPWSTLKVSLLLSV  TLKVSLLLS        0.3419       1236.8                 50.00      Sequence
DRB1_1101  280  IGAFVYNLITDLIGG  FVYNLITDL        0.3335       1354.9                 50.00      Sequence
DRB1_1101  262  GAFLIGLVNIVLMTA  LVNIVLMTA        0.3332       1359.0                 50.00      Sequence
DRB1_1101  182  SRGPVRASMQIRRID  VRASMQIRR        0.3331       1360.5                 50.00      Sequence
DRB1_1101  281  GAFVYNLITDLIGGI  FVYNLITDL        0.3236       1507.2                 50.00      Sequence
DRB1_1101  279  TIGAFVYNLITDLIG  FVYNLITDL        0.3114       1721.1                 50.00      Sequence
DRB1_1101  282  AFVYNLITDLIGGIE  YNLITDLIG        0.3092       1763.0                 50.00      Sequence
DRB1_1101  181  RSRGPVRASMQIRRI  VRASMQIRR        0.3090       1766.1                 50.00      Sequence
DRB1_1101  207  LSVALFFVWMITVAF  LFFVWMITV        0.3023       1898.2                 50.00      Sequence
DRB1_1101  230  GVWAKLNSNVGDLLN  WAKLNSNVG        0.2972       2005.9                 50.00      Sequence
DRB1_1101  187  RASMQIRRIDPWSTL  RASMQIRRI        0.2964       2023.9                 50.00      Sequence
DRB1_1101  212  FFVWMITVAFLYLVL  FVWMITVAF        0.2912       2142.0                 50.00      Sequence
DRB1_1101  283  FVYNLITDLIGGIEV  YNLITDLIG        0.2882       2211.4                 50.00      Sequence
DRB1_1101   73  PPAAADARLNRFISG  DARLNRFIS        0.2874       2230.5                 50.00      Sequence
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DRB1_1101  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.2812       2385.8                 50.00      Sequence
DRB1_1101  216  MITVAFLYLVLGGMG  VAFLYLVLG        0.2798       2421.3                 50.00      Sequence
DRB1_1101  278  ATIGAFVYNLITDLI  GAFVYNLIT        0.2792       2437.2                 50.00      Sequence
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DRB1_1101  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.2771       2493.3                 50.00      Sequence
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DRB1_1101  176  QLSARRSRGPVRASM  QLSARRSRG        0.2728       2613.4                 50.00      Sequence
DRB1_1101   44  PWQRAATRQSQAGHR  WQRAATRQS        0.2722       2630.8                 50.00      Sequence
DRB1_1101  180  RRSRGPVRASMQIRR  RSRGPVRAS        0.2714       2652.8                 50.00      Sequence
DRB1_1101   43  PPWQRAATRQSQAGH  WQRAATRQS        0.2710       2663.2                 50.00      Sequence
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DRB1_1101  188  ASMQIRRIDPWSTLK  SMQIRRIDP        0.2648       2849.9                 50.00      Sequence
DRB1_1101  261  GGAFLIGLVNIVLMT  FLIGLVNIV        0.2571       3095.8                 50.00      Sequence
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DRB1_1101  191  QIRRIDPWSTLKVSL  IRRIDPWST        0.2539       3206.4                 50.00      Sequence
DRB1_1101  277  LATIGAFVYNLITDL  FVYNLITDL        0.2531       3232.5                 50.00      Sequence
DRB1_1101  192  IRRIDPWSTLKVSLL  IRRIDPWST        0.2509       3311.3                 50.00      Sequence
DRB1_1101   45  WQRAATRQSQAGHRQ  WQRAATRQS        0.2481       3413.4                 50.00      Sequence
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DRB1_1101   41  DPPPWQRAATRQSQA  WQRAATRQS        0.2359       3893.4                 50.00      Sequence
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DRB1_1101  284  VYNLITDLIGGIEVT  YNLITDLIG        0.2330       4020.9                 50.00      Sequence
DRB1_1101  206  LLSVALFFVWMITVA  LFFVWMITV        0.2277       4257.8                 50.00      Sequence
DRB1_1101  177  LSARRSRGPVRASMQ  RRSRGPVRA        0.2268       4297.1                 50.00      Sequence
DRB1_1101  178  SARRSRGPVRASMQI  RSRGPVRAS        0.2264       4318.4                 50.00      Sequence
DRB1_1101  287  LITDLIGGIEVTLAD  LIGGIEVTL        0.2233       4463.5                 50.00      Sequence
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DRB1_1101  239  VGDLLNNASGSSAEL  LLNNASGSS        0.2104       5130.9                 50.00      Sequence
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DRB1_1101   19  GLVDRGGAHRAATGP  VDRGGAHRA        0.2018       5634.6                 50.00      Sequence
DRB1_1101  236  NSNVGDLLNNASGSS  VGDLLNNAS        0.2014       5658.4                 50.00      Sequence
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DRB1_1101   20  LVDRGGAHRAATGPG  RGGAHRAAT       0.2006       5707.8                 50.00      Sequence
DRB1_1101   17  ADGLVDRGGAHRAAT  LVDRGGAHR       0.1996       5765.7                 50.00      Sequence
DRB1_1101  276  ALATIGAFVYNLITD  LATIGAFVY       0.1990       5804.5                 50.00      Sequence
DRB1_1101  250  SAELVSSGTIFGGAF  LVSSGTIFG       0.1977       5889.2                 50.00      Sequence
DRB1_1101   72  NPPAAADARLNRFIS  DARLNRFIS       0.1929       6199.2                 50.00      Sequence
DRB1_1101  256  SGTIFGGAFLIGLVN  IFGGAFLIG       0.1924       6234.9                 50.00      Sequence
DRB1_1101  158  AGSSGGRSITAESRD  SSGGRSITA       0.1909       6335.0                 50.00      Sequence
DRB1_1101  156  SAAGSSGGRSITAES  SSGGRSITA       0.1896       6431.0                 50.00      Sequence
DRB1_1101   40  GDPPPWQRAATRQSQ  WQRAATRQS       0.1878       6555.4                 50.00      Sequence
DRB1_1101  163  GRSITAESRDARVQL  SITAESRDA       0.1873       6590.1                 50.00      Sequence
DRB1_1101   23  RGGAHRAATGPGRIP  RGGAHRAAT       0.1853       6730.4                 50.00      Sequence
DRB1_1101  159  GSSGGRSITAESRDA  SSGGRSITA       0.1853       6730.8                 50.00      Sequence
DRB1_1101  249  SSAELVSSGTIFGGA  AELVSSGTI       0.1848       6769.5                 50.00      Sequence
DRB1_1101  214  VWMITVAFLYLVLGG  WMITVAFLY       0.1786       7237.8                 50.00      Sequence
DRB1_1101  205  LLLSVALFFVWMITV  LFFVWMITV       0.1784       7258.5                 50.00      Sequence
DRB1_1101  164  RSITAESRDARVQLS  ITAESRDAR       0.1778       7301.0                 50.00      Sequence
DRB1_1101  160  SSGGRSITAESRDAR  SSGGRSITA       0.1766       7397.0                 50.00      Sequence
DRB1_1101  162  GGRSITAESRDARVQ  SITAESRDA       0.1733       7671.0                 50.00      Sequence
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DRB1_1101  248  GSSAELVSSGTIFGG  AELVSSGTI       0.1674       8174.9                 50.00      Sequence
DRB1_1101  165  SITAESRDARVQLSA  ITAESRDAR       0.1655       8345.2                 50.00      Sequence
DRB1_1101  251  AELVSSGTIFGGAFL  LVSSGTIFG       0.1644       8440.7                 50.00      Sequence
DRB1_1101   22  DRGGAHRAATGPGRI  RGGAHRAAT       0.1643       8452.5                 50.00      Sequence
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DRB1_1101  253  LVSSGTIFGGAFLIG  LVSSGTIFG       0.1522       9637.7                 50.00      Sequence
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DRB1_1101   24  GGAHRAATGPGRIPD  AHRAATGPG       0.1512       9742.9                 50.00      Sequence
DRB1_1101  252  ELVSSGTIFGGAFLI  LVSSGTIFG       0.1487      10001.9                 50.00      Sequence
DRB1_1101   25  GAHRAATGPGRIPDA  AHRAATGPG       0.1475      10131.4                 50.00      Sequence
DRB1_1101  161  SGGRSITAESRDARV  SITAESRDA       0.1464      10260.8                 50.00      Sequence
DRB1_1101   91  PVTGPAAAVRTPQPD  PVTGPAAAV       0.1429      10659.0                 50.00      Sequence
DRB1_1101   90  APVTGPAAAVRTPQP  PVTGPAAAV       0.1425      10700.5                 50.00      Sequence
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DRB1_1101  247  SGSSAELVSSGTIFG  LVSSGTIFG       0.1367      11398.3                 50.00      Sequence
DRB1_1101  234  KLNSNVGDLLNNASG  NSNVGDLLN       0.1353      11561.2                 50.00      Sequence
DRB1_1101  154  GDSAAGSSGGRSITA  SSGGRSITA       0.1352      11574.1                 50.00      Sequence
DRB1_1101  204  SLLLSVALFFVWMIT  SLLLSVALF       0.1344      11674.1                 50.00      Sequence
DRB1_1101  166  ITAESRDARVQLSAR  ITAESRDAR       0.1322      11966.7                 50.00      Sequence
DRB1_1101  254  VSSGTIFGGAFLIGL  IFGGAFLIG       0.1302      12218.3                 50.00      Sequence
DRB1_1101   14  GPNADGLVDRGGAHR  DGLVDRGGA       0.1276      12570.4                 50.00      Sequence
DRB1_1101   89  SAPVTGPAAAVRTPQ  PVTGPAAAV       0.1260      12796.5                 50.00      Sequence
DRB1_1101  233  AKLNSNVGDLLNNAS  NSNVGDLLN       0.1259      12805.3                 50.00      Sequence
DRB1_1101  241  DLLNNASGSSAELVS  LLNNASGSS       0.1198      13675.1                 50.00      Sequence
DRB1_1101   88  ASAPVTGPAAAVRTP  PVTGPAAAV       0.1139      14574.6                 50.00      Sequence
DRB1_1101  242  LLNNASGSSAELVSS  LLNNASGSS       0.1100      15208.9                 50.00      Sequence
DRB1_1101   93  TGPAAAVRTPQPDPD  AAAVRTPQP       0.1042      16186.0                 50.00      Sequence
DRB1_1101   92  VTGPAAAVRTPQPDP  TGPAAAVRT       0.1030      16406.4                 50.00      Sequence
DRB1_1101   94  GPAAAVRTPQPDPDA  AAAVRTPQP       0.0988      17174.0                 50.00      Sequence
DRB1_1101   46  QRAATRQSQAGHRQP  RAATRQSQA       0.0986      17200.4                 50.00      Sequence
DRB1_1101   27  HRAATGPGRIPDAGD  HRAATGPGR       0.0958      17725.5                 50.00      Sequence
DRB1_1101  132  TPRAPQRNPAPARPA  RAPQRNPAP       0.0930      18278.8                 50.00      Sequence
DRB1_1101   87  GASAPVTGPAAAVRT  PVTGPAAAV       0.0917      18540.5                 50.00      Sequence
DRB1_1101  121  YASELPDLSGPTPRA  YASELPDLS       0.0916      18556.0                 50.00      Sequence
DRB1_1101   47  RAATRQSQAGHRQPP  RAATRQSQA       0.0901      18871.0                 50.00      Sequence
DRB1_1101  119  EAYASELPDLSGPTP  YASELPDLS       0.0900      18875.9                 50.00      Sequence
DRB1_1101  120  AYASELPDLSGPTPR  ASELPDLSG       0.0889      19105.4                 50.00      Sequence
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DRB1_1101  131  PTPRAPQRNPAPARP  RAPQRNPAP        0.0876       19372.7                  50.00      Sequence
DRB1_1101  133  PRAPQRNPAPARPAE  RAPQRNPAP        0.0868       19555.3                  50.00      Sequence
DRB1_1101  246  ASGSSAELVSSGTIF  AELVSSGTI        0.0865       19614.6                  50.00      Sequence
DRB1_1101   71  TNPPAAADARLNRFI  AAADARLNR        0.0864       19635.8                  50.00      Sequence
DRB1_1101  122  ASELPDLSGPTPRAP  LPDLSGPTP        0.0846       20012.0                  50.00      Sequence
DRB1_1101   95  PAAAVRTPQPDPDAS  AAAVRTPQP        0.0843       20073.2                  50.00      Sequence
DRB1_1101   13  DGPNADGLVDRGGAH  DGLVDRGGA        0.0831       20342.6                  50.00      Sequence
DRB1_1101  134  RAPQRNPAPARPAEG  RAPQRNPAP        0.0803       20966.7                  50.00      Sequence
DRB1_1101  130  GPTPRAPQRNPAPAR  RAPQRNPAP        0.0761       21947.2                  50.00      Sequence
DRB1_1101  123  SELPDLSGPTPRAPQ  LPDLSGPTP        0.0755       22101.8                  50.00      Sequence
DRB1_1101   62  PVSHPEGRPTNPPAA  SHPEGRPTN        0.0750       22216.7                  50.00      Sequence
DRB1_1101   96  AAAVRTPQPDPDASL  AAAVRTPQP        0.0742       22404.2                  50.00      Sequence
DRB1_1101    5  EPGALSKGDGPNADG  PGALSKGDG        0.0741       22435.0                  50.00      Sequence
DRB1_1101    4  NEPGALSKGDGPNAD  PGALSKGDG        0.0737       22534.3                  50.00      Sequence
DRB1_1101   28  RAATGPGRIPDAGDP  AATGPGRIP        0.0733       22624.0                  50.00      Sequence
DRB1_1101    3  PNEPGALSKGDGPNA  PGALSKGDG        0.0732       22646.7                  50.00      Sequence
DRB1_1101   61  PPVSHPEGRPTNPPA  SHPEGRPTN        0.0727       22760.5                  50.00      Sequence
DRB1_1101  124  ELPDLSGPTPRAPQR  LPDLSGPTP        0.0726       22795.2                  50.00      Sequence
DRB1_1101    6  PGALSKGDGPNADGL  LSKGDGPNA        0.0721       22913.2                  50.00      Sequence
DRB1_1101  118  AEAYASELPDLSGPT  ASELPDLSG        0.0718       22985.2                  50.00      Sequence
DRB1_1101   48  AATRQSQAGHRQPPP  ATRQSQAGH        0.0718       23004.8                  50.00      Sequence
DRB1_1101   63  VSHPEGRPTNPPAAA  SHPEGRPTN        0.0707       23256.8                  50.00      Sequence
DRB1_1101   49  ATRQSQAGHRQPPPV  ATRQSQAGH        0.0702       23404.0                  50.00      Sequence
DRB1_1101   86  SGASAPVTGPAAAVR  SAPVTGPAA        0.0697       23527.2                  50.00      Sequence
DRB1_1101   51  RQSQAGHRQPPPVSH  QSQAGHRQP        0.0692       23644.8                  50.00      Sequence
DRB1_1101  245  NASGSSAELVSSGTI  AELVSSGTI        0.0665       24343.9                  50.00      Sequence
DRB1_1101   52  QSQAGHRQPPPVSHP  QAGHRQPPP        0.0656       24599.1                  50.00      Sequence
DRB1_1101  125  LPDLSGPTPRAPQRN  LPDLSGPTP        0.0643       24933.5                  50.00      Sequence
DRB1_1101  153  RGDSAAGSSGGRSIT  AAGSSGGRS        0.0639       25041.7                  50.00      Sequence
DRB1_1101   29  AATGPGRIPDAGDPP  AATGPGRIP        0.0630       25296.3                  50.00      Sequence
DRB1_1101   50  TRQSQAGHRQPPPVS  QSQAGHRQP        0.0623       25485.9                  50.00      Sequence
DRB1_1101  135  APQRNPAPARPAEGG  RNPAPARPA        0.0618       25620.8                  50.00      Sequence
DRB1_1101  243  LNNASGSSAELVSSG  LNNASGSSA        0.0607       25939.3                  50.00      Sequence
DRB1_1101  107  DASLGCGDGSPAEAY  LGCGDGSPA        0.0598       26168.8                  50.00      Sequence
DRB1_1101  117  PAEAYASELPDLSGP  ASELPDLSG        0.0595       26260.1                  50.00      Sequence
DRB1_1101  106  PDASLGCGDGSPAEA  LGCGDGSPA        0.0591       26367.2                  50.00      Sequence
DRB1_1101   60  PPPVSHPEGRPTNPP  SHPEGRPTN        0.0587       26487.3                  50.00      Sequence
DRB1_1101  129  SGPTPRAPQRNPAPA  TPRAPQRNP        0.0585       26563.9                  50.00      Sequence
DRB1_1101  105  DPDASLGCGDGSPAE  DASLGCGDG        0.0579       26729.1                  50.00      Sequence
DRB1_1101   53  SQAGHRQPPPVSHPE  QAGHRQPPP        0.0569       27014.9                  50.00      Sequence
DRB1_1101   12  GDGPNADGLVDRGGA  DGLVDRGGA        0.0553       27480.1                  50.00      Sequence
DRB1_1101    2  APNEPGALSKGDGPN  PGALSKGDG        0.0547       27660.3                  50.00      Sequence
DRB1_1101   64  SHPEGRPTNPPAAAD  SHPEGRPTN        0.0547       27662.1                  50.00      Sequence
DRB1_1101    7  GALSKGDGPNADGLV  LSKGDGPNA        0.0542       27815.1                  50.00      Sequence
DRB1_1101  136  PQRNPAPARPAEGGA  RNPAPARPA        0.0542       27827.5                  50.00      Sequence
DRB1_1101   38  DAGDPPPWQRAATRQ  PWQRAATRQ        0.0540       27866.6                  50.00      Sequence
DRB1_1101  151  GSRGDSAAGSSGGRS  GSRGDSAAG        0.0538       27931.2                  50.00      Sequence
DRB1_1101  104  PDPDASLGCGDGSPA  DASLGCGDG        0.0528       28251.6                  50.00      Sequence
DRB1_1101  145  PAEGGAGSRGDSAAG  AEGGAGSRG        0.0511       28761.1                  50.00      Sequence
DRB1_1101  244  NNASGSSAELVSSGT  SGSSAELVS        0.0497       29206.7                  50.00      Sequence
DRB1_1101  116  SPAEAYASELPDLSG  EAYASELPD        0.0496       29242.1                  50.00      Sequence
DRB1_1101  128  LSGPTPRAPQRNPAP  TPRAPQRNP        0.0491       29380.4                  50.00      Sequence
DRB1_1101   59  QPPPVSHPEGRPTNP  SHPEGRPTN        0.0483       29660.5                  50.00      Sequence
DRB1_1101  148  GGAGSRGDSAAGSSG  GSRGDSAAG        0.0481       29729.3                  50.00      Sequence
DRB1_1101  150  AGSRGDSAAGSSGGR  GSRGDSAAG        0.0472       29990.0                  50.00      Sequence
DRB1_1101   54  QAGHRQPPPVSHPEG  HRQPPPVSH        0.0462       30344.5                  50.00      Sequence
DRB1_1101  149  GAGSRGDSAAGSSGG  GSRGDSAAG        0.0461       30372.7                  50.00      Sequence
DRB1_1101  146  AEGGAGSRGDSAAGS  GGAGSRGDS        0.0453       30622.5                  50.00      Sequence
DRB1_1101  152  SRGDSAAGSSGGRSI  AAGSSGGRS        0.0439       31111.1                  50.00      Sequence
DRB1_1101    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.0425       31569.2                  50.00      Sequence
DRB1_1101  147  EGGAGSRGDSAAGSS  GSRGDSAAG        0.0424       31588.0                  50.00      Sequence
DRB1_1101   97  AAVRTPQPDPDASLG  AVRTPQPDP        0.0422       31681.8                  50.00      Sequence
DRB1_1101    1  TAPNEPGALSKGDGP  PGALSKGDG        0.0421       31694.1                  50.00      Sequence
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   DRB1_1101  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.0412      32011.9                  50.00     Sequence
   DRB1_1101  108  ASLGCGDGSPAEAYA  LGCGDGSPA        0.0402      32370.3                  50.00     Sequence
   DRB1_1101  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.0393      32671.8                  50.00     Sequence
   DRB1_1101  137  QRNPAPARPAEGGAG  RNPAPARPA        0.0389      32837.0                  50.00     Sequence
   DRB1_1101   58  RQPPPVSHPEGRPTN  SHPEGRPTN        0.0384      32994.8                  50.00     Sequence
   DRB1_1101  144  RPAEGGAGSRGDSAA  AEGGAGSRG        0.0377      33265.0                  50.00     Sequence
   DRB1_1101  138  RNPAPARPAEGGAGS  RNPAPARPA        0.0365      33699.4                  50.00     Sequence
   DRB1_1101   70  PTNPPAAADARLNRF  PAAADARLN        0.0360      33857.6                  50.00     Sequence
   DRB1_1101   57  HRQPPPVSHPEGRPT  HRQPPPVSH        0.0351      34191.9                  50.00     Sequence
   DRB1_1101  143  ARPAEGGAGSRGDSA  AEGGAGSRG        0.0343      34508.2                  50.00     Sequence
   DRB1_1101  103  QPDPDASLGCGDGSP  DASLGCGDG        0.0342      34529.9                  50.00     Sequence
   DRB1_1101  115  GSPAEAYASELPDLS  EAYASELPD        0.0342      34542.2                  50.00     Sequence
   DRB1_1101   55  AGHRQPPPVSHPEGR  GHRQPPPVS        0.0340      34623.0                  50.00     Sequence
   DRB1_1101   98  AVRTPQPDPDASLGC  AVRTPQPDP        0.0322      35305.4                  50.00     Sequence
   DRB1_1101   11  KGDGPNADGLVDRGG  NADGLVDRG        0.0313      35620.5                  50.00     Sequence
   DRB1_1101    0  VTAPNEPGALSKGDG  APNEPGALS        0.0310      35760.6                  50.00     Sequence
   DRB1_1101   56  GHRQPPPVSHPEGRP  HRQPPPVSH        0.0293      36413.1                  50.00     Sequence
   DRB1_1101    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.0289      36556.0                  50.00     Sequence
   DRB1_1101  109  SLGCGDGSPAEAYAS  LGCGDGSPA        0.0289      36573.4                  50.00     Sequence
   DRB1_1101  142  PARPAEGGAGSRGDS  AEGGAGSRG        0.0286      36673.6                  50.00     Sequence
   DRB1_1101   65  HPEGRPTNPPAAADA  RPTNPPAAA        0.0269      37382.7                  50.00     Sequence
   DRB1_1101   37  PDAGDPPPWQRAATR  PPWQRAATR        0.0262      37660.4                  50.00     Sequence
   DRB1_1101  110  LGCGDGSPAEAYASE  LGCGDGSPA        0.0245      38344.6                  50.00     Sequence
   DRB1_1101   69  RPTNPPAAADARLNR  PAAADARLN        0.0241      38541.8                  50.00     Sequence
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   DRB1_1101   30  ATGPGRIPDAGDPPP  ATGPGRIPD        0.0225      39177.1                  50.00     Sequence
   DRB1_1101   66  PEGRPTNPPAAADAR  RPTNPPAAA        0.0224      39240.2                  50.00     Sequence
   DRB1_1101  140  PAPARPAEGGAGSRG  PAPARPAEG        0.0214      39672.7                  50.00     Sequence
   DRB1_1101   10  SKGDGPNADGLVDRG  KGDGPNADG        0.0213      39721.7                  50.00     Sequence
   DRB1_1101  139  NPAPARPAEGGAGSR  PARPAEGGA        0.0212      39745.3                  50.00     Sequence
   DRB1_1101  114  DGSPAEAYASELPDL  EAYASELPD        0.0206      40016.3                  50.00     Sequence
   DRB1_1101   68  GRPTNPPAAADARLN  RPTNPPAAA        0.0204      40102.6                  50.00     Sequence
   DRB1_1101  141  APARPAEGGAGSRGD  AEGGAGSRG        0.0204      40113.0                  50.00     Sequence
   DRB1_1101   67  EGRPTNPPAAADARL  RPTNPPAAA        0.0196      40425.8                  50.00     Sequence
   DRB1_1101  113  GDGSPAEAYASELPD  EAYASELPD        0.0160      42062.4                  50.00     Sequence
   DRB1_1101  112  CGDGSPAEAYASELP  GSPAEAYAS        0.0149      42543.5                  50.00     Sequence
   DRB1_1101   31  TGPGRIPDAGDPPPW  TGPGRIPDA        0.0143      42855.3                  50.00     Sequence
   DRB1_1101  111  GCGDGSPAEAYASEL  GDGSPAEAY        0.0138      43077.1                  50.00     Sequence
   DRB1_1101  101  TPQPDPDASLGCGDG  DASLGCGDG        0.0136      43162.5                  50.00     Sequence
   DRB1_1101   33  PGRIPDAGDPPPWQR  IPDAGDPPP        0.0083      45687.2                  50.00     Sequence
   DRB1_1101   34  GRIPDAGDPPPWQRA  IPDAGDPPP        0.0079      45918.2                  50.00     Sequence
   DRB1_1101  100  RTPQPDPDASLGCGD  RTPQPDPDA        0.0078      45932.1                  50.00     Sequence
   DRB1_1101   35  RIPDAGDPPPWQRAA  IPDAGDPPP        0.0077      46025.1                  50.00     Sequence
   DRB1_1101   32  GPGRIPDAGDPPPWQ  PGRIPDAGD        0.0076      46059.0                  50.00     Sequence
   DRB1_1101   36  IPDAGDPPPWQRAAT  IPDAGDPPP        0.0068      46468.9                  50.00     Sequence
   DRB1_1101   99  VRTPQPDPDASLGCG  RTPQPDPDA        0.0066      46571.1                  50.00     Sequence
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Allele: DRB1_1101. Number of high binders 1. Number of weak binders 34. Number of peptides 290

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1302  266  IGLVNIVLMTALATI  IGLVNIVLM        0.7495         15.0           SB     0.80     Sequence
   DRB1_1302  265  LIGLVNIVLMTALAT  IGLVNIVLM        0.7394         16.8           SB     0.80     Sequence
   DRB1_1302  263  AFLIGLVNIVLMTAL  IGLVNIVLM        0.7285         18.9           SB     0.80     Sequence
   DRB1_1302  264  FLIGLVNIVLMTALA  IGLVNIVLM        0.7225         20.1           SB     0.80     Sequence
   DRB1_1302  261  GGAFLIGLVNIVLMT  IGLVNIVLM        0.6938         27.5           SB     2.00     Sequence
   DRB1_1302  262  GAFLIGLVNIVLMTA  IGLVNIVLM        0.6933         27.6           SB     2.00     Sequence
   DRB1_1302  267  GLVNIVLMTALATIG  IVLMTALAT        0.6776         32.7           SB     2.00     Sequence
   DRB1_1302  260  FGGAFLIGLVNIVLM  IGLVNIVLM        0.6760         33.3           SB     2.00     Sequence
   DRB1_1302  268  LVNIVLMTALATIGA  VLMTALATI        0.6633         38.2           SB     2.00     Sequence
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DRB1_1302  269  VNIVLMTALATIGAF  VLMTALATI        0.6518        43.3        SB      4.00       Sequence
DRB1_1302  198  WSTLKVSLLLSVALF  VSLLLSVAL        0.6304        54.5        WB      4.00       Sequence
DRB1_1302  197  PWSTLKVSLLLSVAL  VSLLLSVAL        0.6228        59.2        WB      4.00       Sequence
DRB1_1302  271  IVLMTALATIGAFVY  VLMTALATI        0.6012        74.8        WB      8.00       Sequence
DRB1_1302  270  NIVLMTALATIGAFV  VLMTALATI        0.6009        75.1        WB      8.00       Sequence
DRB1_1302  199  STLKVSLLLSVALFF  VSLLLSVAL        0.5957        79.4        WB      8.00       Sequence
DRB1_1302  200  TLKVSLLLSVALFFV  VSLLLSVAL        0.5872        87.1        WB      8.00       Sequence
DRB1_1302  201  LKVSLLLSVALFFVW  VSLLLSVAL        0.5844        89.7        WB      8.00       Sequence
DRB1_1302  202  KVSLLLSVALFFVWM  VSLLLSVAL        0.5622       114.1        WB      8.00       Sequence
DRB1_1302  192  IRRIDPWSTLKVSLL  WSTLKVSLL        0.5562       121.8        WB      8.00       Sequence
DRB1_1302  203  VSLLLSVALFFVWMI  VSLLLSVAL        0.5430       140.4        WB      8.00       Sequence
DRB1_1302  272  VLMTALATIGAFVYN  VLMTALATI        0.5390       146.6        WB      8.00       Sequence
DRB1_1302  193  RRIDPWSTLKVSLLL  WSTLKVSLL        0.5350       153.1        WB     16.00       Sequence
DRB1_1302  195  IDPWSTLKVSLLLSV  WSTLKVSLL        0.5209       178.4        WB     16.00       Sequence
DRB1_1302  196  DPWSTLKVSLLLSVA  WSTLKVSLL        0.5121       196.2        WB     16.00       Sequence
DRB1_1302  229  MGVWAKLNSNVGDLL  KLNSNVGDL        0.5011       221.1        WB     16.00       Sequence
DRB1_1302   78  DARLNRFISGASAPV  FISGASAPV        0.4857       261.2        WB     16.00       Sequence
DRB1_1302  194  RIDPWSTLKVSLLLS  WSTLKVSLL        0.4784       282.5        WB     16.00       Sequence
DRB1_1302   79  ARLNRFISGASAPVT  FISGASAPV        0.4774       285.7        WB     16.00       Sequence
DRB1_1302  259  IFGGAFLIGLVNIVL  LIGLVNIVL        0.4754       291.9        WB     16.00       Sequence
DRB1_1302  228  GMGVWAKLNSNVGDL  WAKLNSNVG        0.4748       293.8        WB     16.00       Sequence
DRB1_1302  211  LFFVWMITVAFLYLV  VWMITVAFL        0.4727       300.5        WB     16.00       Sequence
DRB1_1302  230  GVWAKLNSNVGDLLN  KLNSNVGDL        0.4724       301.3        WB     16.00       Sequence
DRB1_1302  281  GAFVYNLITDLIGGI  LITDLIGGI        0.4703       308.4        WB     16.00       Sequence
DRB1_1302  210  ALFFVWMITVAFLYL  VWMITVAFL        0.4663       322.0        WB     16.00       Sequence
DRB1_1302  227  GGMGVWAKLNSNVGD  WAKLNSNVG        0.4635       331.7        WB     16.00       Sequence
DRB1_1302   80  RLNRFISGASAPVTG  FISGASAPV        0.4612       340.1        WB     16.00       Sequence
DRB1_1302  181  RSRGPVRASMQIRRI  RASMQIRRI        0.4599       344.9        WB     16.00       Sequence
DRB1_1302  231  VWAKLNSNVGDLLNN  KLNSNVGDL        0.4590       348.4        WB     16.00       Sequence
DRB1_1302  221  FLYLVLGGMGVWAKL  LVLGGMGVW        0.4575       354.3        WB     16.00       Sequence
DRB1_1302  226  LGGMGVWAKLNSNVG  WAKLNSNVG        0.4527       373.1        WB     16.00       Sequence
DRB1_1302  209  VALFFVWMITVAFLY  VWMITVAFL        0.4525       374.0        WB     16.00       Sequence
DRB1_1302  282  AFVYNLITDLIGGIE  LITDLIGGI        0.4433       412.9        WB     32.00       Sequence
DRB1_1302  274  MTALATIGAFVYNLI  LATIGAFVY        0.4432       413.5        WB     32.00       Sequence
DRB1_1302  208  SVALFFVWMITVAFL  VWMITVAFL        0.4425       416.8        WB     32.00       Sequence
DRB1_1302  223  YLVLGGMGVWAKLNS  LVLGGMGVW        0.4410       423.5        WB     32.00       Sequence
DRB1_1302  222  LYLVLGGMGVWAKLN  LVLGGMGVW        0.4378       438.5        WB     32.00       Sequence
DRB1_1302  182  SRGPVRASMQIRRID  RASMQIRRI        0.4371       441.6        WB     32.00       Sequence
DRB1_1302  248  GSSAELVSSGTIFGG  AELVSSGTI        0.4362       446.1        WB     32.00       Sequence
DRB1_1302  247  SGSSAELVSSGTIFG  AELVSSGTI        0.4355       449.5        WB     32.00       Sequence
DRB1_1302   87  GASAPVTGPAAAVRT  PVTGPAAAV        0.4353       450.3        WB     32.00       Sequence
DRB1_1302  250  SAELVSSGTIFGGAF  AELVSSGTI        0.4343       455.2        WB     32.00       Sequence
DRB1_1302  212  FFVWMITVAFLYLVL  VWMITVAFL        0.4342       455.6        WB     32.00       Sequence
DRB1_1302  219  VAFLYLVLGGMGVWA  LVLGGMGVW        0.4318       467.8        WB     32.00       Sequence
DRB1_1302   81  LNRFISGASAPVTGP  FISGASAPV        0.4295       479.5        WB     32.00       Sequence
DRB1_1302  275  TALATIGAFVYNLIT  LATIGAFVY        0.4294       479.9        WB     32.00       Sequence
DRB1_1302  251  AELVSSGTIFGGAFL  AELVSSGTI        0.4280       487.4        WB     32.00       Sequence
DRB1_1302  218  TVAFLYLVLGGMGVW  LVLGGMGVW        0.4259       498.6        WB     32.00       Sequence
DRB1_1302  220  AFLYLVLGGMGVWAK  LVLGGMGVW        0.4257       499.7        WB     32.00       Sequence
DRB1_1302  249  SSAELVSSGTIFGGA  AELVSSGTI        0.4234       512.3               32.00       Sequence
DRB1_1302   88  ASAPVTGPAAAVRTP  PVTGPAAAV        0.4221       519.6               32.00       Sequence
DRB1_1302  246  ASGSSAELVSSGTIF  AELVSSGTI        0.4192       536.1               32.00       Sequence
DRB1_1302  232  WAKLNSNVGDLLNNA  KLNSNVGDL        0.4151       560.2               32.00       Sequence
DRB1_1302  273  LMTALATIGAFVYNL  LATIGAFVY        0.4113       583.9               32.00       Sequence
DRB1_1302  283  FVYNLITDLIGGIEV  LITDLIGGI        0.4113       584.0               32.00       Sequence
DRB1_1302  276  ALATIGAFVYNLITD  LATIGAFVY        0.4106       588.3               32.00       Sequence
DRB1_1302  285  YNLITDLIGGIEVTL  LITDLIGGI        0.4088       599.6               32.00       Sequence
DRB1_1302  183  RGPVRASMQIRRIDP  RASMQIRRI        0.4079       605.7               32.00       Sequence
DRB1_1302  277  LATIGAFVYNLITDL  LATIGAFVY        0.4015       649.3               32.00       Sequence
DRB1_1302  213  FVWMITVAFLYLVLG  VWMITVAFL        0.3999       660.6               32.00       Sequence
DRB1_1302  284  VYNLITDLIGGIEVT  LITDLIGGI        0.3990       667.1               32.00       Sequence
DRB1_1302   82  NRFISGASAPVTGPA  FISGASAPV        0.3989       667.6               32.00       Sequence
DRB1_1302  187  RASMQIRRIDPWSTL  RRIDPWSTL        0.3988       668.7               32.00       Sequence
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DRB1_1302  184  GPVRASMQIRRIDPW  RASMQIRRI        0.3965        685.0              32.00      Sequence
DRB1_1302   86  SGASAPVTGPAAAVR  PVTGPAAAV        0.3956        691.6              32.00      Sequence
DRB1_1302   89  SAPVTGPAAAVRTPQ  PVTGPAAAV        0.3939        704.6              32.00      Sequence
DRB1_1302  278  ATIGAFVYNLITDLI  VYNLITDLI        0.3921        718.9              32.00      Sequence
DRB1_1302  224  LVLGGMGVWAKLNSN  LVLGGMGVW        0.3908        728.8              32.00      Sequence
DRB1_1302   85  ISGASAPVTGPAAAV  PVTGPAAAV        0.3882        749.8              32.00      Sequence
DRB1_1302  279  TIGAFVYNLITDLIG  VYNLITDLI        0.3802        817.2              32.00      Sequence
DRB1_1302  286  NLITDLIGGIEVTLA  LITDLIGGI        0.3769        846.7              32.00      Sequence
DRB1_1302  189  SMQIRRIDPWSTLKV  RRIDPWSTL        0.3745        869.6              32.00      Sequence
DRB1_1302   83  RFISGASAPVTGPAA  FISGASAPV        0.3727        886.6              32.00      Sequence
DRB1_1302  207  LSVALFFVWMITVAF  LFFVWMITV        0.3664        948.6              32.00      Sequence
DRB1_1302   90  APVTGPAAAVRTPQP  PVTGPAAAV        0.3664        948.8              32.00      Sequence
DRB1_1302  252  ELVSSGTIFGGAFLI  ELVSSGTIF        0.3586       1033.1              32.00      Sequence
DRB1_1302  233  AKLNSNVGDLLNNAS  KLNSNVGDL        0.3554       1068.6              32.00      Sequence
DRB1_1302  190  MQIRRIDPWSTLKVS  RRIDPWSTL        0.3552       1071.4              32.00      Sequence
DRB1_1302  280  IGAFVYNLITDLIGG  VYNLITDLI        0.3540       1085.5              32.00      Sequence
DRB1_1302  287  LITDLIGGIEVTLAD  LITDLIGGI        0.3504       1128.4              32.00      Sequence
DRB1_1302  180  RRSRGPVRASMQIRR  GPVRASMQI        0.3492       1143.4              32.00      Sequence
DRB1_1302  225  VLGGMGVWAKLNSNV  VWAKLNSNV        0.3450       1196.5              32.00      Sequence
DRB1_1302  214  VWMITVAFLYLVLGG  VWMITVAFL        0.3427       1226.1              32.00      Sequence
DRB1_1302   84  FISGASAPVTGPAAA  FISGASAPV        0.3408       1251.8              32.00      Sequence
DRB1_1302  185  PVRASMQIRRIDPWS  RASMQIRRI        0.3378       1292.8              32.00      Sequence
DRB1_1302  245  NASGSSAELVSSGTI  AELVSSGTI        0.3337       1352.4              32.00      Sequence
DRB1_1302  169  ESRDARVQLSARRSR  RVQLSARRS        0.3325       1370.0              32.00      Sequence
DRB1_1302  191  QIRRIDPWSTLKVSL  RRIDPWSTL        0.3319       1378.7              32.00      Sequence
DRB1_1302  188  ASMQIRRIDPWSTLK  RRIDPWSTL        0.3307       1396.0              32.00      Sequence
DRB1_1302  239  VGDLLNNASGSSAEL  LNNASGSSA        0.3281       1435.6              50.00      Sequence
DRB1_1302  186  VRASMQIRRIDPWST  RASMQIRRI        0.3281       1436.3              50.00      Sequence
DRB1_1302   91  PVTGPAAAVRTPQPD  PVTGPAAAV        0.3260       1469.6              50.00      Sequence
DRB1_1302  237  SNVGDLLNNASGSSA  LLNNASGSS        0.3258       1471.8              50.00      Sequence
DRB1_1302  170  SRDARVQLSARRSRG  RVQLSARRS        0.3234       1510.8              50.00      Sequence
DRB1_1302  205  LLLSVALFFVWMITV  LFFVWMITV        0.3234       1511.6              50.00      Sequence
DRB1_1302  234  KLNSNVGDLLNNASG  KLNSNVGDL        0.3214       1544.8              50.00      Sequence
DRB1_1302  179  ARRSRGPVRASMQIR  GPVRASMQI        0.3200       1567.6              50.00      Sequence
DRB1_1302  240  GDLLNNASGSSAELV  LNNASGSSA        0.3165       1627.8              50.00      Sequence
DRB1_1302  238  NVGDLLNNASGSSAE  LNNASGSSA        0.3158       1641.2              50.00      Sequence
DRB1_1302  178  SARRSRGPVRASMQI  GPVRASMQI        0.3113       1721.7              50.00      Sequence
DRB1_1302  168  AESRDARVQLSARRS  RVQLSARRS        0.3099       1749.4              50.00      Sequence
DRB1_1302  258  TIFGGAFLIGLVNIV  FLIGLVNIV        0.3014       1917.1              50.00      Sequence
DRB1_1302  206  LLSVALFFVWMITVA  LFFVWMITV        0.3013       1919.0              50.00      Sequence
DRB1_1302  204  SLLLSVALFFVWMIT  SLLLSVALF        0.3009       1927.0              50.00      Sequence
DRB1_1302  241  DLLNNASGSSAELVS  LNNASGSSA        0.2901       2166.3              50.00      Sequence
DRB1_1302  171  RDARVQLSARRSRGP  RVQLSARRS        0.2809       2393.5              50.00      Sequence
DRB1_1302  217  ITVAFLYLVLGGMGV  YLVLGGMGV        0.2749       2553.2              50.00      Sequence
DRB1_1302  253  LVSSGTIFGGAFLIG  TIFGGAFLI        0.2705       2678.8              50.00      Sequence
DRB1_1302  172  DARVQLSARRSRGPV  RVQLSARRS        0.2683       2744.1              50.00      Sequence
DRB1_1302  242  LLNNASGSSAELVSS  LNNASGSSA        0.2645       2859.7              50.00      Sequence
DRB1_1302  215  WMITVAFLYLVLGGM  MITVAFLYL        0.2615       2951.9              50.00      Sequence
DRB1_1302  236  NSNVGDLLNNASGSS  LLNNASGSS        0.2608       2974.8              50.00      Sequence
DRB1_1302  173  ARVQLSARRSRGPVR  RVQLSARRS        0.2600       2999.9              50.00      Sequence
DRB1_1302  254  VSSGTIFGGAFLIGL  TIFGGAFLI        0.2592       3028.4              50.00      Sequence
DRB1_1302  255  SSGTIFGGAFLIGLV  TIFGGAFLI        0.2574       3086.8              50.00      Sequence
DRB1_1302   15  PNADGLVDRGGAHRA  VDRGGAHRA        0.2571       3097.3              50.00      Sequence
DRB1_1302   22  DRGGAHRAATGPGRI  RAATGPGRI        0.2561       3129.1              50.00      Sequence
DRB1_1302  112  CGDGSPAEAYASELP  PAEAYASEL        0.2556       3148.2              50.00      Sequence
DRB1_1302  235  LNSNVGDLLNNASGS  LNSNVGDLL        0.2531       3235.0              50.00      Sequence
DRB1_1302  111  GCGDGSPAEAYASEL  PAEAYASEL        0.2526       3249.2              50.00      Sequence
DRB1_1302   16  NADGLVDRGGAHRAA  VDRGGAHRA        0.2471       3450.2              50.00      Sequence
DRB1_1302   18  DGLVDRGGAHRAATG  VDRGGAHRA        0.2447       3540.1              50.00      Sequence
DRB1_1302  256  SGTIFGGAFLIGLVN  TIFGGAFLI        0.2434       3592.4              50.00      Sequence
DRB1_1302   23  RGGAHRAATGPGRIP  RAATGPGRI        0.2407       3698.3              50.00      Sequence
DRB1_1302  113  GDGSPAEAYASELPD  PAEAYASEL        0.2394       3748.4              50.00      Sequence
DRB1_1302   17  ADGLVDRGGAHRAAT  VDRGGAHRA        0.2394       3749.3              50.00      Sequence
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DRB1_1302   19  GLVDRGGAHRAATGP  VDRGGAHRA        0.2347       3944.6              50.00      Sequence
DRB1_1302  216  MITVAFLYLVLGGMG  ITVAFLYLV        0.2341       3969.8              50.00      Sequence
DRB1_1302  257  GTIFGGAFLIGLVNI  AFLIGLVNI        0.2338       3983.9              50.00      Sequence
DRB1_1302  167  TAESRDARVQLSARR  ARVQLSARR        0.2266       4306.3              50.00      Sequence
DRB1_1302   24  GGAHRAATGPGRIPD  RAATGPGRI        0.2258       4344.0              50.00      Sequence
DRB1_1302  114  DGSPAEAYASELPDL  PAEAYASEL        0.2243       4413.3              50.00      Sequence
DRB1_1302  115  GSPAEAYASELPDLS  PAEAYASEL        0.2150       4885.1              50.00      Sequence
DRB1_1302   25  GAHRAATGPGRIPDA  RAATGPGRI        0.2140       4934.1              50.00      Sequence
DRB1_1302   63  VSHPEGRPTNPPAAA  RPTNPPAAA        0.2134       4967.7              50.00      Sequence
DRB1_1302  288  ITDLIGGIEVTLADR  LIGGIEVTL        0.2114       5075.8              50.00      Sequence
DRB1_1302  243  LNNASGSSAELVSSG  LNNASGSSA        0.2090       5212.4              50.00      Sequence
DRB1_1302  174  RVQLSARRSRGPVRA  RVQLSARRS        0.2083       5249.2              50.00      Sequence
DRB1_1302  164  RSITAESRDARVQLS  TAESRDARV        0.1982       5854.1              50.00      Sequence
DRB1_1302   14  GPNADGLVDRGGAHR  GLVDRGGAH        0.1978       5879.6              50.00      Sequence
DRB1_1302   26  AHRAATGPGRIPDAG  RAATGPGRI        0.1976       5892.1              50.00      Sequence
DRB1_1302  116  SPAEAYASELPDLSG  PAEAYASEL        0.1942       6118.6              50.00      Sequence
DRB1_1302  289  TDLIGGIEVTLADRD  LIGGIEVTL        0.1920       6263.0              50.00      Sequence
DRB1_1302  163  GRSITAESRDARVQL  TAESRDARV        0.1861       6674.4              50.00      Sequence
DRB1_1302   45  WQRAATRQSQAGHRQ  RQSQAGHRQ        0.1853       6731.6              50.00      Sequence
DRB1_1302  117  PAEAYASELPDLSGP  PAEAYASEL        0.1851       6745.1              50.00      Sequence
DRB1_1302   77  ADARLNRFISGASAP  NRFISGASA        0.1850       6758.7              50.00      Sequence
DRB1_1302   64  SHPEGRPTNPPAAAD  RPTNPPAAA        0.1848       6773.0              50.00      Sequence
DRB1_1302   27  HRAATGPGRIPDAGD  RAATGPGRI        0.1829       6912.5              50.00      Sequence
DRB1_1302  165  SITAESRDARVQLSA  TAESRDARV        0.1826       6933.0              50.00      Sequence
DRB1_1302  161  SGGRSITAESRDARV  TAESRDARV        0.1808       7067.4              50.00      Sequence
DRB1_1302   65  HPEGRPTNPPAAADA  RPTNPPAAA        0.1782       7268.8              50.00      Sequence
DRB1_1302  177  LSARRSRGPVRASMQ  RGPVRASMQ        0.1752       7510.8              50.00      Sequence
DRB1_1302   20  LVDRGGAHRAATGPG  VDRGGAHRA        0.1746       7559.3              50.00      Sequence
DRB1_1302   28  RAATGPGRIPDAGDP  RAATGPGRI        0.1736       7642.5              50.00      Sequence
DRB1_1302  166  ITAESRDARVQLSAR  TAESRDARV        0.1726       7727.7              50.00      Sequence
DRB1_1302  162  GGRSITAESRDARVQ  TAESRDARV        0.1706       7898.5              50.00      Sequence
DRB1_1302   92  VTGPAAAVRTPQPDP  TGPAAAVRT        0.1698       7964.7              50.00      Sequence
DRB1_1302   76  AADARLNRFISGASA  NRFISGASA        0.1641       8472.2              50.00      Sequence
DRB1_1302   66  PEGRPTNPPAAADAR  RPTNPPAAA        0.1638       8501.3              50.00      Sequence
DRB1_1302   13  DGPNADGLVDRGGAH  GLVDRGGAH        0.1620       8667.2              50.00      Sequence
DRB1_1302   46  QRAATRQSQAGHRQP  RQSQAGHRQ        0.1619       8676.6              50.00      Sequence
DRB1_1302   67  EGRPTNPPAAADARL  RPTNPPAAA        0.1613       8732.3              50.00      Sequence
DRB1_1302   44  PWQRAATRQSQAGHR  WQRAATRQS        0.1609       8770.1              50.00      Sequence
DRB1_1302   43  PPWQRAATRQSQAGH  WQRAATRQS        0.1591       8937.6              50.00      Sequence
DRB1_1302   68  GRPTNPPAAADARLN  RPTNPPAAA        0.1547       9380.6              50.00      Sequence
DRB1_1302   41  DPPPWQRAATRQSQA  RAATRQSQA        0.1516       9695.8              50.00      Sequence
DRB1_1302   21  VDRGGAHRAATGPGR  VDRGGAHRA        0.1479      10097.0              50.00      Sequence
DRB1_1302   42  PPPWQRAATRQSQAG  WQRAATRQS        0.1448      10440.1              50.00      Sequence
DRB1_1302   47  RAATRQSQAGHRQPP  RQSQAGHRQ        0.1443      10498.7              50.00      Sequence
DRB1_1302   39  AGDPPPWQRAATRQS  WQRAATRQS        0.1426      10688.2              50.00      Sequence
DRB1_1302   93  TGPAAAVRTPQPDPD  TGPAAAVRT        0.1416      10810.0              50.00      Sequence
DRB1_1302  104  PDPDASLGCGDGSPA  LGCGDGSPA        0.1401      10980.2              50.00      Sequence
DRB1_1302   40  GDPPPWQRAATRQSQ  WQRAATRQS        0.1388      11135.8              50.00      Sequence
DRB1_1302  109  SLGCGDGSPAEAYAS  LGCGDGSPA        0.1385      11177.7              50.00      Sequence
DRB1_1302  110  LGCGDGSPAEAYASE  LGCGDGSPA        0.1372      11331.8              50.00      Sequence
DRB1_1302  105  DPDASLGCGDGSPAE  LGCGDGSPA        0.1364      11434.7              50.00      Sequence
DRB1_1302   62  PVSHPEGRPTNPPAA  GRPTNPPAA        0.1358      11498.9              50.00      Sequence
DRB1_1302   49  ATRQSQAGHRQPPPV  RQSQAGHRQ        0.1346      11656.5              50.00      Sequence
DRB1_1302  244  NNASGSSAELVSSGT  NASGSSAEL        0.1342      11699.1              50.00      Sequence
DRB1_1302   70  PTNPPAAADARLNRF  AADARLNRF        0.1331      11845.7              50.00      Sequence
DRB1_1302  132  TPRAPQRNPAPARPA  QRNPAPARP        0.1318      12015.1              50.00      Sequence
DRB1_1302   75  AAADARLNRFISGAS  AADARLNRF        0.1269      12670.1              50.00      Sequence
DRB1_1302  107  DASLGCGDGSPAEAY  LGCGDGSPA        0.1260      12795.6              50.00      Sequence
DRB1_1302   69  RPTNPPAAADARLNR  RPTNPPAAA        0.1254      12878.9              50.00      Sequence
DRB1_1302  133  PRAPQRNPAPARPAE  QRNPAPARP        0.1233      13173.3              50.00      Sequence
DRB1_1302  106  PDASLGCGDGSPAEA  LGCGDGSPA        0.1232      13183.2              50.00      Sequence
DRB1_1302   48  AATRQSQAGHRQPPP  RQSQAGHRQ        0.1229      13222.4              50.00      Sequence
DRB1_1302  131  PTPRAPQRNPAPARP  QRNPAPARP        0.1227      13258.8              50.00      Sequence
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DRB1_1302   71  TNPPAAADARLNRFI  AADARLNRF        0.1226      13263.4              50.00      Sequence
DRB1_1302  108  ASLGCGDGSPAEAYA  LGCGDGSPA        0.1212      13474.9              50.00      Sequence
DRB1_1302   73  PPAAADARLNRFISG  AADARLNRF        0.1208      13535.8              50.00      Sequence
DRB1_1302  134  RAPQRNPAPARPAEG  QRNPAPARP        0.1178      13979.5              50.00      Sequence
DRB1_1302    0  VTAPNEPGALSKGDG  TAPNEPGAL        0.1172      14067.5              50.00      Sequence
DRB1_1302    1  TAPNEPGALSKGDGP  TAPNEPGAL        0.1151      14394.4              50.00      Sequence
DRB1_1302   74  PAAADARLNRFISGA  AADARLNRF        0.1149      14421.5              50.00      Sequence
DRB1_1302    8  ALSKGDGPNADGLVD  LSKGDGPNA        0.1143      14522.1              50.00      Sequence
DRB1_1302  175  VQLSARRSRGPVRAS  RRSRGPVRA        0.1141      14544.5              50.00      Sequence
DRB1_1302   50  TRQSQAGHRQPPPVS  RQSQAGHRQ        0.1138      14594.8              50.00      Sequence
DRB1_1302  130  GPTPRAPQRNPAPAR  APQRNPAPA        0.1130      14727.1              50.00      Sequence
DRB1_1302   72  NPPAAADARLNRFIS  AADARLNRF        0.1110      15043.7              50.00      Sequence
DRB1_1302    9  LSKGDGPNADGLVDR  LSKGDGPNA        0.1097      15263.1              50.00      Sequence
DRB1_1302  157  AAGSSGGRSITAESR  SSGGRSITA        0.1078      15570.7              50.00      Sequence
DRB1_1302    7  GALSKGDGPNADGLV  LSKGDGPNA        0.1077      15591.9              50.00      Sequence
DRB1_1302  129  SGPTPRAPQRNPAPA  APQRNPAPA        0.1066      15770.9              50.00      Sequence
DRB1_1302  156  SAAGSSGGRSITAES  SSGGRSITA        0.1064      15809.6              50.00      Sequence
DRB1_1302   51  RQSQAGHRQPPPVSH  RQSQAGHRQ        0.1022      16555.3              50.00      Sequence
DRB1_1302  158  AGSSGGRSITAESRD  SSGGRSITA        0.0990      17138.9              50.00      Sequence
DRB1_1302  176  QLSARRSRGPVRASM  RRSRGPVRA        0.0988      17174.6              50.00      Sequence
DRB1_1302  160  SSGGRSITAESRDAR  SSGGRSITA        0.0982      17282.3              50.00      Sequence
DRB1_1302  155  DSAAGSSGGRSITAE  SSGGRSITA        0.0968      17550.6              50.00      Sequence
DRB1_1302  159  GSSGGRSITAESRDA  SSGGRSITA        0.0964      17627.5              50.00      Sequence
DRB1_1302  154  GDSAAGSSGGRSITA  SSGGRSITA        0.0958      17731.4              50.00      Sequence
DRB1_1302   57  HRQPPPVSHPEGRPT  VSHPEGRPT        0.0886      19162.6              50.00      Sequence
DRB1_1302  135  APQRNPAPARPAEGG  QRNPAPARP        0.0863      19655.4              50.00      Sequence
DRB1_1302   58  RQPPPVSHPEGRPTN  VSHPEGRPT        0.0853      19862.8              50.00      Sequence
DRB1_1302  147  EGGAGSRGDSAAGSS  GSRGDSAAG        0.0829      20389.3              50.00      Sequence
DRB1_1302  148  GGAGSRGDSAAGSSG  GSRGDSAAG        0.0827      20433.4              50.00      Sequence
DRB1_1302   94  GPAAAVRTPQPDPDA  AAAVRTPQP        0.0811      20795.4              50.00      Sequence
DRB1_1302    4  NEPGALSKGDGPNAD  LSKGDGPNA        0.0792      21234.0              50.00      Sequence
DRB1_1302  146  AEGGAGSRGDSAAGS  GSRGDSAAG        0.0791      21234.7              50.00      Sequence
DRB1_1302   10  SKGDGPNADGLVDRG  DGPNADGLV        0.0777      21580.1              50.00      Sequence
DRB1_1302  149  GAGSRGDSAAGSSGG  GSRGDSAAG        0.0776      21592.9              50.00      Sequence
DRB1_1302    5  EPGALSKGDGPNADG  LSKGDGPNA        0.0774      21643.4              50.00      Sequence
DRB1_1302  150  AGSRGDSAAGSSGGR  GSRGDSAAG        0.0768      21776.6              50.00      Sequence
DRB1_1302    3  PNEPGALSKGDGPNA  LSKGDGPNA        0.0763      21911.1              50.00      Sequence
DRB1_1302  145  PAEGGAGSRGDSAAG  GSRGDSAAG        0.0758      22009.7              50.00      Sequence
DRB1_1302  128  LSGPTPRAPQRNPAP  RAPQRNPAP        0.0756      22057.9              50.00      Sequence
DRB1_1302  153  RGDSAAGSSGGRSIT  AGSSGGRSI        0.0755      22087.2              50.00      Sequence
DRB1_1302   59  QPPPVSHPEGRPTNP  VSHPEGRPT        0.0752      22155.9              50.00      Sequence
DRB1_1302   61  PPVSHPEGRPTNPPA  VSHPEGRPT        0.0737      22515.3              50.00      Sequence
DRB1_1302    6  PGALSKGDGPNADGL  LSKGDGPNA        0.0720      22934.2              50.00      Sequence
DRB1_1302   11  KGDGPNADGLVDRGG  DGPNADGLV        0.0709      23210.3              50.00      Sequence
DRB1_1302  151  GSRGDSAAGSSGGRS  GSRGDSAAG        0.0704      23349.1              50.00      Sequence
DRB1_1302  152  SRGDSAAGSSGGRSI  AGSSGGRSI        0.0681      23923.0              50.00      Sequence
DRB1_1302   52  QSQAGHRQPPPVSHP  AGHRQPPPV        0.0676      24051.2              50.00      Sequence
DRB1_1302  137  QRNPAPARPAEGGAG  QRNPAPARP        0.0673      24139.3              50.00      Sequence
DRB1_1302   60  PPPVSHPEGRPTNPP  VSHPEGRPT        0.0669      24251.9              50.00      Sequence
DRB1_1302   53  SQAGHRQPPPVSHPE  AGHRQPPPV        0.0663      24400.6              50.00      Sequence
DRB1_1302  136  PQRNPAPARPAEGGA  QRNPAPARP        0.0643      24940.6              50.00      Sequence
DRB1_1302   38  DAGDPPPWQRAATRQ  PPWQRAATR        0.0634      25177.5              50.00      Sequence
DRB1_1302   12  GDGPNADGLVDRGGA  DGPNADGLV        0.0625      25418.4              50.00      Sequence
DRB1_1302   54  QAGHRQPPPVSHPEG  RQPPPVSHP        0.0620      25571.2              50.00      Sequence
DRB1_1302  121  YASELPDLSGPTPRA  DLSGPTPRA        0.0603      26043.1              50.00      Sequence
DRB1_1302   55  AGHRQPPPVSHPEGR  RQPPPVSHP        0.0598      26189.2              50.00      Sequence
DRB1_1302  122  ASELPDLSGPTPRAP  DLSGPTPRA        0.0543      27800.1              50.00      Sequence
DRB1_1302  124  ELPDLSGPTPRAPQR  DLSGPTPRA        0.0535      28029.0              50.00      Sequence
DRB1_1302  118  AEAYASELPDLSGPT  ELPDLSGPT        0.0534      28049.7              50.00      Sequence
DRB1_1302  123  SELPDLSGPTPRAPQ  ELPDLSGPT        0.0531      28137.5              50.00      Sequence
DRB1_1302   97  AAVRTPQPDPDASLG  PQPDPDASL        0.0531      28138.4              50.00      Sequence
DRB1_1302   96  AAAVRTPQPDPDASL  PQPDPDASL        0.0517      28588.0              50.00      Sequence
DRB1_1302  138  RNPAPARPAEGGAGS  RNPAPARPA        0.0516      28614.0              50.00      Sequence
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   DRB1_1302   98  AVRTPQPDPDASLGC  PQPDPDASL        0.0489      29471.5                50.00      Sequence
   DRB1_1302  143  ARPAEGGAGSRGDSA  ARPAEGGAG        0.0472      30004.9                50.00      Sequence
   DRB1_1302   56  GHRQPPPVSHPEGRP  RQPPPVSHP        0.0468      30133.5                50.00      Sequence
   DRB1_1302  125  LPDLSGPTPRAPQRN  DLSGPTPRA        0.0466      30194.5                50.00      Sequence
   DRB1_1302  119  EAYASELPDLSGPTP  ELPDLSGPT        0.0460      30391.8                50.00      Sequence
   DRB1_1302    2  APNEPGALSKGDGPN  GALSKGDGP        0.0459      30436.9                50.00      Sequence
   DRB1_1302  120  AYASELPDLSGPTPR  ELPDLSGPT        0.0458      30455.3                50.00      Sequence
   DRB1_1302  139  NPAPARPAEGGAGSR  ARPAEGGAG        0.0447      30829.3                50.00      Sequence
   DRB1_1302  140  PAPARPAEGGAGSRG  RPAEGGAGS        0.0444      30917.8                50.00      Sequence
   DRB1_1302   99  VRTPQPDPDASLGCG  PQPDPDASL        0.0442      31002.9                50.00      Sequence
   DRB1_1302  141  APARPAEGGAGSRGD  ARPAEGGAG        0.0441      31015.0                50.00      Sequence
   DRB1_1302  102  PQPDPDASLGCGDGS  PQPDPDASL        0.0429      31425.7                50.00      Sequence
   DRB1_1302  142  PARPAEGGAGSRGDS  ARPAEGGAG        0.0427      31490.1                50.00      Sequence
   DRB1_1302   32  GPGRIPDAGDPPPWQ  RIPDAGDPP        0.0427      31507.8                50.00      Sequence
   DRB1_1302   95  PAAAVRTPQPDPDAS  AAAVRTPQP        0.0423      31635.9                50.00      Sequence
   DRB1_1302  126  PDLSGPTPRAPQRNP  DLSGPTPRA        0.0421      31720.2                50.00      Sequence
   DRB1_1302   29  AATGPGRIPDAGDPP  RIPDAGDPP        0.0414      31938.9                50.00      Sequence
   DRB1_1302  127  DLSGPTPRAPQRNPA  DLSGPTPRA        0.0408      32145.5                50.00      Sequence
   DRB1_1302  144  RPAEGGAGSRGDSAA  GAGSRGDSA        0.0404      32293.3                50.00      Sequence
   DRB1_1302   37  PDAGDPPPWQRAATR  PPWQRAATR        0.0397      32533.2                50.00      Sequence
   DRB1_1302   33  PGRIPDAGDPPPWQR  RIPDAGDPP        0.0396      32559.6                50.00      Sequence
   DRB1_1302  100  RTPQPDPDASLGCGD  PQPDPDASL        0.0379      33179.1                50.00      Sequence
   DRB1_1302   34  GRIPDAGDPPPWQRA  RIPDAGDPP        0.0377      33248.8                50.00      Sequence
   DRB1_1302  101  TPQPDPDASLGCGDG  PQPDPDASL        0.0375      33311.9                50.00      Sequence
   DRB1_1302   31  TGPGRIPDAGDPPPW  RIPDAGDPP        0.0355      34038.7                50.00      Sequence
   DRB1_1302   30  ATGPGRIPDAGDPPP  RIPDAGDPP        0.0345      34415.0                50.00      Sequence
   DRB1_1302  103  QPDPDASLGCGDGSP  ASLGCGDGS        0.0295      36346.6                50.00      Sequence
   DRB1_1302   35  RIPDAGDPPPWQRAA  RIPDAGDPP        0.0264      37581.0                50.00      Sequence
   DRB1_1302   36  IPDAGDPPPWQRAAT  GDPPPWQRA        0.0218      39512.9                50.00      Sequence
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Allele: DRB1_1302. Number of high binders 10. Number of weak binders 48. Number of peptides 290

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random      Identity
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   DRB1_1501  222  LYLVLGGMGVWAKLN  VLGGMGVWA        0.7642         12.8         SB     0.40      Sequence
   DRB1_1501  224  LVLGGMGVWAKLNSN  VLGGMGVWA        0.7517         14.7         SB     0.80      Sequence
   DRB1_1501  223  YLVLGGMGVWAKLNS  VLGGMGVWA        0.7515         14.7         SB     0.80      Sequence
   DRB1_1501  221  FLYLVLGGMGVWAKL  VLGGMGVWA        0.7504         14.9         SB     0.80      Sequence
   DRB1_1501  220  AFLYLVLGGMGVWAK  VLGGMGVWA        0.7337         17.8         SB     0.80      Sequence
   DRB1_1501  225  VLGGMGVWAKLNSNV  VLGGMGVWA        0.6696         35.7         SB     4.00      Sequence
   DRB1_1501  219  VAFLYLVLGGMGVWA  VLGGMGVWA        0.6521         43.1         SB     4.00      Sequence
   DRB1_1501  199  STLKVSLLLSVALFF  KVSLLLSVA        0.6358         51.5         WB     4.00      Sequence
   DRB1_1501  200  TLKVSLLLSVALFFV  KVSLLLSVA        0.6310         54.2         WB     4.00      Sequence
   DRB1_1501   78  DARLNRFISGASAPV  RLNRFISGA        0.6295         55.1         WB     4.00      Sequence
   DRB1_1501   79  ARLNRFISGASAPVT  RLNRFISGA        0.6282         55.9         WB     4.00      Sequence
   DRB1_1501  267  GLVNIVLMTALATIG  NIVLMTALA        0.6279         56.0         WB     8.00      Sequence
   DRB1_1501  268  LVNIVLMTALATIGA  NIVLMTALA        0.6195         61.4         WB     8.00      Sequence
   DRB1_1501  269  VNIVLMTALATIGAF  NIVLMTALA        0.6175         62.7         WB     8.00      Sequence
   DRB1_1501  198  WSTLKVSLLLSVALF  KVSLLLSVA        0.6137         65.3         WB     8.00      Sequence
   DRB1_1501  201  LKVSLLLSVALFFVW  KVSLLLSVA        0.6094         68.4         WB     8.00      Sequence
   DRB1_1501   77  ADARLNRFISGASAP  RLNRFISGA        0.5983         77.2         WB     8.00      Sequence
   DRB1_1501  270  NIVLMTALATIGAFV  NIVLMTALA        0.5881         86.2         WB     8.00      Sequence
   DRB1_1501   80  RLNRFISGASAPVTG  RLNRFISGA        0.5873         86.9         WB     8.00      Sequence
   DRB1_1501  266  IGLVNIVLMTALATI  NIVLMTALA        0.5799         94.2         WB     8.00      Sequence
   DRB1_1501   76  AADARLNRFISGASA  RLNRFISGA        0.5681        107.0         WB     8.00      Sequence
   DRB1_1501  265  LIGLVNIVLMTALAT  NIVLMTALA        0.5650        110.7         WB    16.00      Sequence
   DRB1_1501  202  KVSLLLSVALFFVWM  KVSLLLSVA        0.5585        118.8         WB    16.00      Sequence
   DRB1_1501  197  PWSTLKVSLLLSVAL  KVSLLLSVA        0.5391        146.4         WB    16.00      Sequence
   DRB1_1501  264  FLIGLVNIVLMTALA  NIVLMTALA        0.5268        167.4         WB    16.00      Sequence
   DRB1_1501   75  AAADARLNRFISGAS  RLNRFISGA        0.5248        170.9         WB    16.00      Sequence
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DRB1_1501  189  SMQIRRIDPWSTLKV  QIRRIDPWS       0.5168       186.4       WB    16.00      Sequence
DRB1_1501  191  QIRRIDPWSTLKVSL  RIDPWSTLK       0.5143       191.5       WB    16.00      Sequence
DRB1_1501  190  MQIRRIDPWSTLKVS  QIRRIDPWS       0.5127       194.9       WB    16.00      Sequence
DRB1_1501  286  NLITDLIGGIEVTLA  LIGGIEVTL       0.5082       204.6       WB    16.00      Sequence
DRB1_1501  218  TVAFLYLVLGGMGVW  LVLGGMGVW       0.4996       224.6       WB    16.00      Sequence
DRB1_1501  287  LITDLIGGIEVTLAD  LIGGIEVTL       0.4945       237.3       WB    16.00      Sequence
DRB1_1501  186  VRASMQIRRIDPWST  QIRRIDPWS       0.4888       252.5       WB    32.00      Sequence
DRB1_1501  187  RASMQIRRIDPWSTL  QIRRIDPWS       0.4872       256.8       WB    32.00      Sequence
DRB1_1501  188  ASMQIRRIDPWSTLK  QIRRIDPWS       0.4847       263.8       WB    32.00      Sequence
DRB1_1501  273  LMTALATIGAFVYNL  LMTALATIG       0.4827       269.7       WB    32.00      Sequence
DRB1_1501  173  ARVQLSARRSRGPVR  ARVQLSARR       0.4808       275.2       WB    32.00      Sequence
DRB1_1501  272  VLMTALATIGAFVYN  LMTALATIG       0.4806       275.9       WB    32.00      Sequence
DRB1_1501  288  ITDLIGGIEVTLADR  LIGGIEVTL       0.4787       281.6       WB    32.00      Sequence
DRB1_1501  248  GSSAELVSSGTIFGG  ELVSSGTIF       0.4782       283.1       WB    32.00      Sequence
DRB1_1501  285  YNLITDLIGGIEVTL  LIGGIEVTL       0.4736       297.7       WB    32.00      Sequence
DRB1_1501  172  DARVQLSARRSRGPV  QLSARRSRG       0.4724       301.5       WB    32.00      Sequence
DRB1_1501  247  SGSSAELVSSGTIFG  ELVSSGTIF       0.4718       303.5       WB    32.00      Sequence
DRB1_1501   81  LNRFISGASAPVTGP  RFISGASAP       0.4717       303.6       WB    32.00      Sequence
DRB1_1501  249  SSAELVSSGTIFGGA  ELVSSGTIF       0.4693       311.8       WB    32.00      Sequence
DRB1_1501  271  IVLMTALATIGAFVY  LMTALATIG       0.4658       323.7       WB    32.00      Sequence
DRB1_1501  226  LGGMGVWAKLNSNVG  LGGMGVWAK       0.4658       323.8       WB    32.00      Sequence
DRB1_1501  185  PVRASMQIRRIDPWS  QIRRIDPWS       0.4655       324.7       WB    32.00      Sequence
DRB1_1501  289  TDLIGGIEVTLADRD  LIGGIEVTL       0.4649       326.9       WB    32.00      Sequence
DRB1_1501  274  MTALATIGAFVYNLI  ALATIGAFV       0.4647       327.5       WB    32.00      Sequence
DRB1_1501  171  RDARVQLSARRSRGP  ARVQLSARR       0.4630       333.7       WB    32.00      Sequence
DRB1_1501   19  GLVDRGGAHRAATGP  LVDRGGAHR       0.4606       342.3       WB    32.00      Sequence
DRB1_1501  192  IRRIDPWSTLKVSLL  RIDPWSTLK       0.4529       372.3       WB    32.00      Sequence
DRB1_1501  275  TALATIGAFVYNLIT  TIGAFVYNL       0.4521       375.3       WB    32.00      Sequence
DRB1_1501   18  DGLVDRGGAHRAATG  LVDRGGAHR       0.4512       379.3       WB    32.00      Sequence
DRB1_1501  278  ATIGAFVYNLITDLI  FVYNLITDL       0.4483       391.3       WB    32.00      Sequence
DRB1_1501   17  ADGLVDRGGAHRAAT  LVDRGGAHR       0.4451       405.1       WB    32.00      Sequence
DRB1_1501  250  SAELVSSGTIFGGAF  ELVSSGTIF       0.4403       426.6       WB    32.00      Sequence
DRB1_1501  174  RVQLSARRSRGPVRA  QLSARRSRG       0.4374       440.2       WB    32.00      Sequence
DRB1_1501   16  NADGLVDRGGAHRAA  LVDRGGAHR       0.4346       453.5       WB    32.00      Sequence
DRB1_1501  276  ALATIGAFVYNLITD  TIGAFVYNL       0.4309       472.2       WB    32.00      Sequence
DRB1_1501  170  SRDARVQLSARRSRG  ARVQLSARR       0.4290       482.3       WB    32.00      Sequence
DRB1_1501  193  RRIDPWSTLKVSLLL  RIDPWSTLK       0.4281       486.8       WB    32.00      Sequence
DRB1_1501  203  VSLLLSVALFFVWMI  VSLLLSVAL       0.4281       486.9       WB    32.00      Sequence
DRB1_1501  279  TIGAFVYNLITDLIG  AFVYNLITD       0.4255       500.6             32.00      Sequence
DRB1_1501  277  LATIGAFVYNLITDL  ATIGAFVYN       0.4223       518.6             32.00      Sequence
DRB1_1501   74  PAAADARLNRFISGA  RLNRFISGA       0.4193       535.5             32.00      Sequence
DRB1_1501  251  AELVSSGTIFGGAFL  ELVSSGTIF       0.4096       594.6             32.00      Sequence
DRB1_1501  175  VQLSARRSRGPVRAS  QLSARRSRG       0.4051       624.3             32.00      Sequence
DRB1_1501  196  DPWSTLKVSLLLSVA  KVSLLLSVA       0.4034       635.7             32.00      Sequence
DRB1_1501  169  ESRDARVQLSARRSR  ARVQLSARR       0.4016       648.5             32.00      Sequence
DRB1_1501  281  GAFVYNLITDLIGGI  FVYNLITDL       0.3951       695.7             32.00      Sequence
DRB1_1501  227  GGMGVWAKLNSNVGD  GVWAKLNSN       0.3947       699.0             32.00      Sequence
DRB1_1501  184  GPVRASMQIRRIDPW  PVRASMQIR       0.3935       707.9             32.00      Sequence
DRB1_1501   82  NRFISGASAPVTGPA  RFISGASAP       0.3929       712.3             32.00      Sequence
DRB1_1501  252  ELVSSGTIFGGAFLI  ELVSSGTIF       0.3895       738.8             32.00      Sequence
DRB1_1501   15  PNADGLVDRGGAHRA  LVDRGGAHR       0.3889       744.1             32.00      Sequence
DRB1_1501   20  LVDRGGAHRAATGPG  LVDRGGAHR       0.3867       762.1             32.00      Sequence
DRB1_1501  263  AFLIGLVNIVLMTAL  LIGLVNIVL       0.3825       797.0             50.00      Sequence
DRB1_1501  183  RGPVRASMQIRRIDP  PVRASMQIR       0.3809       811.0             50.00      Sequence
DRB1_1501  280  IGAFVYNLITDLIGG  FVYNLITDL       0.3795       823.9             50.00      Sequence
DRB1_1501   83  RFISGASAPVTGPAA  RFISGASAP       0.3788       829.8             50.00      Sequence
DRB1_1501  246  ASGSSAELVSSGTIF  ELVSSGTIF       0.3786       831.4             50.00      Sequence
DRB1_1501  261  GGAFLIGLVNIVLMT  LIGLVNIVL       0.3767       848.6             50.00      Sequence
DRB1_1501  217  ITVAFLYLVLGGMGV  AFLYLVLGG       0.3761       854.0             50.00      Sequence
DRB1_1501  168  AESRDARVQLSARRS  ARVQLSARR       0.3748       866.3             50.00      Sequence
DRB1_1501  262  GAFLIGLVNIVLMTA  LIGLVNIVL       0.3697       915.8             50.00      Sequence
DRB1_1501  207  LSVALFFVWMITVAF  FFVWMITVA       0.3662       951.0             50.00      Sequence
DRB1_1501  194  RIDPWSTLKVSLLLS  RIDPWSTLK       0.3648       966.0             50.00      Sequence
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DRB1_1501  208  SVALFFVWMITVAFL  FFVWMITVA        0.3596       1021.7              50.00     Sequence
DRB1_1501  228  GMGVWAKLNSNVGDL  VWAKLNSNV        0.3589       1029.3              50.00     Sequence
DRB1_1501  284  VYNLITDLIGGIEVT  DLIGGIEVT        0.3558       1064.4              50.00     Sequence
DRB1_1501  253  LVSSGTIFGGAFLIG  LVSSGTIFG        0.3557       1065.8              50.00     Sequence
DRB1_1501  229  MGVWAKLNSNVGDLL  VWAKLNSNV        0.3542       1082.7              50.00     Sequence
DRB1_1501  282  AFVYNLITDLIGGIE  FVYNLITDL        0.3538       1088.0              50.00     Sequence
DRB1_1501  181  RSRGPVRASMQIRRI  PVRASMQIR        0.3536       1090.5              50.00     Sequence
DRB1_1501  176  QLSARRSRGPVRASM  QLSARRSRG        0.3503       1129.4              50.00     Sequence
DRB1_1501  206  LLSVALFFVWMITVA  VALFFVWMI        0.3503       1129.8              50.00     Sequence
DRB1_1501  255  SSGTIFGGAFLIGLV  IFGGAFLIG        0.3480       1158.3              50.00     Sequence
DRB1_1501  254  VSSGTIFGGAFLIGL  IFGGAFLIG        0.3466       1175.3              50.00     Sequence
DRB1_1501  260  FGGAFLIGLVNIVLM  LIGLVNIVL        0.3458       1185.5              50.00     Sequence
DRB1_1501  216  MITVAFLYLVLGGMG  AFLYLVLGG        0.3453       1193.0              50.00     Sequence
DRB1_1501  215  WMITVAFLYLVLGGM  AFLYLVLGG        0.3439       1210.4              50.00     Sequence
DRB1_1501  182  SRGPVRASMQIRRID  PVRASMQIR        0.3430       1222.8              50.00     Sequence
DRB1_1501  214  VWMITVAFLYLVLGG  AFLYLVLGG        0.3423       1231.3              50.00     Sequence
DRB1_1501   14  GPNADGLVDRGGAHR  LVDRGGAHR        0.3414       1243.8              50.00     Sequence
DRB1_1501  180  RRSRGPVRASMQIRR  PVRASMQIR        0.3401       1261.5              50.00     Sequence
DRB1_1501  256  SGTIFGGAFLIGLVN  IFGGAFLIG        0.3370       1305.0              50.00     Sequence
DRB1_1501  209  VALFFVWMITVAFLY  FFVWMITVA        0.3365       1311.8              50.00     Sequence
DRB1_1501  283  FVYNLITDLIGGIEV  FVYNLITDL        0.3328       1365.6              50.00     Sequence
DRB1_1501  230  GVWAKLNSNVGDLLN
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